rickettsia haemophilus escherichia

haemophilus

0912m3 095kkb5 095kcj4 095kcj4 095kcj3 095kgj 095kgj 095kg5 095kg5 095kg5 095kg7 095kg7 095kg3 095kg

091250 018736 0912M3 0912M3 0912M3 090001 090001 090001 090001 090001 090001 090001 090001 090001 090001 090001 090001 090001

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rickettsia

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ALIGNMENTS

neisseria m salmonella

rickettsia salmonella

520.5 520.5 516 511 509 506.5 504.5 504.5 504.4 504.5

sus scrofa rickettsia pseudomonas

Q91950 018758 Q9xc47

haemophilus rickettsia

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1 MNHIYKVIFNKATGTFMAVA.....NGSADTQGHVGAAVGAGFHF 2314
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_unclassified:\*

sp\_rodent:\*

sp\_vertebrate:\*

SUMMARIES

:	Description	Q9pd50 xylella fas	P71401 haemophilus	Q9f3x5 pasteurella	Q9pc04 xylella fas		Q9f2d8 salmonella		Q9f3x6 pasteurella		Q9r169 staphylococ	Q91ch2 staphylococ	Q9zd91 rickettsia	Q52657 rickettsia	Q55582 synechocyst	Q91800 aeromonas s	Q9zhl0 haemophilus	Q9jy30 neisseria m	Q9i120 pseudomonas	Q9rni2 haemophilus
	ID	Q9PD50	P71401	Q9F3X5	Q9PC04	Q9F285	Q9F2D8	048152	Q9F3X6	Q9VTK8	Q9RL69	09гсн2	Q92D91	052657	055582	O9L800	O9ZHL0	Q9JY30	Q91120.	Q9RNI2
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Query	Match	10.5	10.1	8.9	6.4	6.0	5.7	5.6	5.6	5.0	4.9	4.9	4.9	4.8	4.8	4.8	4.7	4.7	4.6	4.6
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1 PRELIMINARY; PRT; 2353 AA. P71401 PREB-1997 (TrEMBLrel. 02, Last sequence update) 01-501-5000 (TrEMBLrel. 14, Last annotation update) 01-5000 (TrEMBLrel. 14, Last annotation update) HSF PROTEIN. HASF PROTEIN. Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae; Haemophilus. CRET_TAXID=727;	
SEQUENCE FROM N.A. STRAIN=C54; MEDILINE=97047989; Pubmed=8892830; Geme J.W., Cutter D. III, Barenhamp S.J.; Geme J.W., Cutter D. III, Barenhamp S.J.; "Characterization of the genetic locus encoding Haemophilus influenzae type b surface fibrils."; J. Bacteriol. 178:6281-6287(1996). EMBL; U41852; AAC44560.1; SEQUENCE 2353 AA; 243844 MW; 53E491B51A897B77 CRC64;	a & a & a
Query Match  10.1%; Score 1177.5; DB 2; Length 2353; Best Local Similarity 23.3%; Pred No. 3.4e-41; Matches 644; Conservative 349; Mismatches 908; Indels 865; Gaps 1  MATCHES 644; Conservative 349; Mismatches 908; Indels 865; Gaps 1  MATCHES 644; Conservative 149; Mismatches 908; Indels 865; Gaps 1  MATCHES 644; Conservative 149; Mismatches 908; Indels 865; Gaps 1  MATCHES 644; Conservative 15: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:	127; 09 09 09 09 09

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-- DDETITVGKDGTQNGKTVNTLKLKGENGLTVATNKDG---TVTFGINTQSGL 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NFTYSLQDALTGLTSITLGGTTNGGNDAKTVINKDGLTITPAGNGGTTGTNTIS 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STKADCGLEKDGDIIKLKVDNQNTDNVLTVGNNGTAVTKGGFETVKTGATDADR 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAKVSDTLTIGGNTPTGGTTATPKVNITSTADGLN--FAKETADASGSKNVYLK 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGNATTAKVTYDETNQTSKVTYDVNVDEKTIELTGDNGKTNKIGVKTTTLTT 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFSTTDND-----ALVNAKDIAENLNTLAKEIHTTKGTADTALQTFKVKKD 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----DSTTLNKDGLSIKNPA----SNEQIQVGADGVK-----FAKVDK-- 985
                                                                                   250
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GGKNTESVDLVSAYNNVEFIT--GDKNT-----LDVVLTAK-ENGKTTEVKF 269
                                                                                                                                                                                                                                                       309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GTVDENKPYLDKD 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAATVGDLRKLGWVVSTKNGTKEESNQVKQADEVLFTGAGAATVTSKSENGKHT 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPYLDKKQLQVGGVKITKDSGINAGDQKISNVKD-ATDDTDAVTYKQLKQVQQD 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |----AGAKSSHVDLNVDATK-KSNAASIEDVLRAGWNIQGNGNNVDYVAT 904
-----TDESTNASSFTYSLKKDLTDLTSVATEKLSFG----ANGDKVDITSD 159
                                                                                                                                                                                                                                                                                                       -----TSV----IKEKDGKLFTGKENNDTNK------VTSNTATD 302
                                                                                                                                                                                                                                                                                                                                                          353 3LFSIGSSTIKRKIINVGAGYEDTDAVNVAQLKAVENLAKRQ------ 353
                                                                                                                                                                                                                                                                                                                                                                                                              347 SLV-----TAKAVI------DAVNKAGWRVKTTTANGONGDFATVASGTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | | | | | | | | OGTTASVTKDTNGKYDAKVGDGLKFDSDKKIVADTTALTVTGGKVAEIA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----GLTFTPTTNASTD-KTVYGTDGLKFT--DNSNTALEDTTR 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFSIRDEKGOEFTISNLYSNG--NTPNTFETITF-AGEN-----GISISNDIA
                                                                                                                                                   A EGHASTAVGAMAYAKGHFANAFGTRSTA EGNY SLAVGLTAKA EKGYTLA IGS
                                                                                                                                                                                                                                                          GALALGADTRVDLDYGIALGYGSQILNNNNNNNNNKAYVPEGNGSNIKSSKAT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----DDNGTGV--------KKKLGET--LTIKGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STLNNGGL-----TVNNTIGGSN--KQ----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----IQVGADGIKFADVNVNVSNAAKFGT--TRITE-----EEIGFADAD-
                                                ORNSTNSKYPNGLLSTL---IQNHTVL---
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986 1113		Db
		Db Qy
1054 NSNDAV		Db Qy
1114 SDVIT: : : : 1248 ANEVE		Db
1161 - IDSK : : 1308 TVDAT	-IDSKDGQNTITGLSNTLANVIN-DGAGHALSQGLANDTDKTRAASIGDV 1208 	Db Qy
	LNAGENLQCNGEAVDFVSTYDTVDFIDGNATTAKVTYDDTSKTSKVVYDVNVDNK 1263	do VQ
1264 TIEV 1406 TIEV	VKTTTLTKTS     VK	Db Qy
1324 SQAS	SQASSASYVDADGNKVIYDSTDKKYYQVNDKGQVDKNKEVAKDKLVAQAQIPDGTLAQM 1383	qa
	NVKSVINKEQVNDANKKOGINEDNAFIKGLENAAKDIKTKNAAVTVGDLNAVOT 1438  NVKSVINKEQVNDANKKOGINEDNAFIKGLENAAKDIKTKNAAVTVGDLNAVOT 1438  1	RES OD ID
1492 GAL 1439 PLTI	PLIFAGDIGITAKKLGETILIKGGOTDINKLTDNNIGVVAGIDGFTVKLAKDLT 1492 PLIFAGDIGITAKKLGETILIKGGOTDINKLTDNNIGVVAGIDGFTVKLAKDLT 1492 VDEVAGNOMITSVIVESKDNGKRTEVKIGAKTSVIKDHNGKLFTGKELKDAN 1598	DT DT DE
	NLNSVNAGGTRIDEKGISFVDANGQAKANTPVLSANGLDLGGRRISNIGAAVDDNDA 1549  NLNSVNAGGTRIDEKGISFVDANGQAKANTPVLSANGLDLGGRRISNIGAAVDDNDD- 1549	00 00 00 00 00 00 00 00 00 00 00 00 00
1550 VNF	KQFNEVAKT 	X N R R
1609 NAN	NANGVPVDKDGKPITDADKLANLAAHGKPLDAGHQVVASLGGNSDAITLINIKSTLP 1665	RATE RETE
1666 QII	QIDTPUTGNANAGQAQSLPSLSAAQQSNAASVKDVLNVGFNLQTNHNQVDFVK 1718	os 
1737 1719 AY	AGKEGTGEVDPANSAGAEVRAGO NYITAROOMMININGAGAA AYDTVNEVNGTGADITSVRSADGFMSNITVNTALAATDDDGNVLIKAKDGKEYK 1772	
1773 AD	ADDLMPNGSLKAGKSASDAKTPIGLSLVNPNAGKGSTGDAVALNNLSKAVFKSK 1826 :	
	TTTVSSDGISIQGKDNSSI	
1880 DL	DLTNLDEKGAUNNPTVAUNTAALVOLANDON OOI NEVRNILGIG- NAGNDNADGNOVNI ADITKEDPNGGSSSNRTVIKAGTV 1928	
	RNANEVKEKSGNGINVSGKTLNGTRVITFELAKGEVVKSNEFTVKNADGSETNLVKVGDM 1990	

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132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 NSKIAFGTT-----GNNDNASASNEASIAIGSLAKAHANQAIAIG-----GSKP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2249 AMASMPQAYIPGRSMVTGGIATHNGOGAVAVGLSKLSDNGGWVFKINGSADTQGHVGAAV 2308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 ATGTFMAVAECAKSHSGGSSSSTAGQVGSSPVIRLTRVATL--AILVIGATLNGSAYAQN 69
                                                                                                                                                                                                                                                                                                                                                                         2192 RRIGNVAAGEVSATSTDAVNGSQLYKATOGIAN---ATNELDHRIHQNENKANAGISSAM 2248
                                                                                                                                                                                                                                                                                                                                                                                               2228 VVIDNVANGEISATSTDAINGSQLXAVAKGVTNLAGQVNNLECKVNKVGKRADAGTASAL 2287
                                                                                                                                                                                                                       2096 TUKRDINSYSVGNNNQFIDATQIDVFGV---GNNITVT-----ESNSVALGSNSAISAG- 2145
                                                                                                                                                                                                                                                                                                                                 2168 VDANGKKVVKVTENGÅDKMYYTNÅDGAADKTKĠEVSNDKÅSTDEKHVVRLDPNNQSNÄKG 2227
                                                                                                                                                                                                                                                       2119 FVKTD------VELPLTQIYNTDANGNKIVKKADGKWYELNADGTASNKEVTLGN 2167
                                                                                                                                                                                                                                                                                               2146 --THAGTQAKKSDGTAGTTTTAGATGTVKGFAGQTAVGAVSVG------ASGAE 2191
                                                                                                                                               2042 -----ADGEAAVAIGROTQAGNOSIAIGDNAQATGDQSIAIGTGNVVTGKHSGAIGDPS 2095
1929 LGGKGNND--TEKLATGGVQVGVDKDGNANGDLSNVWYVTQKDGSKKALLATYNAAGQTN 1986
                                   1991 YYSKEDIDPATSKPMTG----KTEKYKVENGKV-----VSANGSKTEVTLTNKGSG---
                                                                                               2080 KAETVNAHDKVRPANGLNTKV---SAATVESTDANGDK-----VTT----T
                                                                         1987 YLTNNPAEAIDRINEQGIRFFHVNDGNOEPVVOGRNGIDSSASGKHSVALGFQAK----
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
NCBL_TaxID=747;
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STRAIN=PM70;
Henderson I.R., Nataro J.P., Cappello R., Stein C.;
Henderson I.R., Nataro J.P., Cappello R., Stein C.;
"Evolutionary origins of the autotransporter proteins.";
"Evolutionary origins of the EMBL/Genbank/DDBJ databases.
SUBMILIA AJ277636; CAC14203.1;
EMBL, AJ277636; CAC14203.1;
SEQUENCE 2712 AA: 276154 MW; 3F5579D6F32FFA3D CRC64;
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Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Le
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:  :     :	EGNYSLAVGLTAKAEKGYTIAIGSNAQAINYGALALGADTRVDLDYGIALGYGSQILNNN   ::   :  :    ::    :    :     :	NNNNNKAYVPEGNGSNIKSSKATGNGLF8IGSSTIKRKIINVGAGYEDTDAVNV 	AQLKAVENLAKRQITFKGDDNGTGVKKKLGETLTIKGGE			GTDGLKFTDNSNTALEDTTRITKDKIGFSNKAGTVDENKPYLDKDK-LKVGN	STLNNGGLTVNNTIGGSNKQIQVGADGIKFADVNVNVS	NAAKEGTTRITEEEIGFADAD  :    :     ::    :  KSHAKGLASIAFGTNOVYSGONSGSIGYAGELGNAKATVINGEGTYSLGNTNSTLTANES		KDATDDTDAV-TYKQLKQVQQDAD-GALQSFSIRDEKGQEF	-TISNLYSNGNTPNTFETITFAGENGISISNDIAKGKII	VKVGIDPINGLTTPKLTVGSDKDGKTQLVIEQVASGNDTKN	IIRGLSPTLPSITNAGGVRTTEQGNTITSDEDKSKAASIGDILNTGFNL	KNNSNSVGFVSTYNTVDFIDGNATTAKVTYDETNQTSKVTYDVNVD 	EKTIELTGDNGKTNKIGVKTTTLTTNANGKATNFSTTDNDALVNAKDIAENLN :	TLAKEIHTTKGTADTALQTFKVKKDGATDDETITVGKDGTQNGKTVNTLKLKGE	NGLTVATNKDGTVTFGINTQSGLKAGDSTTLNKDGLSIKNPASNEQ	IQV-GAD-GVKFAKVDKG-NSTGIDGTSRITKDQIGFTGANGSLDTTKPHLT:
549	227 595	287	341	380	416	458 857	509	547	568	606	645 1134	681 1194	722	771	817 1353	871	925	971
qq	Oy Db	Qy Db	Qy Db	OY Dp	QY	Oy Dp	Qy Dp	Oy Dp	QY	Oy Dp	Qy Dp	Qy Db	Oy Db	QY Dp	Qy Db	Qy	Qy Db	Οÿ

Q D	1509 V	VDVKGATANTVWDNFDKGQNIMTRVEGNTITVALAKALSGLTSATFGDPASNPKDSTVIN 156	89
Qy	1021 K	KDKLKVGEVEITNTGINAGGKKITNIQSGDITQNSNDAVTGGRVYDLK 106	890
qa	1569 K	-	628
Οy	1069 T	AKTAQNSLHEFSVADEQGNHFTVSNPYS	28
qα	1629 Ţ	TAINNITNGTTGDSNVNTK 167	173
07	6	FGLSNTLANVTN 11	80 7
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δλ	m	<pre>GEAVDEVSTYDTVDFID 1</pre>	32
ДD	1726 D	GSEGAISLIGOPATOGAAAPTAKIKVAEGNPDLENTSDDPANPN 177	170
Qy	1236 G	GNATTAKVIYDDTSKTSKVVYDVNVDNKTIEVTSDKKLGVKTTLTKTSANGNA 128	683
QQ	1771 0	QNKKT-RITYDIAGPNGTTVTEQLATLNDGLKFGANTGDVHDAKLNTRVDVKGKA 182	824
δλ	1290 T	NTLAGDIQTAKGASQASSSASYVDADGNKVIYDSTDKKY 13	449
QQ	1825 E	ENTIMANFDAGQNIMTQISGNTITVALAKALAGLDSATFGNPADGSK 187	371
δλ	1350 Y	FLAQMNVK	101
qq	1872 -		394
QY	1408 A	AFIKGLENAAKDTKTKNAAVTVGDLNAVAQTPLTFAGDTGTTAKKLGETLTI 145	53
qq	1895 -		38
Qy	1460 K	Ϋ́	118
qu	1939 K		994
ογ	1519 -		574
qq	1995 E	EISLANDITLGKNGADGVDGSLGVNGKDGASVVLNGKDGSIGLT 203	38
٥y	1575 L	PQKAIKGADGKYYHANANGVPVDKDGKPIT 1	623
qq	2039 G		93
Oy	1624 D	NIKSTLPQ	983
qa	2094 D	DGMKFVGNDGKEVTRKLNETLDIKGGLDAATVADNAKVSSSNLG 213	137
Qy	1684 P	SLSAAQQSNAASVKDVLNVGFNLQTNHNQVDFVKAYDTVNFVNGTGADITSVRSADGTM 17	743
qq	2138 -	:::: VKTNAEGIGLEIVMKERPTF 21:	157
Qy	1744 S	SNITVNFYKADDLMP 177	178
qq	2158 S	:     :	217
Οy	N 6771	GSLKAGKSASDAKTPTGLSL-VNPNAG	323
QQ	2218 N		271
٥y	1824 K	KSKDGTTTTTVSSDGISIQKDNSSITLSKDGLNVGGKVISNVGKG 186	698
QQ	2272 -	IIIII	330
ΟŸ	1870 -	TKDTDAANVQQLNEVRNLLGLGONGNDNADGNQVNIAD 190	100
qq	2331 S	PNSTDAVNGSQLNAVKETAEAGWHLTANGADSSNVKPRNTVDLNNTDGNIVISKTNTAD 23	068
Qy	1908 I	KKDPNSGSSSNRTVIKAGTVLGGKGNNDTEKLATGGVQVGVDKDGNANGDLSNVWVKTQ 19	196
qo	2391 -	:	42

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Best Local Similarity
Matches 352; Conserv
         Query Match
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RECOLURE FROM N.A.

REDINE=20365717; Pubbmed=10910347;

RA ALVES L.M.C., Arraya J.E., Bala G.S., Baptista C.S.,

RA ALVES L.M.C., Arraya J.E., Bala G.S., Baptista C.S.,

RA ALVES L.M.C., Arraya J.E., Bala G.S., Baptista C.S.,

RA ALVER C. ALVES L.M.C., Arraya J.E., Bala G.S., Baptista C.S.,

RA ALVER C. Alves L.M.C., Camargo L.E.A., Carraro D.M., Carrer H.,

RA BERTOS M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Carrer D.M., Carrer D.M., Carrer D.M., Carrer D.M., Colombo C., Costa F.F., Costa M.C.R., Costa N.C. R.

RA COULIND L.L., CIISTOGENI M., Dlass Netco E., Docena C., El-Dorry H.,

RA Fraqa J.S., Frracia S.C., Franco M.C., Frohme M., Furlan L.R.,

RA Garnier M., Goldman G.H., Goldman M.L., Kemper E.L., Kitajima J.P.,

RA Michael J.D., Jungueira M.L., Lambais M.R., Lette L.C.C.,

RA Machado M.A. Madeira J.B., Madeira H.M.F., Marino C.L.,

RA Machado M.A. Madeira A.M.B., Madeira H.M.F., Marino C.L.,

RA Machado M.A., Matca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,

Marques M.V., Martins E.A.L., Mattista M.A.,

RA Mond D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,

RA Mond N.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,

RA Mond N. J., Marca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,

RA G. Oliveira M.C., de Oliveira R.C., Pelmieri D.A., Paris A.,

RA G. Souza A.P., Terenzi M.F., Truffi D., Pasquero J.B.,

RA G. Souza A.P., Terenzi M.F., Truffi D., Setubal J.C.;

RA Asliva A. C.R., da Silva A.M., da Silva F.R., Silva M.A. J., A da Silva A.M., da Silva F.R., Salva M.A., Tsulako M.A.,

RA Aslama M.A., Zatz M., Meidanis J., Setubal J.C.;

RA Matter A. C. R., Sarchilli R.V., Sawsaski H.E.,

RA Matter A. C. R., Sarchilli R.V., Sawsaski H.E.,

RA Aslama H. Van Sluys M.A., Verjovski Almeida S., Vettore A.L.,

RA Matter A. C. R., Salva A.M., da Silva F.R., Silva M.A., Tsulako M.A.,

RA Matter A. C. R., Sarchilli M.B., Tsulako M.A., Tsulako M.B., The Genome Sequence of the plant pathogen Xylella A.C., Sarchilla J.C.;

RA Matter A. C. R., Sarchilla M.A., Tsulako M.
                                                                                                                                                                                                                                                                                                                                                                                                                                            2204 ATSTDAVNGSQLYKATQGI---ANATNELDHRIHQNENKANAGISSAMAMASMPQAYIPG 2260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---HSGAIGDPSTVKADNSYSVGNNNOFIDATOTDVFGVGNNITVTESNSVALGSNSAIS 2143
                                             2443 KDGKDAVAISGKDGVG-TIGLT-GPAGA-DGKNANAI--IGVNDS-----VKGLDGNDGK 2492
                                                                                                                                                                                                                                                                           2544 KNIETEVAGDIIRVRLKDNIDVKGIN------VTENLTVKEGAKINMGNNV---
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1968 KDGSKKALLATYNAAGQTNYLTNNPAEAIDRINEQGIRFFHVNDGNQEPVVQGRNGIDSS
                                                                                                             ASGKHSVAIGFQAKADGEAAVAIGRQTQAGNQSIAIGDNAQATGDQSIAIGTGNVVTGK-
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09PC04:
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01-OCT-2000 (TrEMBLrel. 15, La
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1682 SLPSLSAAQQ---SNAASVKDVLNVGFNLQTNHNQVDFVKAYDTVNF----VNGTGADI 1733
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                                                                                                                                                                                                                                            -GIVIDSKDGQNTITGLSNTLANVINDG--AGHALSQGLANDTDKTRAASIGDVLNAGFN 1214
                                                                                                                                                                                                                                                                                                       1215 LOGNGEAVDEVSTYDTVDEIDGNATTAKVTYDDTSKTSKVVYDVNVDNKTIEVTSDKKLG 1274
                                                                                                                    1064 -VYD-----LKTELESKINSAAKTA------ONSLHEFSVADEOGNHFTVSNPY 1105
                                                                                                                                                                                                                                                                          DSIAIGSGQGSKT-----DGNTSGATVAQGL------RSIAIGTTARS--- 217
                                                         1010 GSLDTTKPHLTKDKLKVGE----VEITNTGINAGGKKITNIQSGDITQNSNDAVTGGR-- 1063
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                                                                                                                                                  63 KLHDRRQLHIVLITVLAASTGYTGKVAAQVYVNSDSTENCVEILGDSSQTSFIHSASNDK 122
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                                Gaps
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                                                                                                                                                                                    1106 SSYDTSKTSDVITFAGEN---GITTKVNKGVVRVGIDOTKGLT-TPKL-TVGNNNGK---
                                                                                                                                                                                                     ----QSQDAISIGTGASTTGNFAI
                                                                                441;
Length 1190;
                                   Indels
   6.4%; Score 743.5; DB 2;
ilarity 24.1%; Pred. No. 2e-23;
Conservative 188; Mismatches 481;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SLGSIVFLSTGPVFAADITVSTQAELSAALSNGTYDKIILGADITLIGSLTVNMTSNQVV 120
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         KG--NNDTEKLATGGVQVGVDK-----DGNANGDLSNV-WVKTQKDGSKKALLATYNAAG
                                                   QTNYLTNNPAEAIDRINEQGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKAD
                                                                VGTVSVGDASKGETRTVSNVADAKEATDAVNLRQLDRVAQDANRYVDNKIESLSEGQTFV
                                                                                                                                                                                    ESNSVALGSNSA--ISACTHA-----GTQAKKSDGTA-GTTTTAGATGTVKGFAGQTAVG
                                                                                                                                                                                                  -----AVSVGASGAERRIQNVAAGEVSATSTDAVNGSQLYKATQGIANATNELDHR
                                                                                                                                                                                                                                          2233 IHONENKANAGISSAMAMASMPQAYIPGRSMVTGGIATHNGQGAVAVGLSKLSDNGQWVF
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                          797 MGLVITDGPSVTSSGINAGSQKITNVAAGTADTDAVNLSQLNTAMAGS-----
                                                                                              2044 GEAAVAIGRQTQA-GNQSIAIGDNAQATGDQSIAIGTG-----NVVTGKHSG----
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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"Evolutionary origins of the autotransporter proteins.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ277631; CAC14227.1;
SEQUENCE 3705 AA; 370756 MW; 714FDF16455968C9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                3705 AA
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948 KAGDSTTLNKDGLSIKNPASNEQIQVGADGVKFAKVDKGNSSTGIDGTSRITKDQIGFTG 1007 1008 ANGSLDTTKPHLTKDKLKVGEVEITNTGINAGGKKITNIQSGDITQNSNDAVTGGRVYDL 1067 1068 KTELESKINSAAKTAQNSLHEFSVADEQGNHFTVSNPYSSYDTSKT-----SDVITFAG 1121 ---NDGTITSTTAGIAISSA----SIKEISVDNTDGTITATAGTGVNV--LASALLNLFG 472 503 605 608 999 716 814 IGAGTGSAIVNNSANVSLEQASMFAGTWQVNQGG----ALTASNSNQLGSAKIGLDGTLN 869 854 TDNDALVN-----AKDIAENLNTLAKEIHTTKGTADTAL-----QTFKVKKDGA---- 897 870 LDNIALFNHVLTGNGTLNVAKNLATTAFDFGSTVGGAFSGIVNLTKTTFALSADNAAALA 929 SLAVGLTAKAEKGYTIAIGSNAQAINYGALALGADTRVDLDYGI-----ALGYGSQILNN 285 NNNNNNKAYVPEGNGSNIKSSKATG-----NGLFSIGSSTIKRKIINVGAGYEDTD 336 564 651 694 PDPRNQAANQKAGSHAKGKESIAIGGDVLAEGDASIAIGSDDLYLDRNSTNSKYPNGLLS 172 TGRFHVTHT-----GSSVTSFVSTGGANNTST----MDFASGADVKIDRTGSTGD--- 275 LTSTGVNAFA---YTFADGASFELIANQNVFSGTTTNRGLEIGSYNSIDGFGSGVKIVLQ 332 LKVGNSTLN--NG-----GLTVNNTIGGSNKQIQVGADGIKFADVNVNVSNAAKFGTT 554 TI----TFAGENGISISNDIAKGKVKVGIDPINGLTTPKLTVGSDKDGKTQLVIEQVASG ----TDDETITVGKDGTQNGKTVNTLKLKGENGLTVATNKDGTVTF-GINTQ---SGL 330 SATLKLSDDSVTTVG----TTDRTLHGLDLSG-----GTLIFDGAVPQSQTSGV PTTNASTDKTVYGTDGLKF - - TDNSNTALEDTTRITKDKIGFSNKAGTVDENKPYLDKDK ----KDATDDTDAVTYKQLKQVQQDADGALQSFSIRDEKGQEFTISNLYSNGNTPNTFE 609 TALQITDGIDNTTTIG----NEIQLNAENAT------AINFLGSSSKTLNNNG 652 TIKGSVIFAGVADHIINN-------NGTLDGTLTTGA---GNDTLVLDSSSQS 717 NDTKNIIRG-LSPTLPSITNAGGVRTTEQGNTITSDEDKSKAASIGDI-LNTGFNLKNNS 1025 VTGDIDAL-----DLLVNGTAITSG------TQG-----TQG SRSDGS---IISGNGIDNATINAAGINNNASGDANVIYNLGTGSI-LKATNTG-----AVNVAQLKAVENLAKRQITFKGD------DNGTGVKKKLGETLTIKGGETQADKLT DNNNIGVVTDNNTGLKVKLAKNLSGLETVSTKNLTASEKVTVGSGNNTAELQSGCLT-FT RITEEEIGFADADGKVDKKSPYLDKKQLQVGGVKI---TKDSGIN-AGDQKISNV---------TSKVTYDVNVDEKTIELTGDNGKTNKIGVKTTTTLTTNAN--GKA----TNFST 181 IDFLGSSQLIYMGAYGAATNSIMTFGDIL------NDVVVNDRAQEIGEVNKLAF T - - LIQNHTVLRQIRDSNGSQKYRRTAAEGHASTAVGAMAYAKGHFANAFGTRSTAEGNY NSV------GFVSTYNTVD----FIDGNATTAKVTYDETNQ------οy

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QLYKATQGIANATNELDHRIHQNENKA-----NAGISSAMAMASMPQAYIPGRSMVTGG 2267
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                                                                                                                                                                                                                                                                                                                              ADGEAAVAIGROTQAGNOSIAIGDNAQAT-GDOSIAIGTGNVVTGKHSGAIGDPSTVKAD 2100
                                                                                                                                                                                                                                                                                                                                                                                                             IEQG------IRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAK 2041
                                                                                                                                                                                                                                                                                        ----TVLGGKG-----NNDTEKLATG-----GVQVGVDKDGNANGDLSNV----- 1962
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YLATTAFDXGSTVGXXFSGIVNLT----NTTFALSADNAAALARATLKLSDDSVTTVG 2157
                             ----TVSSDGISIQGKDNSSITLSKDGLNVGGKVISNVGKGTKDTD---- 1874
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eria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
nonella.
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                                                   DRILHGLDLNGGTLIFDGSPPQSQANGVVTVTDLALNSG--TISITGAGNMENEHPVT
                                                                                         NIVQQLNEVRN -- LLGLGNAGNDNADGNQVNIADIKKDPNSGSSSNRTVIKAG-----
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FNGTFGNSVTGSGVLQVTDDAE 2668
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1076 132	1136 152	1196 181	1253 235	1311 <sup>°</sup> 291	1371	1430 356	1487	1541	1597 496	1657 536	1712 580	1753 640	1810 686	1870 739	1930	1984 825	2037 876
17 PHLTKDKLKVGEVEITNTGINAGGKKITNIQSGDITQNSNDAVTGGRVYDLKTELESKIN	7 SAAKTAQNSLHEFSVADEQGNHFTVSNPYSSYDTSKTSDVITFAGENGITTKVNKGVVRV	7 GIDQTKGLTTPKLTVGNNNGKGIVIDSKDGQNTITGLSNTLANVTNDGAGHALSQGLAND :	1 T-DKTRAASIGDVLNAGFNLQGNGEAVDFVSTYDTVDFIDGNATTAKVTYDDTSKTSK	44 VVYDVNVDNKTIEVTSDKKLGVKTTLTKTSANGNATKFSAADGDALVKASDIATHLN : :   :	2 TLAGDIQTAKGASQASSSASYVDADGNKVIYDSTDKKYYQVNDKGQVDKNKEVAKDKLVA	2 QAQTPDGTLAQMNVKSVINKEQVNDANKKQGINE-DNAFIKGLENAAKDTKTKNAAVTVG	11 DLNAVAQTPLTFAGDTGTTAKKLGETLTIKGGQT-DTNKLTDNNIGVVAGTDGFTVKL	488 AKDLTNLNSVNAGGTRIDEKGISFVDANGQAKANTPVLSANGLDLGGKRISNIG :	542 AAVDDNDAVNFKQFNEVAKTVNNLNNQSNSGASLPFVYTDANGKPIN-GTDGKPQKA	598 IKGADGKYYHANANGVPVDKDGKPITDADKLANLAAHGKPLDAGHQVVASLGGNSDAITL :     :     :     :	658 THIKSTLPQIDTPNTGNANAGQAQSLPSLSAAQQSNAASVKDVLNVGFNLQTNHN :	713 QVDFVKAYDTVNFVNGTGADITSVRSADGTMSNITVNTALA :	754 ATDDDGNVLIKAKDGKFYKADDLMPNGSLKAGKSASDAKTPTGLSLVNPNAGKGSTG- 	######################################	871 KDTDAANVQQLNEVRNLLGLGNAGNDNADGNQVNIADIKKDPNSGSSSNRTVIKAGTVLG 	11 GKGNNDTEKLATGGVQVGVDKDGNANGDLSNVWVKTQKDGSKKALLATYNAAGQ	985TNYLTNNPAEAIDRINEGGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIG  : ::  :      ::   1: 826 NVGQLKVTDAQVSRNTQSITNLNTQVSNLDTRVTNIENGIGDIVTTGSTKY
Qy 1017 Db 97	Qy 1077 Db 133	Oy 1137 Db 153	Qy 1197 Db 182	Qy 1254 Db 236	Oy 1312 Db 292	Oy 1372 Db 323	Qy 1431 Db 357	Qy 1488 Db 402	Qy 154 Db 45	Oy 159 Db 49	Qy 1658 Db 537	Qy 1713 Db 581	Oy 1754 Db 641	Qy 1811 Db 687	Qy 1871 Db 740	Oy 1931 Db 773	Qy 1985 Db 826

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2038 FQAKADGEAAVAIGRQTQAGNQSIAIGDNAQATGDQSIAIGTGNVVTGKHSGAIGDPSTV 2097
                                                                 2098 KADNSYSVGNNNQFIDATQTDVFGVGNNITVTESNSVALGSNSAISAGTHAGTQAKKSDG 2157
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SEQUENCE FROM N.A.
STRAIN 11;
MEDLINE-BO332658; PubMed-8730864;
MEDLINE-96332658; PubMed-8730864;
Barenkamp S.J., St Geme J.W. III;
"Identification of a second family of high-molecular-weight adhesion proteins expressed by non-typable Haemophilus influenzae.";
Mol. Microbiol. 19:1215-1223(1996).
EMBL; 038617; AAC43721.1; -.
FRMEL; 038617; AAC43721.1; -.
FROUENCE 1098 AA; 114100 MW; D977335A89F7333D CRC64;
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                     917 DEANTVSVGSSTQ-----QLRRITNVAAGVNNTDAVNVA------QLKASE-
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
NCBI_TaxID=727;
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                                                                                                                                                                                                                                                                         2273 GQGAVAVGLSKLSDNGQWVFKINGSADTQGHVGAAVGAGFHF 2314
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KINSAAKTAQNSLHEFSVADEQGNHFTV----SNPYSSYDTSKTSDVITFAGENGITTKV 1129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SKAASIGDILNIGFNLKNNSNSVGFVSTYNTVDFIDGNATTAKVTYDETNQTSKVTYDVN 814
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                                                                                                                                                                                                                                                                                                                         tch 5.6%; Score 653.5; DB 2; Length 1299; al Similarity 23.3%; Pred. No. 1.3e-19; 402; Conservative 207; Mismatches 554; Indels 563;
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ia; Proteobacteria; gamma subdivision; Pasteurellaceae;
rella.
axID=747;
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Ison I.R., Dationary Origins of the autotransporter proteins.";
ited (APR-2000) to the EMBL/GenBank/DDBJ databases.
AJ277635; CAC14202.1; ... BBCCEOEB66CDB428 CRC64;
ICE 1299 AA; 130963 MW; BBCCEOEB66CDB428 CRC64;
                                Created)
Last sequence update)
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PRT; 1299 AA
                                (TrEMBLrel. 16, C
(TrEMBLrel. 16, L
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     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                              KDVLNVGFNLQTNHNQVDFVKAYDTVNFVNGTG-ADITSVRSADGTMSNITVNTALAATD 1756
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                                                                                                           1464
                                              QVDKNKEVAKDKLVAQA-----QTPD-----GTLAQMNVKSVINKEQVNDANKKQGINE 1405
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                                                                                                                           -----ALGFGAK-SDTKAQAVSICYNSNAKGYQAIAFGSBAKTT-ENAGSSIAF-GTKA
                                                                                                                                                                         DTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGTRIDEKGISFVDANGQAKANTPV
                                                                                                                                                                                                                                                                                                 1578 VVTDANGKPINGTDGKPQKAIKGADGKYYHANANGVPVDKDGKPITDADKLANLAAHGKP
                                                                                                                                                                                                                                                                                                                                                                LDAGHQVVASLGGNSDAITLTNIKSTLPQIDTPNTGNANAGQAQSLPSLSAAQQSNAASV
                                                                                                                                                                                                                                                                                                                                                                                               ---GSQLYLALN-----ALGNVGNTL-----VTNVLGGDA-----AIVKEGDEAGT
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                                                                                                                                                                                                       QTRASASIAIGMGAET-GFD-------GGQALD--GSDAVALGREAKAK---
                                                                                                                                                                                                                                      LSANGLDLGGKRISNIGAAVDDNDAVNFKQFNEVA-----KTVNNLNNQSNSGASLPF
                                                                                                                                                                                                                                                                    710 -RQNALAFGYK-----AVADHKDAVALGAGAETAAAEGTNEATVNEFKYSGFAGI----
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                                                                                                                                                            Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
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19.0%; Pred. No. 1.9e-16;
ive 369; Mismatches 1085; Indels 732;
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2586 AA; 260194 MW; 8EBB2435A9FEAE5B CRC64;
                                                                                          Last sequence update)
Last annotation update)
                       2586 AA
                                                                     Created)
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Best Local Similarity 19.0%
Matches 513; Conservative
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SEQUENCE FROM N.A.
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qq	2251PEVD 2282	qq	100 AQPN
δλ	2046 AAVAIGRQTQAGNQSIAIGDNAQATGDQSIAIGTGNVVTGKHSGAIGD 2093	Qy	123 KAGS
QQ	Q9NA	qa	154 PANA
Qy	2094 PSTVKADNSYSVGNNNQFIDATQTDVFGVGNNITVTESNSVALGSNSAI 2142	δλ	167 PNGL
qq	2331 TTTTTSTNGSKSSKILTVPKVDA-GISIDGGISGSTSTKTIKITSKNSAVPKASSSF 2386	qq	214 VNGY
Qy	2143 SAGTHAGTQAKKSDGTAGTTTTAGATGTVKGFAGQTAVGAVSVGASGAERR 2193	QY	219 AFG-
QQ	1387 KTTTTTTSKTSSVPKTESKYSWSSSSKKTSNPIRLTLPNINAGISVGGGDSSGSWSKLI 2446	qo	 254 ALGR
Οy	STD	Qy	259 ALAL
qq	2447 KRSTSSDETNASDGPSLSGSIDSRVTVPVPRDLRDIRIRLGREQSGNDAQSQNSN 2501	qa	314 ATVN
Οy	2252 SMPQAYIPGRSMVTGGIATHNGQGAVAVGLSKLSDNGQWV 2291	δλ	300 GSNI
qq	2502 SWTQSATQGSESLANGAITANGLSLEGSGSSGGVATTIPGGSVGVTGQYPYWGNGRWV 2560	qa	374 GSHL
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So	ning. Bankaria, Birmington, Banillus (Clastridium graum.	ag .	527 L
388	Dacteria, Finiatories, Bacillas/Libiladum 910up; Bacillas/Staphylococcus group; Staphylococcus. MCBI THE TASTER 1980.	ον	511 LNNG
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R 5	STRAIN-COL;	οy	556 ITEE
RA R	MEDLINE-97302526; PubMed=9158773; Wu S., de Lencastre H., Sali A., Tomasz A.;	q	:  : 631 VTQD
r r r	A prospringluccontractive gene essential for the optimal expression of methicillin resistance in Staphylococcus aureus: molecular cloning and DNA sequencing ":	Qy	615 VTYK
. J. 3	Microb. Drug Resist. 2:277-286(1996).	đ	679 ITPT
R R S	141 SCHOENCE FROM N.A.	Qy	666 GENG
X & 6	MEDINE-704, MEDINE-71478; PubMed-9286983; MEDINE-717 GN C GN VER UCITATION TO CONTACT U	qa	: 730 DIDA
<b>8</b> 8 5	o., de mendastre n.,	Qy	722
RT	whice remains gene from oraphytococcus aureas, the interiuption of which results in reduced methicillin resistance, encodes a phosphodiucosamine mutase ".	qa	789 EVAE
2 2 Z	Frogrammer and a sectoriol 179:5321-5325(1997).	Qy	778 GFVS
8 P	SCUENCE FROM N.A.	qa	846 KQAA
RX a	SIGNATOUS.  MEDLINE-9255121; PubMed=10332717; Min C As Issastra U .	Qy	830 -NKI
RT	"Mrp-a new auxiliary gene essential for optimal expression of methicillin registance in Graphylococus auxilia.".	qa	902 LDKI
R.	Microb Ing Resist. 5.9-18(1999). FMRL: Y09927: CAR55329 1: -	0y	888 QTFK
ÖS	SEQUENCE 2478 AA; 263029 WW; 6B9859A02D023C74 CRC64;	qa	956 QEAR
ć	40.	Qy	948 KA
, B	Best Local Similarity 20.8%; Pred. No. 4.7e-16; Matches 545; Conservative 329; Mismatches 1033; Indels 708; Gaps 120;	qa —	996 KAEI
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EAIERINAAKVSGVKAIEATTTAQDLERVKNEEISKIENITDSTQTKMDA---YNEV 845
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                     SHAKGKESIAIGGDVLAE-----GDASI-----AIGSDDLYLDRNSTNSKY 166
                                                                                                                                                               LLSTLIQN-----HTVLRQ--IRDSNGSQKYRRTAAEGHASTAVGAMAYAKGHFAN 218
                                                                                                                                                                                                                                               ---LAVGLT----AKAEKGYTIAIGSNAQAINYG 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -IIRGLSPTLPSITNAGGVRTTEQGNTITSDEDKSKAASIGDILNTGFNLKNNSNSV 777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATARKAQ----NATVSNATNEEVAEADAAVDAAQKQGLHDIQVVKSKQEVADTKSKV 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I-GVKTTTLTTTNANGKATNFSTTDNDALVNAKDIAENLNTLAKEIHTTKGTADTAL 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVKKDGATDDETITVGKDGTQNGKTVNTLKLKGENGLTVATNKDGTVTFGINTQSGL 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -GDSTTLNKDGLSIKNPASNEQIQVGADGVKFAKV-------DKGNSSTGI 992
                                                                                                         :|:
DEVAALVTKINNDKNNAIAEINKQTTAQGVTTEKDNGI-------AVLEQDV
                                                                                                                                                                                                                                                                         LGADT --------RVDLDY ---GIALGYGSQILNNNNNNKAYVPE---GN
                                                                                                                                                                                                                                                                                                                                                                                                                                           AKRQITF-KGDDNGTGVKKKLGETLTIKGGETQADKLTDNNNIGVVTDNNT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDGLKFTDNSNTALEDTTRITKDKIGFSNKAGTVDENKPY----LDKDKLKVGNST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEIGFADADGKVDKKSPYLD-KKQLQVGGVKITKDSGINAGDQKISNVKDATDDTDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GISISNDIAKGKVKVGIDPIN---GLTTPKLTVGSDKDGKTQLVIEQVASGNDTKN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GLKVKLAKNLSGLETVSTKNLTASEKVTVGSGNNTAELQSGGLTFTPTTNASTDKT
                                                                                                                                                                                                                                               ----TRSTAEGNYS-----
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: :   : :     Db	OY 1981 AAGQTNYLTNN	Db 2040 DKTQTNAEVAELQNV		Qy 2086 KHSGAIGDPSTVKAD	Db 2118 NSDAÀIGETTATSAI OV 2128 VTESNSVALGSNSA <sup>1</sup>	2178		Db 2235 SKQNAEVNNSAESQ	Db 2295 VPSNTSKDKEESTT	QY 2273 GQGAVAVGLSKLSD	Db 2351 KEKMISTNLSQKDD	RESULT 11 Q9LCH2 TO OGLCH2	Q9LCH2;	DT 01-00T-2000 (17EMB) DT 01-0CT-2000 (TYEMB) DT 01-0CT-2000 (TYEMB) DE FMTB.	GN FMTB. OS Staphylococcus aure			RC STRAIN=COL; RA KOMATSUZAWA H.;	RT "Staphylococcus au			Query Match Best Local Similarity Matches 545; Conse	Qy 67 AQNNSKIAFGTTC	Db 100 AQPNTQPA(	Qy 123 KAGSHAKGKESI	Db 154 PANAPAAAQPAA	Qy 167 PNGLLSTLIQN-	VNGY -	Qy 219 AFGTRSTA
	1056 EATLAAITPDANVKPAAKQAIADKVQAQETAIDGNNGS-TTEEKAAAKQQVQTEKTTADA	OY 1032TINTGINAGGKKITNIOSGDITQ-NSNDAVIGGRVYDLKTELESKINSAAK 1080	VITEAGENGITTKV	:   :   :   :   :   :   :   :   :   :			1271	1249 SKTSKVVYDVNVDNKTIEVTSDKKLGKKTTTLTKTSANGNATKESAAGADGAAVAAS 1.1.   .   .     .     .     .       .     .       .         .	DIATHLNTL	1361 DAGKNSIQSTQPATAVKSNAKN-DVDQAVTTQNQAIDNTTGATTEEKNAAKDLV			1474	1437	1487		VVTDANGKPINGTDGKPQKAIKG		QY 1601 ADGKYYHANANGVPVDKDGKPITDADKLANLAAHGKPLDAGHQVVASLGGNSDAITLINI 1660	Db 1670 -EGKAKINAVKTFSEYKKDALAKIEDAYNAKVNEADNSNASTSSEI 1/14	1661 KSTLPQIDTPNTGNANAGQAGSLPSLSAAQQSNAAGSKDVLANGFNLGINNEVJUENAGI     1   1   1   1   1   1   1   1   1	QY 1721 DIVNEVNGTGADITSVRSADGTMSNITVNTALAATDDDGNVLIKAKDGKFYKADDLMPNG 1780 QY 1721 DIVNEVNGTGADITSVRSADGTMSNITVNTALAATDDDGNVLIKAKDGKFYKADDLMPNG 1780	-TIPTCKKESATTDLYAYADQKKNNISADINATQDENOQAIANAYOGANGATTOLYOGANGATTOLYOGANGAGATTOLYOGATTOLYOGANGAGATTOLYOGANGAGATTOLYOGATTOLYOGANGAGATTOLYOGATTOLYOGATTOLYOGATTOLY	1781SLKAGKSASDAKIPIGLSLVNFNAGAG 	1813	1814	1871	OY 186 GNOINDIDGE CONTROLL	1925

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4.9%; Score 578; DB 2; Length 2478;
ty 20.9%; Pred. No. 4.7e-16;
ervative 334; Mismatches 1033; Indels 698; Gaps 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----HTVLRQ--IRDSNGSQKYRRTAAEGHASTAVGAMAYAKGHFAN 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEGNYS-----LAVGLT---AKAEKGYTIAIGSNAQAINYG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGNNDNASASNEASIAIGSLAKAHANOAIAIGGSKPDPRNQAA----NQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :IAIGGDVLAE-----GDASI-----AIGSDDLYLDRNSTNSKY 166
                                                                                                                                                                                                                                                                                                              AISAGTHAGTQAKKSDGTAGTTTTAGATGTVKGFAGOTAVGAVSVGA 2187
                                                                                                                                                                                                                                        E----- 2225
                                                                                                                                                                                                                                                              OSTNDKVAQPKSENKAKAEKDGSDSTNQSMVESTTETLPSADITEPN 2294
                                                                                                                                                                                                                                                                                          TNELDHRIHQNENKANAGISSAMAMASMPQAYIPGRSMVTGGIATHN 2272
                                                                                                                                                      GROTOAGNOSIALGDNAQA----TGDQSIAIGTGN-----VVTG 2085
                                                                                                         AD---NSYSVGNNNQFIDA---- 2127
INPAEAIDRINEQGIRFFHVNDGNOEPVVQGRNGIDSSASGKHSVAI 2036
                                                             ureus gene for affecting the methicillin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      999) to the EMBL/GenBank/DDBJ databases.
AAA93438.1; -
AA: 262993 MW; 1C118EBEODD03B34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
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ttes; Bacillus/Clostridium group;
ococcus group; Staphylococcus.
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                                                                                                                                                                                                                                                                                                                                                                  PRT; 2478 AA.
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DSELITINFTTMQTUSKQGATULVIKDAKKNTELGIALGYGSQILNNNNNNNRAYVPEGN	GENSIDQVTPTVNK 1222 TLANVTNDGAGHALSQGLA 1194
	AEEIAAANADVDNAVTQANSNIEAANSQNDVDQAKTTGENSIDQVTPTVNK RVGIDQTKGLTTPKLIVGNNNGKGIVIDSKDGQNTITGLSNTLANVTNDGAGHALSQGLA   ::
254 ALGRN 255 ALALL 314 ATVNN 300 GSNI- 374 GSHL) 374 GSHL) 374 GSHL) 429 NN 480 FPDK 480 FPDK 480 FPDK 480 FPDK 481 ILNNG 611 DTDA 611	1172 AE 1135 RV
da       9	Db 11

1872 DIDAANVQQLNEVRNLLG--LGNAGNDNADGNQVNIADIKKDPNSGSSSNRTVIKAGTVL 1929 1308 DQLQATQINVINNDQNATTEEKEAAIQQLATAVTDAKNNIT--AATDDNGVDQAKDAGKN 1365 1348 KYYQ-----VNDKGQVDKN------KEVAKDKLVAQAQTPDGTLAQMNVK 1386 1492 TNLNSVNAGGTRIDEKGISFVDANGQAKANTPVLSANGL--DLGGKRISNIGA----AVD 1545 1628 QTPNASQQEINDAKQEVDTELNQAKTNVDQ------SSTNEYVDNAVK--EGK- 1672 1666 QIDTPNTGNANAGQAQSLPSLSAAQQSNAASVKDVLNVGFNLQTNHNQVDFVKAYDTVNF 1725 1726 VNGTGADITSVRSADGTMSNITVNTALAATDDDGNVLIKAKDGKFYKADDLMPNG---- 1780 1817 1818 VDDALTQGKAAIDAIQVD--ATVKPKANQAIEVKAEDTKESIDQSDQLTAEEKTEALAMI 1875 1575 --LNNINAATTTGD-----VTTAKDTAVQKVQQLHANPVKKPAGKKELDQAAADKKTQIE 1627 1781 ---SLKAGKSASDAKTPTGLSLVNPNAGKG-----STGDAV------ALNNL 1818 SKAVFKSKDGTT--TTTVSSDGISIQGK---DNSSI--TLSKDGLNVGGKVISNVGKGTK 1871 2091 IGDPSTVKAD---NSYSVGNNNQFIDA------TQTDVFGVGNNIT---VTESN 2132 -----KATARNEITAILNNKLQEIQATPDATDEEKQAADAEANTENGKANQAISAATT 1275 1310 LNTLAGDIQTAKGASQASSSASYVDAD----GNKVIYDST-------DK 1347 1442 FAGDTGTTAKKLGETLT-----IKGGQTDTNKLTDNNIGVV--AGTDGFTVKLAKDL 1491 1986 N----YLTNNPAEAIDRINEQGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAK 2041 2042 ADGEAAVAIGRQTQAGNQSIAIGDNAQA----TGDQSIAIGTGN------VVTGKHSGA 2090 1387 SVINKEQVN---DANKKQG-INEDNAFIKGLENAAKDTKTKNAAVTVGDLNAV-AQTPLT 1760 GKKESATTDLYAYADQKKNISADT--NATQDEKQQAIKQVDQNVQTALESINNGVDNGD 1253 ---KVVYDVNVDNKTIEVTSDKKLGVKTTTLTKTSANGNATKFSAADGDALVKASDIATH 1546 DNDAVNFKQFNEVAKTVNNLNNQSNSGASLPFVVTDANGKPINGTDGKPQKAIKGADGKY 1606 YHANANGVPVDKDGKPITDADKLANLAAHGKPLDAGHQVVASLGGNSDAITLTNIKSTLP 1930 GGKGNNDTEKLATGGVQVGVDKD----GNANGDLSNVWVKTQKDGSKKALLATYNAAGQT 1195 N-DIDKTRAASIGDVLNAGFNLQGNGEAVDFVSTYDTVDFIDGNATTAKVTYDDTSKTS-1673 --AKINAVKTFSEYK----KDALAK-----IEDAYNAKVNEADNSNASTSSEI----2045 NAEVAELONVTIPALEALVPQNDP--DANDTN-----NGID------1366 1223 qq qq οy g q οy qq QQ δ QQ δ q δ g δλ QQ ò q Ôγ QQ δ QQ ōλ Dp Qγ qq g ολ QΥ δý ò ò

us-09-361-619-11.rspt

	Db 400 SVN-GLLDTDCVIFNNSNYNGGILLIANANIACION CONTRACTOR	559 PETITEA 659 PETITEA 533 - KVIIIA 530 LEQVASG 1:     590 LDLGAGG	650 821 698	Qy 864 DIAENLNTLAKEIHTTKGTADTALQTFKVKKDGATDDETJ Db 755 IITTAGNNSGKLIFTGNGG1TGNIGANGAALQEVV Qy 923 GENGLYTANKDGTVTFGINTQSGLKAGDSTTLNKDG Db 803QNFTVAHSAANVVITGLTT-GALKYKDTGTITAHGGL)	QY 970 VERILGDGAMIDGSVLCNGGVAGTLDF Db 850 -KFILGDGAMIDGSVLCNGGVAGTLDF QY 1037 -NAGGKKITNIQSGDITONSNDAVTGGRVY Db 888 DNANSISTINIQ-GDNTKNVIJANDIFVDNIHFTNGGIL QY 1087 HEFSVADEGGNHFTN	Db 928IGNLTTHNIDF-GANGG Qy 1147 PKLTVGNNNGKGIVIDSKDGONTITGLSNTLANVTND Db 949GNNTYNLNAIIVNGONGILNAFTNLK Qy 1204 SIGDV-LNAGFNLQGNGEAVDFVSTXD-TVDFIDGNA-7 Db 987 NIGQIGTPQNFTIQVNNKNLTLVSSVNSSINFGDANSO	OY 1254VVYDVNVDNKTIEVTSDKLGVKTTITITITISTSDKN  1
QY 2133 SVALGSNSALSAGTHAGTQAKKSDGTAGTTTAGATGTVKGFAGQTAVGAVSVGASGAER 2192  Db 2183 NATPAESTTNNNSTTTATNENAPTGSTATAPTTASTEAASSADSKDNASVNDSKQNA 2239  QY 2193 RIONVAAGEVSATSTDAVNGSQLXKATGGIANA 2225  Db 2240 EVNNSAESQSTNDKVAQPKSENKAKAEKDGSDSTNQSWVESTTETLPSADITEPNVPSNT 2299	OY 2226TUBLIDHRIHQNENKANAGISSANAMASHIQAYIPGRANATGGIATHGGOAY 2277  11: 1	11.00	OS RICKETTSIA PTOWAZEALI: OC BACTERIA: PTOWAZEALI: OC RICKETTSIACEAE; RICKETTSIA. OX NCBI_TAXID=782; RN [1] RP SEQUENCE FROM N.A. RC STRAIN=MADRID E;	RX MEDLINE-9993499; PubMed-9423893; RA Andersson S.G.E., Zomorodipour A., Andersson J.O., RA Andersson S.G.E., Zomorodipour A., Andersson J.O., RA Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., RA Eriksson AS., Winkler H.H., Kurland C.G.; RT "The genome sequence of Rickettsia prowazekii and the origin of RT mitochondria."; RT mitochondria."; RT MA133271; CAA14908.1. DR EMBL, AJ33271; CAA14908.1. SEQUENCE 2340 AA; 247862 MW; CC4070F93C165F26 CRC64;		118 QAANQKAGSHAKGKESIALGGDVLAEGDASIAIGSDDLYLDRNSTVSKYPNGLLST	Db 153 -NITTRIDNTV\GNNGSITFEGSGIISNHIGYTNSLLGINVGNG 195  Qy 290 NNRAYVPEGNGSNIKSSRATGNGLFSIGSSTIKRKIINVGAGYEDTDAVNVAOLKAVENL 349  Qy 290 NNRAYVPEGNGSNIKSSRATGNGLFSIGSSTIKRKIINVGAGYEDTDAVNVAOLKAVENL 349  Db 196 EAKIXAPEANNITINAKNGUKKKLGETLTIKGGETQADKL-TDNNNIGVYTDNN 398  Qy 350 AKRQI-TFKGDDNGTGVKKKLGETLTIKGGETQADKL-TDNNNIGVYTDNN 398  Db 226 CDGNITTLKGNINNTTEIDGGGILNLAYDLGSSSIITGDIGNIGSLDTINVLGSATFNS 285

λζ	399 TGLKVKLAKNLSGLETVSTKNLTASEKVTVGSGNNTAELOS
o v	GGITETPTTHASTDKTVYGTDGLKFTDNSNTALEDTTRITKDKIGESNKAGTV 49:
QQ	
δō.	DENKPYLDKDKLKVGNSTLNNGGLTVNNTIGGSNKQLQVGADGIKADVNVN 07
g 2	400 SVN-GLLDJDCVIFINGSNINGGIELENGEN STATE SNAAKFGITKDSGINAG 598
; 음	3 PSAGDISDIRIADNTIYTIDAKNGNVNLLNNNAKIIFEGADSMLALINTG 50
οy	599 DOKISNVKDATDDTDAVTYKQLKQVQQDADGALQSFSIRDEKGQEFTISNLYSNGNTPNT 658
QQ	KDGKTOLV 70
QY	59 FETITFAGENG-ISISNDIAKGKVKVGIDTNGLITALIVGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
a :	533 - NVIIITRINGSGITTICEIRGLSPILPSITINAGGVRTTEQGNTITSDEDKSKAASIG 761
<u> </u>	:: E
QY	2 -DILNTGENLKNNSNSVGFVSTYNTVDEIDGNATTAKVTYDETNQTSKVTYDVNVDEKTI 8:
dd	650 ADPYTCSANVFASVALTNPSSVLILADGVTLTGEVTTHNNTKGVLSLG 697
δ	BLIGDNOKTNKIGVKTTLLTTNANGKATNFSTONDALVNAK 8
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Qy	GENGLITVATUKDGTVIFGINIQSGLKAGDSTTLNKDGLSIKNYASNEQIQGVGNO
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QQ	- KFILGDCAMIDGSVLCNCAMORENESKINSAAKTAONSL
δ	NAGGKKITNIOSGDITONSNDAVIGANALOSGENIOS
qq	B DNANSISTINIQ-GDNTKNVTJANDIFVDNITETNOCIDES  B DNANSISTINIQ-GDNTKNVTJANDIFVDNITETNOCIDES  B DNANSISTINIQ-GDDTKNVTJANDIFVDNITETNOCIDES  B DNANSISTINIQ-GDDTKNTTNOCIDES  B DNANSISTINIC-GDDTKNTTNOCIDES  B DNANSI
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, d	1047 GIITLDSNGNNLTISGNNGIKLGSKGNELSSLNIKGKVTVTNDLDIQNIHQLNINNGALF 11
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qq	1107 DDQSLTSAKIKNINIGTVAGGATYTLDAINDNFDLNTSGMVFKHQDSILELKNSSNTNDH
	138 TOTAL THE THE TAXABLE TO THE TAX

RESULT 13 Q52657  TO Q6  TO TEMBLrel. 01, Created)  TO Q1-NOV-1996 (TrEMBLrel. 06, Last annotation update)  TO Q5 (TrEMBLrel. 06, Last annotation update)  TO Q5 (TrEMBLrel. 06, Last annotation update)  TO Q5 (TrEMBLrel. 06, Last annotation update)  TO Q6 (TrEMBLrel. 16 (NPA).)  TO CREATIST PROPANA.  TO CREATIST PROPANA.  TO CREATIST PROPALIST 7:  TO CREATIST PROPALIST	Query Match 4.8%; Score 565.5; DB 2; Length 2021; Best Local Similarity 23.2%; Pred. No. 1.2e-15; Matches 497; Conservative 206; Mismatches 691; Indels 745; Gaps 113; Qy 253 QAINYGALALGADTRVDLDYGIALGYG-SQILNNNNNNNNKAYVPEGNG 300 :	OY 301 SNIKSSKATGNGLFSIGSSTIKRKIINVGAGYEDTDAVNVAQLKAVENLAKRQ 353    :	NGGG NTIG NTIG OKKO	QY         622 QVQQDADGALQSFSIRDEKGQEFTISNLYSNCNTPNTFETITFAGENGISISNDIAKG 679           1
	1718   KAYDTVNFVNGTGADITSVR-SADGTMSNITVNTALAATDDDGNVLIKAKDG   1768	D F O-O F	1729   IVEVITALINE	2118 DVFGVGNNITYTESNSVALG-SNSAISAGTHAGTQAKKSDGTAGTTTTAGATGTV 2171

VIEGG 451 ALVNAKDIAENLNTLAKEIHTTKGTADTALQTFKVKKDGATDDETITVGKDGTQNGKTVN 917	NGLTVAINKDGTVTFGINTQSGLKAGDST	VKF-AKVDKGNSSTGIDGTSRIT-KDOIGFTGANGSLDTTKPHLTKDKLKVGEVEITNTG 1035  VKF-AKVDKGNSSTGIDGTSRIT-KDOIGFTGANGSLDTTKPHLTKDKLKVGEVEITNTG 1035  ATLGGAIRKTTTKLTDNASAVTFTNPVVVTGAIDNTG 556	INAGGKKITNIOSGDITONSNDAVTGGRVYDLKTELESKINSAAKTAONSLHEESVADEQ 1095 INAGGKKITNIOSGDITONSNDAVTGGRVYDLKTELESKINSAAKTAONSLHEESVADEQ 1095	GNHFTVSNPYSSYDTSKTSDVITFAGENGITTKVNKGVVRVGIDQTKGLTTPKLTVG 1152  GNHFTVSNPYSSYDTSKTSDVITFAGENGITTKVNKGVVRVGIDQTKGLTTPKLTVG 1152  AGKATLGGAIIKATTTKLTDNASAVTFTNPVVVTGALDNTG 628	N-NNGKGIVIDSKDGQNTITG-LSNTLANVT-NDGAGHALSGGLANDTDKTRAASIG 1206    N-NNGKGIVIDSKDGQNTITG-LSNTLANVT-NDGAGHALSGGLANDTDKTRAASIG 1206   N-NNGKGIVIDSKTGIVITG   N-NDGAGHALSGAIIKATTTKLTNAASVL 684	DVLNAGFNLQGNGEAVDFVSTYDTVDFIDGNATTAKVTXDDTSKTSKVVYDVNVDN 1262  DVLNAGFNLQGNGEAVDFVSTYDTVDFIDGNATTAKVTXDDTSKTSKVVYDVNVDN 1262    V	KTIEVTSDK-KLGVKTTTLTKTSANGNATKFSAADGDALVKASDIATH 1309	ATINGGAGANILOGANILAGASASSASYUDADGANUIYDSTDKKYXQ-VADKGOVD 1359 L-NTLAGDIQTAK	KNKEVAKDKLVAQA OTPDGTLAQMNVKSVINKEQVNDANKKQGINEDNAFIKGLE 1414  KNKEVAKDKLVAQA OTPDGTLAQMNVKSVINKEQVNDANKKQGINEDNAFIKGLE 1414	-NTUNANNALVIERODDIN 1467NAAKDIKTKNAAVTGDLNAVAQTPLIFAGDTGTTAKKLGETLIIKGGGTDIN 1467NAAKDIKTKNAAVT	KLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGTRIDEKGISFVDANGQAKANTPVLSA 1527 KLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGTRIDEKGISFVDANGAKANTPVLSA 1527 :	ALALYNVO CONTROL GAAVDDNDAVNFKQFNEVAKTVNNLNNQSNSGASLPFV 1578  NG-LDLGGKRISNIGAAVDDNDAVNFKQFNEVAKTVNNLNNQSNSGASLPFV 1578  NG-LDLGGKRISNIGAAVGNNAILNVNTKSLTASHLTIGTV-AEINIGAGNLFAIDA 1035	VIDANGKPINGTDGKPQKAIKGADGKYYHANANGVPVDKDGKPITDADKLANLAAH 1634VIDANGKPINGTDGKPQKAIKGADGKYYHANANGVPVDKDGKPITDADKLANLAAH 1634FRALDSALVLSNITGVGVNNILLAADLVAP 1079	SAGUVILLMAZUI  GKPIDAGHQVVASLGGNSDAITLINIKSTLPQIDIPPNTGNANAGQAQSLPSLSAAQQSNA 1694  :	GVDEGTVVFDGG	LAATD-DDGNVLIKAKDGKFYKADDLMPNGSLKAGKSASDAKTPTGLSLVNP- 1802 LAATD-DDGNVLIKAKDGKFYKADDLMPNGSLKAGKSASDAKTPTGLSLVNP- 1802   :       :     :       :	NAGKGST-GDAVALNNLSKAVFKSKDGTTTTTVSSDGISIQGKDN 1846
419 VTF 858 ALVNAKDIAEN  ::	452 AIIKAT 918 TLKLKGENGLT			_			1263 KTIEVTSDK			1415 NAAKDTE		1528 NG-LDLGG		1036 SAGDVILL 1635 GKPLDAGH			1803 NAGK
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MEDLINE-97061201; Pubmed-8905231;

MEDLINE-97061201; Pubmed-8905231;

MEDLINE-97061201; Pubmed-8905231;

Miyajima N., Mirosawa M., Suqiura M., Sasamoto S., Kimura T.,

Miyajima N., Hirosawa M., Suqiura M., Nakazaki N., Naruo K., Okumura S.,

Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Yamada M., Yasuda M.,

Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda S.,

Tabata S.,
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BMBI., DG3999; BAAI.0087.1; -.
BYPOCHACICAL POCCEIN.
SEQUENCE 3029 AA: 308789 WW; BEE0BB57E822A4FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1494 NSNITGS------GTTLTLGANQVIYTGTGSFTDTLTLNTTFDGAAKSGG 1537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2137 GSNSAISAGTHAGTQAKKSDGTAGTTTTAGA-----TGTVK------GFAGQTAVGA 2182
                                                                                                                                                                                                                                                                                                                                                                                                                                           2077 IGTGNVVTGKHSGAIGDPSTVKADNSYSVGNNNOFIDATQTDVFGVGNNITVTESNSVAL 2136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1369 GEIQGTGTNT-----LTLPAHFKLTG------SINKTGGQALKLNFMNGGSVSG 1411
SSITLSKDGL-----NVGGKVISNVGKGTKDTDAANVQQLNEVRNLLGLGLGNAGNDNADG 1900
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                                                                                                                                                                                                                                                                                                                                 2017 VVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGRQTQAGNQSIAIGDNAQATGDQSIA
                                                                                                                                                                                                                                                                                                                                                                      1957 GDLSNVWVKTQKDGSKKALLATYNAAGQTNYLTNNFAEAIDRINEQGIRFFHVNDGNQEP
                                                                                                            NOVNIADIKKDPNSGSSSNRTVIKAGTVLGGKGNNDTEKLA---TGGVQVGVDKDGNAN-
                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-PCC6803;
Tabata S.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBI_TaxID=1148;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 308.8 KDA PROTEIN.
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1067 LKTELESKINSAAKTAQNSLHEFSVADEQGNHFTVSNPYSSYDTSKTSDVITFAGENGIT 1126 1127 TKVNKGVVRVGIDQTKGLTTPKLTVGNNNGK--GIVIDSKDGQNTITGLSNT----LANV 1180 1228 YDTVDFIDGNA---TTAKVTYDDT---SKTSKVVYDVNVD-NKTIEVTSDKKLGVKTTTL 1280 1675 TGNSATATQT-----IVVDTTAPTVTINAIAVDDIINAVEAGSPVAVSGTTTGVEDG 1726 1399 KKQGINEDNAFIKGLENAAKDTKTKNA---AVTVGD-LNAV-AQTPLTFAGDTGTTAKKL 1453 2058 TEEVVATVSDLAGNPATPATRNITVDTTAPTVTINAIAVDDIINAVEAGSPVAVSGTTTG 2117 1372 SVTATNPT-----VDTTAPT 1397 1019 LTKDKLKVGE-----VEITNTGINAGGKKITNIQSGDITQNSNDAVTGGRVYD 1066 : | | : : | | : : | | | : : | | | | : : | : | : | : | : | : | | : | : | : | : | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 1281 TKTSANGNATKFSAADGDALVKASDIATHLNTLAGD--IQTAKGASQASSSASYVDADGN 1338 1339 KVIYDSTDKKYYQVNDKGQVDKNKEVAKDKLVAQAQTPDGTLAQMNVKSVINKEQVNDAN 1398 1727 QVVTVTIDGNTYTATVTG-----1766 1454 GETLTIK-GGQTDTNKLTDN----NIGV--------VAG-----TDGFT 1484 1485 VKLAKDLTNLNSVNAGGTRIDEKGISFVD-----ANGQAKA-NTPVLSANGLDLGG 1534 1535 KRISNIGAAVDDNDAVNFKQFNEVAKTVNNLNNQSNSGASLPFVVTDANGKP----- 1586 1939 VTANGAĞEWTLDYTGTLLAD-GDYELSVTATNPTGNSATATQTİVVDTTAPTVTINAIAV 1997 1998 DDIINAVEAGSPVAVSGTTTGVEDGQVVTVTIDGNTYTATVTGNAWTFNIPVADIANFEA 2057 1616 ------DKDGKPITDA----- 1637 1638 LDAGHQVVASLGGNSDAITLTNIKST--LPQIDTPN-------TGNANAGQAQ 1681 1682 SLPSLSAAQQSNAASVKDVLNVGFNLQTNHNQVDFVKAYDTVNFVNGTG-ADITSVRSAD 1740 1741 G-TMSNITVNTALAATDDDGNVLIKAKDGKFYKADDLMPNGSLKAGKSASDAKTPTGLSL 1799 1800 VNPNAGKGSTGDAVALNNLSKAVFKSK----DGTTTTTVSSDGISIQGKDNSSITLSKDG 1855 960 -LSIKNPASNEQIQVGADGVKFAKVDKGNSSTGIDGTSRITKDQIGFTGANGSLDTTKPH 1587 ---INGTDGKPQKAIKGA-----DGKYYHANANG-----VPV-----= ::::::::

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                                                                                                                                                                       2478 DIVAPAVIIDSISDDIGAQANDFIINDDILVFNGTAEADSTVVVSLDGIEIGTVTANGAG 2537
                                                                                                                                                                                                                                                                                                                               GTAGITITAG--ATGIVKGFAGQTAVGAVSVGASGAERRIQNVAAGEVSATSTDAVNGSQ 2214
2278 VVDTTAPTVTINALAVDDIINAVEAGSPVAVSGTTT-----GV----EDGQVVTVTIDG 2327
                   LNVGGKVISNVGK-GTKDTDAANVQQLNEVRNLLGLGNAGNDNADGNQVNIADIKKDPNS 1914
                                                                                                                       -- ANGDLSNVWVKTQKDGSKKALLATYNAAGQTNYLTN
                                                                                                                                                                                                                                                        TDVFG-----VGNNITVTES------NSVALGSNSAISAGTHAGTQAKKSD
                                                               GSSSNRTV-------VD
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                                                                                                                                                                                               KHSVAIGFQAKADGEAAVAIGRQTQAGN----QSIAIGDNAQATGDQSIAI-----
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                                         --VATVSDLAGNPAT
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PRINTS; PR00313; CABNDNGRPT.
PROSTIE; PS00018; EF_HAND; UNKNOWN_1.
PROSTIE; PS000130; HEMOLYSIN_CALCIUM; 4.
SEQUENCE 2747 AA; 280202 WW; 208FE380E44A5F37 CRC64;
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STRAIN=ATCC 33658;
Braun M., Frey J., Kuhnert P.;
"1280 kDa RTX protein of Aeromonas.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF218037; AAF27914.1; -.
InterEro; IPR001343; -.
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15, Last sequence update)
16, Last annotation update)
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4.8%; Score 558.5; DB 2;
Best Local Similarity 20.3%; Pred. No. 3.6e-15;
Matches 571; Conservative 350; Mismatches 983;
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                                         NTYTATVTGNAWTFNIPVADIANFEATEEV----
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01-0CT-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
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Aeromonas salmonicida
                                                                                                            1951 KDGN-----
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                                                                                                                   114 A-AAGGAPAAGGGNIGGVAGASGNGGFVTIDRTGDTTIAAAGFDTANQTDAGVTGDAAAG 172
                                                                                                                                                                                                                                                                     152 SDDLY-----LDRNSTNSKYPNGLLST-LIQNHTVLRQIRDSNGSQKYRRTAAEGH 201
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99
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7 VIENKATGTFMAVAECAKSHSGGSSSSTAGQVGSSPVIRLTRVATLAILVIGATLNGSAY
                                                                                        67 AQNNSKIAFGTTGNNDNASASNEA-----SIAIGSLAKAHANQAIAIGGSKPDPRNQA
                                                                                                                                                                                 ---AIGGDVLAEGDASI----AIG
                                        12 VVVTQLKGNIYLVAA-----DGSQKQLAEGDI-----LPRDAVL-ITPEGASFNG-
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JOURNAL Submitted (11-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).	The BDGs is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoryo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecost digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be	found at http://bacpac.med.buffalo.edu/drosophila_bac.htm. Location/Qualifiers 1. 1101 Source /organism="Drosophila melanogaster" /db.xref="taxon.7227" /clone_lib="RPCI-98" /clone="RAKERPIP" /note="end : TET3" BASE COUNT 469 a 6 c 69 g 151 t 406 others	Query Match  0.9%; Score 66.2; DB 219; Length 1101;  Matches 95; Conservative 198; Mismatches 228; Indels 0; Ga 2903 aaagccatcacagggctgtccccaacactgcctagcattgccgatcaagtagccgcaac  :::: ::::: ::::  ::::  1100. MMMMHHTTMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM		920 3143 860 3203 800	3263 gctaatggtaatacagcaactaactttaatgttaactctagtgatgaagatgcccttgtt 3322	Oy 3383 ggcacagcagcaccgccctacaaacctttaccgttaaaaa 3423
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% Query core Match Le			,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		 	CNSOOLT2 IDDOSOPABLE mela BACR48P19 of RI fly), genomic a ALO78714 GSS	fruit fly. Drosophila melano Eukaryota; Metazo Pterygota; Neopte Muscomorpha; Ephy I (bases 1 to 111 Genoscope. Direct Submission

RESULT 1 CNSOOLT2/c LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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FEATURES
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Submitted (12-ARR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon ngroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

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                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygi; Neopterygi; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

[ (pases l to 806)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetler, F., Saurin, W., Bernot, A. and Weissenbach, J.

Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          692 АСТАСТААТААТААТААТАСТААТААТСАТААТААМААТААТАСТАСТАСТАСТ
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8e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="095624"
/clone_llb="G"
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                                                       AL281759
AL281759.1 GI:8020086
GSS; genome survey sequence.
Tetraodon nigroviridis.
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Best Local Similarity 40.7%
Matches 240; Conservative
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail: segref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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3335 atcgccgaaaatctaaacaccctagccaaggaaattcacaccaccaaaggcacagcagac 3394
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachyeera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                     2892 acgcaggtggtaaagccatcacagggctgtccccaacactgcctagcattgccgatcaaa
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                             accgccctacaaacctttaccgttaaaaaggtagatgaaaataataatgctgatgacgcc
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/db_xref="taxon:7227"
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/clone="BACN03G04"
/note="end : SP6"
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This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tetraodon nigroviridis genome survey sequence PUC-Or1 end of clone 224F10 of library G from Tetraodon nigroviridis, genomic survey
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Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
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Roset-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
aaaataat aatgetgatgacgecaaegecateaeegtgggteaaaagaaegeaaataat 3490
                                                                                                                                cccatgataccgctaacaaaaccagtaaagtggtatatgtgatgtgaatgtggatgatacaa 3191
                                                                                                                                                                                               ccattcatctaacaggcactgatgacaataaaaaacttggcgtcaaaaccaccaaactga 3251
                                                                                                                                                                                                                                                              acaaaacaagtgctaatggtaatacagcaactaactttaatgttaactctagtgatgaag 3311
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                                                                                                                                                                                                                                                                                                                                                                                             acaccaccaaaggcacagcagacaccgccctacaaacctttaccgttaaaaaggtagatg 3431
                                                                                    819 MMMTMMMCTYHMWCNMYAHHYHYCTMWHMHTHWHCHYMTCHYMTHHHYHTMYTAAA 760
                                                                                                                                                                                                                                                                                 519 АЙИСТИНТИВНАИАМНАНИНАМИНМАНАМАААСНИНМИМАМАМАМАНИМИКСААААМАИМА 460
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                                                              3072 ttgtctccacttatgacattgttgactttgccaatggcaatgccaccaccgccacagtaa
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                             /organism="Tetraodon nigroviridis"
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                                       Tetraodontidae; Tet:
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melanogaster genome using these BACS. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the enfire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
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Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                    Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                           Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
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Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                        Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                        אסימים (הי Fizames,C., Fizames,C., Fisher,C. Bouneau, E., Billault,A., Quetler,F., Saurin,W., Bernot,A. and Weissenbach,J.
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/clone="268H14"
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/clone_lib="G"
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I 105 c 170 g 282 t 50 others
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41.1%; Pred. No. 0.0013;
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Tetraodon.
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/GD xref="taxon:5759"
/GD xref="taxon:5759"
/Glone_lib="Entamoeba histolytica Sheared DNA"
/Glone_lib="Vector: PHOS1; Site_1: BSt !; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kD). The v + 1 method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                            Entamocba histolytica

Eukaryota; Entamocba histolytica

Eukaryota; Entamocbidae; Entamocba.

I (bases 1 to 816)

Loftus, B., Van Aken, S. and Fraser, C.

Determination of clone end sequences from Entamocba histolytica

HWI:IMSS sheared DNA library

Unpublished (2000)

Contact: Brendan J Loftus

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Fax: 301 838 0200

Fax: 301 838 0200

Fax: 301 838 cond

Email: bloftus@tigr.org

Clones are derived from the Entamocba histolytica HMI:IMSS sheared
                                                                                                                                                                       GSS 03-NOV-2000
DNA Entamoeba histolytica
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Pred. No. 0.0052;
0; Mismatches 253; Indels
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/strain="HM1:IMSS"
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High quality sequence stop: 8
Location/Qualifiers
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Seq primer: M13-Reverse
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                                                                                                                                                                                                            genomic, DNA sequence.
AZ535744
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Best Local Similarity 44.9%;
Matches 206; Conservative
                                                                                                                                                                  AZ535744 816 bp
ENTCQ25TR Entamoeba h
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Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI disestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; on bw sp, the same strain used for the BDGP's pl and bow to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr
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Ptertygota: Neoptera: Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR29B23"
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fly), genomic survey sequence.
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                                               AL069706.1 GI:4949849
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Direct Submission
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The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutcyo Gsoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Esogenic strain v2: nb wsp, the same strain used for the BDGP's pland EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or fullters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Lirect Submitsion
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNSOODKY 928 bp DNA GSS 04-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR27A24 of RPCI-98 library from Drosophila melanogaster (fruit
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    4751 accgataacaagtactatcaagccaaaaatgatggcacagttgataaaaccaaagaagtt 4810
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                             GAATTAGAAGACGATGATGAAGAAGACGATGATGAAGAGACGATGATGAAGAAGACGAT
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/db_xref="texon:7227"
/clone_lib="RPCI-98"
/clone="BACR27A24"
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Direct Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruifily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutcyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pland by the order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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BACR31021 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL071063
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Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilldae; Drosophila.
1 (bases 1 to 996)
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                                   taacgcatttgtaaaaatcattgcgccctttatgtgtatcatatgaatagaatattatg
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/db_xref="taxon:7227"
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36.0%; Pred. No. 0.0093;
:1vc 52; Mismatches 170; I
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Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR24D09 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL057419
AL057419.1 GI:4937885
243 cagaatggtgatgctatatgatgatgcctacgagttgatttgggttaatcactctatgat 302
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Location/Qualifiers
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR24D09"
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TITLE
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Length 1101;

53; DB 219; No. 0.012;

Score Pred.

0.8%;

Query Match Best Local Similarity

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l (bases 1 to 641)
El-Sayed, N., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C., Earsayed, C., Zhao, H., Gill, S., Suh, E., Melville, S., Donelson, J., Fraser, C. and Adams, M.
Determination of clone end sequences from Trypanosoma brucei GUTat 10.1 sheared DNA library
Oupublished (1999)
Other_GSSs: Sheared DNA-46J23.TF
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Sheared DNA-46J23.TR Sheared DNA Trypanosoma brucei genomic clone
Sheared DNA-46J23, DNA sequence.
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                                                                                      tgatatgatttaacatgtgacatgatttaacattgtttaatactgttgccatcattacca 142
                                                                                                                                    taatttagtaacgcatttagtaacgcatttgtaaaaatcattgcgcccctttatgtgtat 202
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  Gaps
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241;
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/strain="TREU927/4 GUTat 10.1"
/db_xref="taxon:5691"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MC
Fal: 301 838 0200
Fax: 301 838 0208
Email: nelsayed@tigr.org
  Mismatches
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AQ946120.1 GI:6769385
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Trypanosoma brucei
Conservative
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/clone="Sheared DNA-46J23"

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fruit fly
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   /clone_inb="Sheared DNA"
/clone_inb="Sheared DNA"
/clone_inb="Sheared DNA"
/clone_inb="Sheared DNA"
/clone_weetor: pUC18; Site_1: SmaI; Constructed at The Institute for Genomic Research (T1GR), Reckville, MD.
Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically Sheared to give a tight size distribution (approx 2 kb).
The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C.
(Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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AL206908

GSS; genome survey sequence.

Tetracdon nigroviridis.

Eutracdon nigroviridis

Eukaryota: Metazca: Chordata: Craniata; Vertebrata; Euteleostomi;

Actinopterygii: Neopterygii; Teleostei; Buteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetracdontiformes;
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
153PO4 of library G from Tetraodon nigroviridis, genomic survey
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                                                                                                                                                                                                                                                                                   Score 52.8; DB 236; Length 641;
Pred. No. 0.011;
0; Mismatches 297; Indels 0;
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Best Local Similarity 43.8%;
Matches 231; Conservative
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
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                                                                                                                                                                                   Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J. Human gene number estimate provided by genome wide analysis using Unpublished
                 Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Welssenbach, J.
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN17A05 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
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PUC-Or1"
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                                                                               Charaterization and repeat analysis of the compact genome freshwater pufferfish Tetraodon nigroviridis Unpublished
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/db_xref="taxon:99883"
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/clone_lib="G"
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(bases 1 to 1190)
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Genoscope.
Direct Submission
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Matches 147; Conservative
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Gossyplum arboreum
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossyplum.
1 (bases I to 780)
Wing, R.A., Frisch, D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xreef="taxon:29729"
/db_xreef="taxon:29729"
/clone="GA_Eb0033M02f"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2990 aaagacaaatccaacgctgccagcattaatgatatattaaatacaggctttaacctaaaa 3049
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Pred. No. 0.02;
0; Mismatches 280;
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/organism="Gossypium arboreum"
                                                                                                                                                                                                                                                                              Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, US
Tel: 864 656 7288
                                                                                                                                                                                                                                                                                                                                                                                       Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
High quality sequence stop: 200.
Location/Qualiflers
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  GI:11209757
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                                                                                                                        Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr )
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.adgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etded Ur Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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GA_Eb0033M02f Gossypium arboreum 7-10 dpa fiber library Gossypium
arboreum cDNA clone GA_Eb0033M02f, mRNA sequence.
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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  Drosophila melanogaster
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Search completed: September 13, 2001, 03:33:34 Job time: 53636 sec

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APPLICANT: SASAKI, Ken
APPLICANT: HARKNESS, Robin E.
APPLICANT: HARKNESS, Robin E.
APPLICANT: HARKNESS, Robin E.
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: LOOSMORE, Sheena M.
AUTILE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER
TITLE OF INVENTION: MEMBRANE PROTEIN OF MORAXELLA
NUMBER OF SEQUENCES:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
CONTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IDM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,370
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US/08/478,370
FILING DATE: Michael I
REGISTRATION NUMBER: 1038-502
TELEPOMMUNICATION NUMBER: 1038
TELEPOMMUNICATION INFORMATION:
TELEPAX: (416) 595-1155
TELEPAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRACTERISTICS:
LENGTH: 6973 base pairs
TUTE APPLICATION ACIDA
SECONDENCE CHARACTERISTICS:
LENGTH: 6973 base pairs
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                 US-08-801-898A-23
US-08-962-690-12
US-08-962-690-12
US-08-992-403A-1
US-08-996-797-1
US-08-728-323A-1
US-08-770-379-20
US-08-770-379-20
US-08-757-669A-20
US-08-928-361B-1
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nter than or equal to the score of the result being printed,
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438	1 CGGTTGACTTTGTCTCCACTTATGACACCGTCAACTTTGCCGATGGCAAŢGCCACCG	4440
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468	0 aaggggcaagccaagcgaacaactcagcaggctatgtggatgctgatggcaataaggtca 	4739
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480	O ccaaagaagttgccaaagacaaactggtcgcccaagcccaaaccccagatggcacattgg 	4859 4860
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510	00 gtgggcaaacagacaccaataagctaaccgataataacatcggtgtggtagcaggtactg 	5159 5160
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27;

<pre>Qy 6600 atggtcaatgggtatttaadatcaatggttcagccgatacccaaggccatgtaggggcgg 6659                                      </pre>	Query Match 63.1%; Score 4396.8; DB 4; Length 9542; Best Local Similarity 80.8%; Pred. No. 0; Matches 5599; Conservative 0; Mismatches 992; Indels 337; Gaps 27
<pre>Qy 6660 cagttggtgcaggttttcacttttaagccataaatcgcaagattttacttaaaaatcaat 6719</pre>	Oy 324 ctattgacttaaatcaccatatggttataatttagcataatggtaggctttttgtaaaaa 383 
Oy 6720 ctcaccatagttgtataaaacagcatcagcatcagtcatattactgatgtttt 6779	Qy 384 tcacatcgcaatattgttctactgttactaccatgcttgaatgacgatcccaatcaccag 443
Oy 6780 tatcacttaaaccattttaccgctcaagtgattctctttcaccatgaccaaatcgccatt 6839	Oy 444 attcattcaagtgatgtgtttgtatacgcaccatttaccctaattattcaatcaa
Oy 6840 gatcatagtaaacttattgagtaaattttatcaatgtagttgttagatatggttaaaat 6899 	Oy 504 ctatgtcagcatgtatcattttttaaggtaaaccaccatgaatcacatctataaagtca 563
Qy 6900 tgtgccattgaccaaaaatgaccgatttatcccgaaaatttctgattatgatccgttga 6959 	Oy 564 totttaacaaagccacaggcacatttatggcagtggcagagtacgccaaatcccacagca 623 
Oy 6960 cctgcaggtcgac 6972 	Oy 624 cgggggggggggggggggggggggggggggggggggg
RESULT 2 US-08-968-685A-9 . Sequence 0 April (20+10) IIC/08068605A	Oy 684 gtattgccgcgctcgctgtcctcgtgatcggtgcaacgctcagtggcagtgcttatgctc 743
; Sequent No. 6214981 ; GENERAL INFORMATION: ; APPLICANT: TUCKER, KENNETH	Oy 744 aaaaaaaagataccaaacatatcgcaattggtgaacaaaaccagccaagacgctcaggca 803 
	Oy 804 ctgccaaggcggacggtgatcgagccattgctattggtgaaaatgctaacgcacagggcg 863 
) 45 (I)	Qy 864 gtcaagccatcgctatggtagtagtagtaaaaactgtcaatggaagcagtttggataaga 923 
	Qy 924 taggtaccgatgctacgggtcaagagtccatcgccatcggtggtgatgtaaaggctagtg 983
COMPUTER: IN PC Compatible  COMPUTER: PARTING SYSTEM: PC-DOS/MS-DOS  CONTRARE: Patentin Release #1.0, Version #1.30	Oy 984 gigatgcctcgattgccatcggtagtgatgacttacatttgcttgatcagcatggtaatc 1043
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; NAME: Baldwin, Geraldine F. ; REGISTRATION NUMBER: 31,232 ; REFERENCE/POCKET NUMBER: 7969-060	Oy 1104 aaatacgaagctcaaaggataatgatgtaaaatatagacgcacaaccgcaagcggac 1160
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	Qy 1221 gtacacgggcaacagctaaaagtgcctattccttggcagtgggtcttgccgccacagccg 1280
TOPOLOGY: Tine MOLECULE TYPE: D S-08-968-685A-9	Qy 1281 agggccaatctacaatcgctattggttctgatgcaacatctagctcgttgggagcgatag 1340 
	Oy 1341 cccttggtgcaggtactcgtgctcagctacagggcagtattgccctaggtcaaggttctg 1400

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	Db 6666 ACTGATGCTGATGTT  Qy 6822 Catgaccaaatcgcc	Qy 6942 ctgattatgatccgt	GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: St. General APPLICANT: Barenkam; TITLE OF INVENTION: NUMBER OF SEQUENCES:		COMPOTER TACADADE PO COMPUTER: ELDE COMPUTER: IBM PC COPERATING SYSTEM: SOFTWARE: PATENTION CURRENT APPLICATION PILING DATE: 29-1	0 D D D D		ILLEFAX: (%12) 57729 57 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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Tloppy disk
Compatible
M: Compatible
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CON DATA:
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amp, Stephen J.
HAEMOPHILUS ADHESION PROTEINS
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ER: US 08/409,995
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                                                                                                                                           Length 2037;
                                                                                                                                         Query Match 1.2%; Score 83.6; DB 4; Length 2
Best Local Similarity 54.1%; Pred. No. 2e-13;
Matches 198; Conservative 0; Mismatches 159; Indels
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APPLICANT: Barenkamp, Stephen I.
APPLICANT: Barenkamp, Stephen I.
APPLICANT: St. Geme III, Joseph W.
TITLE OF INVENTION: Heemophilus Adhesion Proteins
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbe
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,995
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NAME: $110a, Robin M.
RECISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61053/RFT
TELECOMUNICATION INFORMATION:
TELECOMUNICATION: (415) 781-1989
TELEPHAX: (415) 398-3249
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TYPE: nucleic acid
STRANDEDNESS: unknown
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                                     TOPOLOGY: unknown MOLECULE TYPE: DNA US-08-913-942-14
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Pred. No. 4.6e-13;
0; Mismatches 237; Indels
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STREET: Four Embarcadero Center, Suite 3400
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US-08-685-467-1
Sequence 1, Application US/08685467
Patent No. 6060059
GENERAL INFORMATION:
APPLICANT: St. Geme III, Joseph W. APPLICANT: Bt. Geme III, Joseph W. TITLE OF INVENTION: HAEMOPHILUS ADHESION PROTEINS NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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APPLICATION NUMBER: US/08/685,467
                                                                                                                                                                                                                        Ouery Match 1.2%;
Best Local Similarity 49.8%;
                  SEQUENCE CHARACTERISTICS:
LENGTH: 3294 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: United States
                                                                                                                                                                                                                                                                          Matches 244; Conservative
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
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                                                                                                                         ; TOPOLOGY: unknown
US-08-409-995-1
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
CORRESPONDENCE ADDRESS:
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US-08-913-942-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                     STATE: Ca
COUNTRY:
ZIP: 9411
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                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.2%; Score 82.8; DB 3; Length 3 Best Local Similarity 49.8%; Pred. No. 4.6e-13; Matches 244; Conservative 0; Mismatches 237; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: St. Geme, Joseph
APPLICANT: Barenkamp, Stephen J.
AITLE OF INVENTION: HAEMOPHILUS ADHESION PROTEINS
NUMBER OF SEQUENCES: 19
                                                                                                                      RECISTRATION NUMBER: 38,304
REPERENDE/DOCKET NUMBER: A-61053-2/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEFAX: 910-277299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/409,995
FILING DATE: 24-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION UNBER: 38,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08913942
Patent No. 6200578
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic) US-08-685-467-1
 22-JUL-1996
                                                                                                                                                                                                                                                                               LENGTH: 3294 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                        unknown
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STRANDEDNESS:
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ADDRESSEE: Flehr Hobbach Test Albritton & Herbert LLP STREET: Four Embarcadero Center, Suite 3400 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                       SUFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/913,942
FILING DATE: 29-DEC-1997
CLEASIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05/04/09,995
FILING DATE: 24-MAR-1995
FILING DATE: 22-MAR-1996
ATCHING DATE: 39,054
REFERENCE/DOCKET NUMBER: A-61053-1/RFT/RMS/DAV
TELECOMMUNICATION INDERER: 3-0004
                                                                                                                                                                                                                                                                                                 Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 4.6e); Mismatches
                                                                                                                                                                                      COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSCHWARE: Patentin PATENT
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49.8%; Pred
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 398-3249
TELEX: 910 277289
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 3294 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                   RY: United States 94111-4187
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4311 acaaaacccgtgccgccagcattgttgatgtgctaagcgcaggctttaacttgcaaggca 4370
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      6491 gcgtccatgccacaagcctacattcctggcagatccatggttaccggggggtattgccacc 6550
                                                                                                                                4371 atggtgaagcggttgactttgtctccacttatgacaccgtcaactttgccgatggcaatg 4430
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                                                                                                                                                                                                                                              Length 5738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Barenkamp, Stephen I.
APPLICANT: St. Geme III, Joseph W.
TITLE OF INVENTION: Heemophilus Adhesion Proteins
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Sulte 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 0.9%; Score 64.8; DB 1; 1 Similarity 66.4%; Pred. No. 8.6e-08; 93; Conservative 0; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38,304
ER: A-61053/RFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08409995 Patent No. 5646259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 24 WAR-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: S.11VA, RODIN M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELERAX: (415) 398-3249
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGIH: 5738 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
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Matches 93; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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STATE: CACOUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-409-995-3
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3223 ATTATTCGCTTGTCAGGCACAACCAATAGTCAAGGTAAAAACAGGCGTTGCAGCAGGTGT 3282
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                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08913942
Patent No. 6200578
GENERAL INFORMATION:
APPLICANT: Barenkamp, Stephen J.
TITLE OF INVENTION: HARMOPHILUS ADHESION PROTEINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 29 DEC1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,995

FILING DATE: 24 MAR: 1995
PRIOR APPLICATION NUMBER: PCT/US96/4031
APPLICATION NUMBER: PCT/US96/4031
FILING DATE: 22 MAR: 1996
ATTORNEY/AGENT INFORMATION:
NAMM: VANCE: DOILY A.
REGISTRATION NUMBER: 39,054
REFERENCE/DOCKET NUMBER: 39,054
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/913,942
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Pred. No. 1.6e-11;
0; Mismatches 168;
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Best Local Similarity 52.8%;
Matches 198; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7291 base pairs
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EDNESS: unknown
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US-08-913-942-3
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1918 cttatcgcggcgaagccggttacgccatcggctactccagtatttccgacggcggaaatt 1977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: PEAK, Ian Richard Anselm APPLICANT: PEAK, Ian Richard Anselm APPLICANT: PENINGS, Michael Paul APPLICANT: JANINGS, Michael Paul ITILE OF INVENTION: Rover SURFACE ANTIGEN FILE REFERENCE: 06504/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
APPLICANT: PEAK, Ian Richard Anselm APPLICANT: JENNINGS, Michael Paul APPLICANT: MONZON, E. Richard TITLE OF INVENTION: NOVEL SURFACE ANTIGEN TILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
PRIOR FILING NUMBER: PATENTALE TO SECULIAR DATE: 1997-12-12
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US-09-377-155-12
Sequence 12, Application US/09377155
Patent No. 6197312
                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Neisserla meningitidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: (276)...(2051)...
US-09-377-155-1
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SOFTWARE: Patentin Ve
SEQ ID NO 12
LENGTH: 1797
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                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: St. Geme III, Joseph W.
APPLICANT: Barenkamp, Stephen J.
TITLE OF INVENTION: HAEMOPHILUS ADHESION PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE MADRESS:
ADDRESSE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUWRRY: United States
: 21P: 9411-4187
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 22-JUL-1996
CLASSIFICATION T424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,995
FILING DATE: 24-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: S110-X ROBIN M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: 38,304
REFERENCE/DOCKET NUMBER: 3-461053-2/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELEPATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: 3-461053-2/RFT/RMS
TELEPATION NUMBER: 3-49
TELEPATION SOURCE TO NO: 3:
SEQUENCE CHARACTERISTICS:
LENTH: 5738 base pairs
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Pred. No. 8.6e-08;
0; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                            Sequence 3, Application US/08685467
Patent No. 6060059
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            4431 ccaccaccgctaaggtgacc 4450
                                                         2741 CAGGTACAACAACGGTAACC 2760
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Best Local Similarity 66.4%
Matches 93; Conservative
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STRANDEDNESS: unknown
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; MOLECULE TYPE:
US-08-685-467-3
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Query Match
Best Local S
Matches 60
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0
                                                                                                                                        Length 1797;
                                                                                                                                        Score 60.2; DB 4; Length 1
Pred. No. 7.9e-07;
0; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08478370
Patent No. 5808024
GENERAL INFORMATION:
APPLICANT: SASAKI, Ken
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: KIELN, MICHEL H. MICHEL H. MICHEL H. MICHEL OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER TITLE OF INVENTION: MEMBRANE PROTEIN OF MORAXELLA NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,370
FILING DATE: 07-JUN-1995
AMPLORALY ASSERTED TO THE PROBLEM OF THE PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-502
TELECOMMUNICATION INFORMATION:
                                                                                                                                        0.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 4:
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Best Local Similarity 52.13
Matches 134; Conservative
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COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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TYPE: nucleic acid
STRANDEDNESS: single
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; LOCATION: (1)..(1794)
US-09-377-155-12
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     Length 60;
0.9%; Score 60; DB 1; Lallarity 100.0%; Pred; No. 8.9e-08; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michard Paul
APPLICANT: JENNINGS, Michard
ITILE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 06504/0128
CURRENT PELING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR APPLICATION NUMBER: GB 9726398.2
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Patent No. 6197312
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILLE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
                                                                                                                                                                                                                                                                                       ; Sequence 4, Application US/09377155; Patent No. 6197312
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SOFTWARE: PatentIn Ver. 2.0
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; LOCATION: (1)..(1794)
US-09-377-155-4
                           1 Similarity
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Search completed: September 12, 2001, 12:51:16 Job time: 698 sec
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Best Local Similarity 51.4%; Pred. No. 6.3e-06;
Matches 132; Conservative 0; Mismatches 125; Indels
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Pred. No. 6.3e-06;
0; Mismatches 125; Indels
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CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-13
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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Patent No. 6197312
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anseln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Neisseria meningitidis
                                                                                                                                                                           TYPE: DNA ORGANISM: Nelsseria meningitidis
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Best Local Similarity 51.4%;
Matches 132; Conservative
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; LOCATION: (1)..(1773)
US-09-377-155-10
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; LOCATION: (1)..(1767)
US-09-377-155-18
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US-09-377-155-10
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         GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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                                                        OM nucleic - nucleic search, using sw model
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5340 5460 5520 4680 4920 4980 5100 5100 51.60 5220 5280 5400 5400 GGTTGACTTTGTCTCCACTTATGACACCGTCAACTTTGCCGATGGCAATGCCACCACCGC 4440 aggcatcaatgaagacaacgcctttgttaaaggacttgaaaaagccgcttctgataacaa 4381 4501 4561 4741 4741 4801 4921 5101 5341 5401 5461 4441 4621 4621 4681 4681 4801 4861 4861 4921 4981 4981 5041 5041 5101 5161 5161 5221 5221 5281 5281 5341 5401 5461 4441 4501 4561 g QQ Op Op qq Op Db g ò ò QQ ò ά οy δ qq Q οy g οy g οχ Q οy g οy g οy g ργ δ δ ò õ ò

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                                      1 (bases 1 to 6973)
Sasaki,K., Harkness,R.E., Loosmore,S.M. and Klein,M.H.
Nucleic acids encoding high molecular weight major outer
protein of moraxella
Patent: US 5808024-A 1 15-SEP-1998;
Location/Qualifiers
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Sequence 1 from patent US 5808024
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3541 CCGACAAA 3600 aaagcacc 3601 AAGCCGCII 3601 AAGCCGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	9.29
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outer membrane
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Recombinant high molecular weight ma
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CONNAUGHT LABORATORIES LIMITED (CA)
Location/Qualifiers
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Moraxella catarrhalis
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Best Local Similarity 100.0%;
Matches 6972; Conservative 0
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Loosmore, S.M., Sasaki, K., Yang, Y.P. and Klein, M.H.
Recombinant high molecular weight major outer membrane protein
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CONNAUGHT LABORATORIES LIMITED (CA)
Location/Qualifiers
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DEFINITION Sequence 8 from Patent W00107619.  ACCESSION AX079920 6159 bp DNA AX079920.  AX079920.1 GI:13159440  KEYWORDS AX079920.1 GI:13159440  KEYWORDS Woraxella catarrhalis.  ORGANISM Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;  MOTAXELLA CASANCHA: No 6159)  AUTHORS LOOSMORE, S.M., Sasakl, K., Yang, Y.P. and Klein, M.H.  REFERENCE 1 (bases 1 to 6159)  AUTHORS LOOSMORE, S.M., Sasakl, K., Yang, Y.P. and Klein, M.H.  RECOMBINAL PATENTE MO 1007619 A 8 01-FEB-2001;  CONNAUGHT LABORATORIES LIMITED (CA)  FEATURES 1. 6159  AUTHORS COUNT 2035 a 1386 c 1385 g 1353 t  ORIGIN  AX079920.1 GI:13159440  FATTLE MOTAXELLA CATARCHA!  AV079920.1 GI:13159440  FEATURES 1. 6159  AUTHORS 1. 6159  AUTHORS 1. 6159  AUTHORS 1. 6159  AUTHORS 2035 a 1386 c 1385 g 1353 t	Duery Match  58.8%; Score 4101.6; DB 10; Length 6159; Best Local Similarity 81.3%; Pred. No. 0; Matches 5063; Conservative 0; Mismatches 1009; Indels 156; Ga 542 atgaatcacatctataaagtcatcttaaacaagccacaggcacattatggcagtga 1	DD 121 GTACGACTCTAAAGCTTTGCCCGCACTGCTGTCTCGTGATCGTTGGTT 297  QY 836 ALGGGGATAAACAACGCTGAAAGGCGATGCCTAGCGACGTGAAGCATCCATTGGTT 297  QY 836 ALGGGTGATAAACAACGCTGAAAGGCGATGCCTAGCGACGGTGATCGGTAGATCGTAAACAAAAACCAAAAGGCACAAGCTTGATCGTATCGGTAGTCGTAAAAACCAAAAACAAAC	956 gccatcggtggtgatgtaaaggtagtgatgcctcgattgccatcggtagtgatgacgccatcggtgatgatgatgatgatgatgatgatgatgatgatgatg

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5231 gatgacaaaggcgtcttttgtagactcaagcggtcaagccaaagcaaacacccctgtg 5290	1981 aaagacggcaacgctaacggcatttaagcaatgtttgggtcaaaacccaaaagatggc 565 [11111111111111111111111111111111111	2221 GATGGCAATCAGGAGCTGTGTTHININININININININININININININININININI	6011 atcggcgacccaagcactgttaaggctgataacagttacagtgtggtaata [111111111111111111111111111111111	6191 caagccaaaaaatctgacggcacagcaggtacaaccacagcaggtgcaaccggtacg 6250
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28; .xella. | bases 1 to 6942) | smore,S.M., Sasaki,K., Yang,Y.P. and Klein,M.H. | smore,S.M., Sasaki,K., Yang,Y.P. and Klein,M.H. 0199 6490 2940 2880 gocaaatcccacagcacggggggggggtagctgtgctacaggggcaagttggcagt 661 37.1%; Score 2590; DB 10; Length 6942; 66.9%; Pred. No. 0; Live 0; Mismatches 1105; Indels 1269; Gaps ygcagtgettatgeteaaaaaaaagataceaaacatategeaattggtgaacaa 781 22-FEB-2001 xella catarrhalis. xella catarrhalis eria; Proteobacteria; gamma subdivision; Moraxellaceae; agccagttgtacaaagccacccaaagcattgccaacgcaaccaatgagcttgac PAT 1. .6942 /organism="Moraxella catarrhalis" /db\_xref="taxon:480" / 1621 c 1564 g 1471 t nt: WO 0107619-A 10 01-FEB-2001; AUGHT LABORATORIES LIMITED (CA) Location/Qualifiers 9922 6942 bp DNA ence 10 from Patent WO0107619. 9922 9922.1 GI:13159441 acttttaa 6685 CACTTTAA 3135 Conservative ilarity æ 286

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2401 GGCGATCAATCCATCGCTACGGTACAGGCAATGTGGTAGCAGGTAAG
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Berthet, F.X., Dalemans, W.L., Denoel, P., Dequesne, G.S., Lobet, Y.S., Poolman, J.S., Thiry, G.S., Lhonnard, J.S. and Genetically engineered bleb vaccine
Patent: WO 0103350-A 52 08-FEB-2001;
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ASKTYVKEGNNITVEEAADGSRYTVARDYGTKDVKFDSVVAGGTKIDANGLIFYDDOG

TKIDNTPSISKTGIDAGNVYTNVQNGNIAKDSKDAVNGGQLPAGGEGVKNIIGGDTT
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YTVATAKEVTFDKTTVGSVVTDKNTNDITGLSNKTLGGDNFAKNGRAASEEQLNATQT
NLATLLGGNAQNTNGNVAMTDIGGTGKNNINDAIKASRNEVKOGKNMVVTPTTGANGQ
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GTYVNADEAVRSALTAGSTTKEINAKETTDNKYYIEASNTVALGTRALATQLAAVAIG
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COMplement (6493...7833)
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/gene="PM1571"
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/codon_start=1
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                              AE006194 10533 bp DNA BCT 08-MAR-2001
Pasteurella multocida PM70 section 161 of 204 of the complete
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                                                                                                                                                                                                                                                    Pasteurella multocida.
Pasteurella multocida
Bacteria; proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
1 (bases 1 to 10533)
May B.J., Zhang,Q., Li,L.L., Paustian,M.L., Whittam,T.S. and Kapur,V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete genomic sequence of Pasteurella multocida, Pm70 Proc. Natl. Acad. Sci. U.S.A. 98 (6), 3460-3465 (2001) 21145866
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/gene="yfkJ"
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/transl_table=11
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AE006194.1 GI:12721958
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91. .804
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Zhang,Q. and Kapur,V.
Direct Submission
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EDSLDQTHSYYDOMDWEKYISAEORNLAYLKETVRAIYAALLETEEAVSKKFGLATF
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2124 c 2065 9 3349 L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tch 1.4%; Score 97; DB 1; Length 10533; al Similarity 56.0%; Pred. No. 3.3e-10; 209; Conservative 0; Mismatches 155; Indels
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N Pasteurella multocida mapA gene.
AJ277635 1 GI:10945096
MapA protein.
                                                                                                                                                                                                                                                                                                                                               /protein_id="AAK03658.1"
/db_xref="GI:12721967"
                                                                                                                                 /protein_id="AAK03657.1"
/db_xref="GI:12721966"
                                                 complement(8810. .9262)
                                                                                                                                                                                                                                               /Journel PM1574"
9420. 10412
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/codon_start=1
/transl_table=11
complement(8810.
                                                                                /codon_start=1
/transl_table=11
                                                                                                                   /product="AsnC"
                                                                                                                                                                                                                                                                                                                                   /product-"AsnA"
                 /gene="asnC"
/note="PM1573"
                                                                                                                                                                                                                9420. .10412
/gene="asnA"
                                                                   /gene="asnC
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Best Local S
Matches 209
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VERSION
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/ Transl_dab_pilotein"
// product="MapA pilotein"
// product="MapA pilotein
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NATLLGGAROQNTNGNVAANTDIGGTRKNINDRINSTRASRNEWSKOKOKVYTPTTGANGO
TIYEVATADKVAFDRVGGTTIDATTNKISGIAKGDI SENSTDAVNGSQLYELLQOKI
AKSGDNYNILNNRINKVDKDLRAGIAGANAAGLPQAYIPGKSWVAVAAGTYKGONAI
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Pasteurella multocida.
Pasteurella multocida
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (25-APR-2000) Henderson I.R., Center for Vaccine
Development, University of Maryland School of Medicine, 685
Baltimore St, MD 21202, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6388 caaagccacccaaagcattgccaacgcaaccaatgagcttgaccat-----cgtat
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                                                                                                                                 l (bases 1 to 3900)
Henderson, I.R., Nataro, J.P., Cappello, R. and Steln, C.
Evolutionary origins of the autotransporter proteins
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="putative autotransporter protein"
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Pred. No. 1.2e-09;
0; Mismatches 153;
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/organism="Pasteurella multocida"
/strain="PMYO"
/db_xref="taxon:747"
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                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 3900)
Henderson, I.R.
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                                                           BASE COUNT
ORIGIN
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1 (bases 1 to 3700)
Barenkamp, S.J. and St Geme, J.W. 3rd.
Identification of a second family of high-molecular-weight adhesion proteins expressed by non-typable Haemophilus influenzae
MOI. Microbiol. 19 (6), 1215-1223 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTNVTFASGNGTTATVTNGTDGITVKYDAKVGDGLKLDGDKIAADTTA_TVNDGKNAN
NPKGKVADVASTDEKKLVTAKGLVTALNSLSWTTTAAEADGGTLDGNASEQEVKAGDK
VTFKAGKNLKVKQEGANFTYSLQDALTGLTSITLGTGNNGAKTEINKDGLTITPANGA
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DKVTTTFVKTDVELPLTQIYNTDANGKKITKVVKDGQTKWYELNADGTADMTKEVTLG
NVDSDGKKVVKDNDGKWYHAKADGTADKTKGEVSNDKVSTDEKHVVSLDPNDQSKGKG
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DLTTGQPKLKDGNTVAAKYQDKGGKVVSVTDNTEATITNKGSGYVTGNQVADAIAKSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MNKIFNVIWNVVTQTWVVVSELTRTHTKCASATVAVAVLATLLS
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EDNTAATVGNLRKLGWVLSSKNGTRNEKSQQVKHADEVLFEGKGGVQVTSTSENGKHT
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TVHLNGIGSTLTDTLVGSPATHIDGGDQSTHYTRAASIKDVLNAGWNIKGVKAGSTTG
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KANKETNKVDGANATEDADEGKGLVTAKDVIDAVNKTGWRIKTTDANGQNGDFATVAS
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                                                                                                                                                     St.
                                                                                                                                                                                                                                                                                                                          HIU38617 3700 bp DNA BCT 21-MAR-1996
Haemophilus influenzae adhesin (hia) gene, complete cds.
U38617
2 (bases 1 to 3700)
Barenkamp, S.J.
Direct Submission
Bubmitted (16-OCT-1995) Stephen J. Barenkamp, Pediatrics, S
University School of Medicine, 1465 South Grand Boulevard,
Louis, MO 63104-1095, USA
Location/Qualifiers
                                                                                                                                 /standard_name="Haemophilus influenzae adhesin"
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/strain="Nontypeable strain 11"
/db_xref="taxon:727"
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/db_xref="G1:1235666"
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/transl_table=11
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/gene="hia"
251. .3547
/gene="hia"
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VERSION
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AUTHORS
TITLE
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JOURNAL
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REFERENCE
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SOURCE
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ALAASQLPQATMPGKSMVAIAGSSYQGQNGLAIGVSRISDNGKVIIRLSGTTNSQGKT
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                                                                                                                                                                                                                                                                                                                                                                            encoding
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The present invention describes an isolated and purified nucleic acid (I) that encodes a 200 kba outer membrane protein of Moraxella catarrhalis. The 200 kba outer membrane protein (II) has antibacterial activity and can be used in vaccines. (II), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarrhalis infections, particularly otitis media in humans. (II) is also used as antigen in immunoassays for detecting specific antibodies (Ab), and to generate Ab. (I) are used for recombinant production of (II) and its fragments are used as probes for identifying/cloning 200 kba protein genes from other strains, and for diagnostic detection of M. catarrhalis. (I) makes possible production of large amount of recombinant immunogens. (I) makes possible production of large amount of recombinant immunogens. (I) makes possible production of large amount of recombinant immunogens. (I) makes possible production of III) reduces toxicity of the protein towards the Escherichia coll host. The present sequence represents the constitution of the protein constitution of structure and the protein constitution of structure and the scherichia coll host. The present sequence represents the constitution of the protein constitution of the constitution of the protein constit exemplification of the present invention. 247pp; 3A-W; Fig ï Claim 

C; 1532 G; 1620 T; 0 other Sequence 6972 BP; 2265 A; 1555

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that encodes a 200 kba outer membrane protein of Moraxella catarrhalis. The 200 kba outer membrane protein (II) has antibacterial activity and can be used in vaccines. (II), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarrhalis antifections, particularly otitis media in humans. (II) is also used as antigen in immunoassays for detecting specific antibodies (Ab), and to generate Ab. (I) are used for recombinant production of (II) and its fragments are used as probes for identifying/cloning 200 kba protein genes from other strains, and for diagnostic detection of M. catarrhalis. (I) makes possible production of large amount of recombinant immunogens. Expression of truncated versions of (II) reduces toxicity of the protein towards the Escherichia coll host. The present sequence represents the M. catarrhalis strain 4223 immodaRMBLS clone 200kba gene, which is used in the exemplification of the present invention.

present invention describes an isolated and purified nucleic acid (I)

3; Fig 2A-W; 247pp; English.

Example

New nucleic acid encoding Moraxella catarrhalis outer membrane protein, useful in protective vaccines and for diagnosis

Ψ Klein

Υ, Yang

Sasaki K, LAB

Loosmore SM,

CONNAUGHT

2001-159722/16.

P-PSDB; AAB69133

26-JUL-2000; 2000WO-CA00870.

99US-0361619

27-JUL-1999;

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99.8%; Score 6961; I
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iive 0; Mismatches
Query Match 99.8
Best Local Similarity 100.
Matches 6972; Conservative
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200kDa outer membrane protein; antibacterial; immunogenic; infection;
otitis media; detection; ds.
                                                                                                                                                                                                                                                                                      catarrhalis strain 4223 lambdaEMBL3 clone 200kDa gene SEQ ID
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240 240 300 300 360 360 420 420 480

catarrhalis

WO200107619-A1

1;

Gaps

1;

Sequence 6973 BP; 2265 A; 1555 C; 1533 G; 1620 T; 0 other;

ttaaggtaaaccac 540                  ttaaggtaaaccac 540	tttatggcagtggc 600                tttatggcagtggc 600	agggcaagttggca 659                  agggcaagttggca 660	cgtgatcggtgcaa 719 	cgcaattggtgaac 779 	agccattgctattg 839                   agccattgctattg 840	tagtaataaaactg 899                   tagtaataaaactg 900	agagtccatcgcca 959 	gtagtgatgacttac 1019 	tgattaacgatctta 1079                   tgattaacgatctta 1080	atgatgtaaaatata 1139 	tgtcatatgcacagg 1199 	cctattccttggcag 1259 	gttctgatgcaacat 1319 	agctacagggcagta 1379 	ctagaccggcctata 1439 	atacgaaggcgggtc 1499 	teggtgcaggtgtta 1559                   teggtgcaggtgtta 1560
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                                                                                                                                                                                                                                                                                                                                                           media strain 4223 includes the coding region for a 1992-amino acid protein (W04505) identified as an approx. 200 kDa outer membrane protein (OMP). The DNA was isolated from a strain 4223 genomic library in phage lambda BMBL3 by screening with an anti-200 kDa protein guinea pig antiserum. The gene can be used for the recombinant expression of the OMP (for use in procedure), for the preps. of hybridisation probes, or may be
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                                                                             immunogen; vaccine; otitis media;
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Best Local Similarity 100.0%; Pr
Matches 6970; Conservative 0;
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          BP.
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          DNA;
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          AAT38740 standard;
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The present invention describes an isolated and purified nucleic acid (I) that encodes a 200 kba outer membrane protein of Moraxella catarhalis. The 200 kba outer membrane protein of Moraxella catarhalis. The 200 kba outer membrane protein (II) has antibacterial activity and can be used in vaccines. [II), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarhalis infections, particularly offitis media in humans. [II] is also used as antigen in immunoassays for detecting specific antibodies (Ab), and to generate Ab. (I) are used for recombinant production of (II) and its fragments are used as probes for identifying/Cloning 200 kba protein genes from other strains, and for diagnostic detection of M. catarhalis. (I) makes possible production of large amount of recombinant immunogens. Expression of truncated versions of (II) reduces toxicity of the protein towards the Escherichia coil host. The present sequence represents the M. catarhalis M56 200kba gene in pk8348, which is given in the
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200kDa outer membrane protein; antibacterial; immunogenic; infection;
otitis media; detection; ds.
tgccattgaccaaaaatgaccgatttatcccgaaaatttctgattatgatccgttgacc
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m SEO}$ sednence coding arrhalis strain 4223; major outer nembrane protein; antibacterial; in detection; ds. 200kDa strain 4223 genomic BP 6144 entry) atgatccgttgacctgca ||||||||||||||||||||||atgatccgttgacctgca DNA; Moraxella catarrhalis 200kDa outer membrane otitis media; detectio catarrhalis (first standard; catarrhalis 24-APR-2001 AAF59103 5942 6348 5642 6408 8889 5462 5522 6288 5582 5702 6468 5762 6528 5822 6588 5882 6648 6708 6002 6768 6062 6828 6122 6182 6948 6242 6168 6228

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The present invention describes an isolated and purified nucleic acid (I) that encodes a 200 kDa outer membrane protein of Moravella catarrhalis. The 200 kDa outer membrane protein of Moravella catarrhalis. Can be used in vaccines. [II), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarrhalis infections, particularly ottis media in humans. (II) is also used as antigen in immunoassays for detecting specific antibodies (Ab), and to generate Ab. (I) are used for recombinant production of (II) and its fragments are used as probes for identifying/cloning 200 kDa protein genes from other strains, and for idagnostic detection of M. catarrhalis. (I) makes possible production of large amount of recombinant immunogens. Expression of truncated versions of (II) reduces toxicity of the protein towards the Escherichia coli host. The present sequence represents the M. catarrhalis strain 4223 genomic 200kDa coding sequence, which is given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                     New nucleic acid encoding Moraxella catarrhalis outer membrane protein, useful in protective vaccines and for diagnosis
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Sequence 6144 BP; 2014 A; 1403 C; 1399 G; 1328 T; 0 other;

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Query Match 85.8 Best Local Similarity 100. Matches 5979; Conservative

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that encodes a 200 kba outer membrane protein of Moraxella catarrhalis. The 200 kba outer membrane protein of Moraxella catarrhalis. The 200 kba outer membrane protein (II) has antibacterial activity and can be used in vaccines. (II), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarrhalis infections, particularly otitis media in humans. (II) is also used as antigen in immunoassays for detecting specific antibodies (Ab), and to generate Ab. (I) are used for recombinant production of (II) and its fragments are used as probes for identifying/cloning 200 kba protein genes from other strains, and for diagnostic detection of M. catarrhalis. (I) makes possible production of large amount of recombinant immunogens. Expression of truncated versions of (II) reduces toxicity of the protein M. catarrhalis strain 4223 lambdaEmBh3 clone 200kba coding sequence, which is used in the exemplification of the present invention.
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                            gagettgaccategtatecaceaaaaegaaaataaggeeaatgeagggattteateageg
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P-PSDB; AAB69133.
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toggtgtggtaaaagaggctgataatagtggtctgaaagttaaacttgctaaaact 177 [1] [1] [1] [1] [1] [1] [1] [1] [1] [1]	argoagaaacaacagcagcaatcggcactactcgtattaccagagataaaattggc Ii cccgagatggtgatgttgatgaaaaacaagcaccatatttggataaaaaacaactt 20 	grtaagagtggcaatgttaccgccccaacttacaacattggcgtgaaaaccaccgag 2:	
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3181 gtgacaggcgaagatttatgatttaaaaaccgaacttgaaaacaaaatcagcagtact 3240 3947 gccaaaacagcacaaaactcattacacgaattctcagtagcagatgaacaaggtaataac 4006 [	127 gaccaaaacaaagcttaaccacgcctaagctgaccagggtaataataatggcaaagc 418	4307 gaagacaaaacccgtgccgccagcattgttgatgtgctaagcgcaggctttaacttgcaa 4366	4487 gatgtcaatgtggatgatacaaccattgaagttaaagataaaaaacttggcgtaaaaacc 4546 [	4667 atccaaactgccaaaggggcaagccaagcgaacaactcagcaggctatgtggatgctgat 4726	gcacattggctcaaatgaatgtcaaatcagtcattaacaaagaacaagtaaatgat 49
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                                                                                          media;
                                                                                                                                                                                                                                     Genomic library; bacteria; human upper airway; otitis
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                                                                                                                                                                                                                                                                                                         Patterson
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              The present invention relates to a Moraxella catarrhalis genomic library comprising of a combination of 41 nucleic acid molecules (see AAR789514 AAR28554). The library has a number of uses described in the specification e.g. is useful for aidentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as otitis media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis
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Page 293-308; 545pp; English.
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towards the Escherichia coli host. The present sequence represents the M. catarrhalls strain Q8 200kDa gene, which is given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                            that present invention describes an isolated and purified nucleic acid (I) that accodes a 200 kDa outer membrane protein of Moraxella catarrhalis. The 200 kDa outer membrane protein (II) has antibacterial activity and can be used in vaccines. (II), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarrhalis infections, particularly otitis media in humans. (II) is also used as artigen in immunoassays for detecting specific antibodies (Ab), and to generate Ab. (I) are used for recombinant production of (II) and its fragments are used as probes for identifying/cloning 200 kDa protein genes from other strains, and for diagnostic detection of M. catarrhalis. (I) makes possible production of large amount of recombinant immunogens. (I) makes protein of large amount of recombinant immunogens.
                                                                                                                                                                                                                                                              nucleic acid encoding Moraxella catarrhalis
ul in protective vaccines and for diagnosis
                                                                                                                                                                              Klein MH
                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 4A-V; 247pp; English
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P-PSDB; AAB69135.
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outer membrane protein,

1015 297 357 781 542 atgaatcacatctataaagtcatctttaacaaagccacaggcacatttatggcagtggca 601 actgicaatggaagcagiitiggalaagalaggiaccgaigciacgggicaagagiccaic ctcagtggcagtgcttatgctcaaaaaaaaaaataccaaacatatcgcaattggtgaacaa ctcaatggcagtgcttatgctcaacaaattactacca---agatcgaaattggtcaaaca aaccagccaagacgotc----aggcactgccaaggcggacggtgatcgagccattgct 836 attggtgaaaatgctaacgcacagggcggtcaagccatcgccatcggtagtagtaataaa 298 tttggtagtcttctaaggcacaaggctctcaagctattgctatcggtagtgtcaaacca Length 6159, Indels 156; DB 22; Score 4101.6; DB 22; Pred. No. 0; ); Mismatches 1009; ; 58.8%; 81.3%; Conservative Similarity 5063; Query Match Best Local S: Matches 5063, 926 121 181 782 602 61 662 722 QC g δ ò g δ ò qq á qq ò a ò δ q

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The present invention describes an isolated and purified nucleic acid (1) that encodes a 200 kba outer membrane protein of Moraxella catarrhalis. The 200 kba outer membrane protein of Moraxella catarrhalis. The 200 kba outer membrane protein (11) has antibacterial activity and can be used in vaccines. [11], and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarrhalis infections, particularly otitis media in humans. (11) is also used as antigen in immunoassays for detecting specific antibodies (Ab), and to generate Ab. (1) are used for recombinant production of (11) and its fragments are used as probes for identifying/cloning 200 kba protein cannot be as probes for identifying/cloning 200 kba protein (1) makes possible production of large amount of recombinant immunogens. Expression of truncated versions of (11) reduces toxicity of the protein cowards the Escherichia coli host. The present sequence represents the M. catarrhalis less 200kba gene, which is given in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding Moraxella catarrhalis outer membrane protein, useful in protective vaccines and for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moraxella catarrhalis strain Q8; major outer membrane protein;
200kDa outer membrane protein; antibacterial; immunogenic; infection;
otitis media; detection; ds.
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P-PSDB; AAB69136.
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                                            Length 6942;
          0 other;
          Ë
                                         Score 2590; DB 22;
Pred. No. 0;
0; Mismatches 1105;
          G; 1471
          BP; 2286 A; 1621 C; 1564
                                          37.1%;
66.9%;
                                                      Best Local Similarity 66.9
Matches 4802; Conservative
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          Sequence
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Db	Qy Db	Qy Dp	Qy Dp	Qy Db	Q.y D.b	Qy	Qy Db	oy Db	Oy Op	δ	QQ	Oy Db	oy Dp	Oy Dp	δ <del>ζ</del>	oy og	δ S	oy dg	Óγ

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                                                                                                                                                                                         agtgccaccagcaccgatgcggtcaatggtagccagttgtacaaagccacccaaagcatt
                                                                                                                                                 gtagcaggtaagcactctggtgccatcggcgacccaagcactgttaaggctgataacagt
                             atcggtgataacgcacaagccacgggcgatcaatccatcgccatcggtacaggcaatgtg
                                                                                                                                                                                                                                                                                               M. catarrhalis strain 4223 200kDa partial nucleotide sequence.
                                                                                                                                                                                                                               BP.
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                                                                                                                                                                                                                                                                   AAF59129 standard; DNA; 720
                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                              Moraxella catarrhalis
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The present invention describes an isolated and purified nucleic acid (I) that encodes a 200 kbs outer membrane protein of Moraxella catarrhalis.

The 200 kba outer membrane protein of Moraxella catarrhalis.

The 200 kba outer membrane protein (II) has antibacterial activity and can be used in vaccines. (II), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarrhalis infections, particularly otitis media in humans. (II) is also used as antigen in immunoasays for detecting specific antibodies (Ab), and to generate Ab. (I) are used for recombinant production of (II) and its fragments are used as probes for identifying/Cloining 200 kba protein genes from other strains, and for identifying/Cloining 200 kba protein genes from other strains, and for diagnostic detection of M. catarrhalis.

(I) makes possible production of large amount of recombinant immunogens. Expression of truncated versions of (II) reduces toxicity of the protein towards the Escherichia coli host. The present sequence represents a moral strains and strains and sequence represents a moral sequence.
                                                                                                                                                                                                                          New nucleic acid encoding Moraxella catarrhalis outer membrane protein, useful in protective vaccines and for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 720 BP; 201 A; 142 C; 140 G; 237 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used in an example from the present invention.
                                                                                                     Klein MH
                                                                                                                                                                                                                                                                                                           Example 14; Fig 17; 247pp; English.
                                                                                                     Yang Y,
99US-0361619.
                                                  (CONN-) CONNAUGHT LAB LTD
                                                                                                  Sasaki K,
                                                                                                                                                     2001-159722/16.
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                                                                                                     Loosmore SM,
27-JUL-1999;
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 Length 720;
                      Indels
 Score 720; DB 22;
Pred. No. 1.3e-176;
                        .;
0
                      0; Mismatches
 10.3%; ; 100.0%;
Query Match 10.3
Best Local Similarity 100.
Matches 720; Conservative
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BP. AAF91426 standard; DNA; 1000 AAF91426; AAF91426

(first entry)

04-MAY-2001

Moraxella catarrhalis omp106 gene upstream sequence, SEQ ID:52.

Modified Gram-negative bacterium; outer membrane vesicle; bleb; vaccine; genetically modified; protective antigen expression; LPS detoxification; LPS; lipid A; homologous recombination vector; immunisation; immunoprotective; non-toxic; paediatric; ds

Moraxella catarrhalis

WO200109350-A2.

08-FEB-2001.

31-JUL-2000; 2000WO-EP07424.

99GB-0018319 03-AUG-1999; (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

Lobet Y; Feron C, ο, Dequesne ď Denoel P, Dird J, Voet Thonnard J, Dalemans WLJ, Thiry G, Thonn FJ, J, Berthet Poolman 

WPI; 2001-138654/14.

New isolated polynucleotide useful for outer membrane vesicle preparation from Gram-negative bacterial strain for vaccination of useful for microbial infections -New isolated

Claim 46; Page 90; 128pp; English.

The invention relates to a genetically-engineered outer membrane vesicle
(bleb) preparation from a Gram-negative bacterium for use as a vaccine.
The blebs of the invention are improved with respect to their
contains the invention are improved with respect to their
contains the invention are improved with respect to their
changes to the chromosome of the bacterium from which the blebs are
derived. The changes made include the upregulation of protective antigen
expression, and genetic changes which result in detoxification of the
capression, and genetic changes which result in detoxification of the
chromopasses modified Gram-negative bacterial strains from which the bleb
preparations are made, a vector suitable for performing recombination
concepts of lippoplysaccharide (LPS). The invention is useful
concepts and non-toxic Gram-negative bleb, ghost, or killed whole
cell vaccine suitable for paediatric use. The bleb preparation is useful
immunoprotective and non-toxic Gram-negative bleb, ghost, or killed whole
call vaccine suitable for paediatric use. The bleb preparation is useful
concepts the manufacture of a medicament for immunishing human host against a
disease caused by infection of one or more of the following:
meningitidis, Neisseria gonorrhoeae, Haemophilus influenza, Moraxella
catarrhalis, Pseudomonas aeruquinosa, Chlamydia trachomatis, and Chlamydia
preumonia. The invention may also be used to provide immunisation against
the influenza virus. Bacterially derived nucleotide sequences of the
invention are used in the performance of homologous recombination events

for

il nucleic acid encoding Hemophilus influenzae adhesin protein, f as antigens and vaccines and for treating Hemophilus influenzae

Claim 1; Fig 21; 275pp; English.

infection

Novel

¥.

Klein

Yang Y,

Loosmore SM,

2000-618897/59.

P-PSDB; AAB23857

16-MAR-2000; 2000WO-CA00289.

21-SEP-2000

99US-0268347

16-MAR-1999;

(CONN-) CONNAUGHT LAB

us-09-361-619-5.rng

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   either
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up to 1000 bp upstream of a bacterial chromosomal gene in order to eithe increase or decrease expression of that gene. Immunoprotective and non-toxic Gram-negative bleb, ghost, or killed whole cell vaccines are more immunogenic, less toxic and safer, and are particularly useful for paediatric use. The present sequence represents a specifically
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                                                                                                               DB 22; Length 1000;
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                                                                                                                                     Indels
                                                                               Sequence 1000 BP; 287 A; 233 C; 174 G; 306 T; 0 other;
                                                         claimed Moraxella catarrhalis nucleic acid sequence
                                                                                                               Score 426.8; DB 22
Pred. No. 1.7e-100;
0; Mismatches 7;
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                                                                                                               Query Match 6.1%;
Best Local Similarity 91.9%;
Matches 509; Conservative (
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The present sequence represents a Haemophilus influenzae adhesin (Hia) gene from the non-typeable Haemophilus influenzae (NTH1) strain M407. Hia genes and proteins have antiinflammatory, auditory and antibacterial activities, and proteins have antiinflammatory, auditory and antibacterial activities, and can be used in the production of a vaccine. An immunogenic composition comprising an Hia gene, a polypeptide encoded by an Hia gene, or a recombinant Hia polypeptide is useful for inducing protection against disease caused by Haemophilus strains in a susceptible host, preferably a human. An Hia protein is useful as an antigen, in immunogenic preparations including vaccines, as a carrier for other immunogens, and in the generation of diagnostic reagents. Hia is useful for treating diseases caused by the infection of Haemophilus influenzae such as meningitis, epiglottitis, septicaemia and otitis media. Recombinant production of Hia favours high recovery of the protein compared to the low recovery of native protein from Haemophilus influenzae species. A truncated protein has a significantly higher
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Pred. No. 6.1e-28;
); Mismatches 190;
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Hia genes and proteins have antiinflammatory, auditory and antibacterial activities, and can be used in the production of a vaccine. An immunogenic composition comprising an Hia gene, a polypeptide encoded by an Hia gene, or a recombinant Hia polypeptide is useful for inducing protection against disease caused by Haemophilus strains in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 influenzae such as meningitis, epiglottitis, septicaemia and otitis media. Recombinant production of Hia favours high recovery of the protein compared to the low recovery of native protein from Haemophilus
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                                                                                                                                                                                                                                                                                   Hia; adhesin; Haemophilus influenzae adhesin; NTHi; infection; vaccine; non-typeable Haemophilus influenzae; antiinflammatory; auditory; antibacterial; meningitis; epiglottitis; septicaemia; otitis media; diagnosis; immunogenic; antigen; ds.
Novel nucleic acid encoding Hemophilus influenzae adhesin protein, fuse as antigens and vaccines and for treating Hemophilus influenzae infection
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                                                                                                                                                            AAA92493 standard; DNA; 3036 BP.
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Hia; adhesin; Haemophilus influenzae adhesin; NTH1; infection; vaccine; non-typeable Haemophilus influenzae; antiinflammatory; auditory; antibacterial; meningitis; epiglottitis; septicaemia; otitis media;
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                                2615 tttgccggtgcaacggcgcacggtgcggtttctgtcggcgaagcggcgaagaagacgt
                                                                                                        2675 atccaaaacgttgcggcaggcgaatttccgctacttccaccgatgcgattaacggcagc
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tttgctggacaaacggcggttggtgcggtctccgtgggtgcctcaggtgctgaacgccgt
                                                                        atccaaaatgtggcagcaggtgaggtcagtgccaccagcaccgatgcggtcaatggtagc
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P-PSDB; AAB23858.
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3023 tggtaa 3028
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Gaps

12;

Score 146.4; DB 21; Length 3036; Pred. No. 1.6e-27; 0; Mismatches 191; Indels 12;

2.1%; 58.2%;

Best Local Similarity 58.2 Matches 283; Conservative

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Query Match

6200 aaatctgacggcacagcaggtacaaccaccacagggtgcaacggtacggttaaaggc 6259

diagnosis; immunogenic; antigen; ds.

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His genes and proteins have antilnflammatory, auditory and antibacterial activities, and can be used in the production of a vaccine. An activities, and can be used in the production of a vaccine. An immunogenic composition comprising an His gene, a polypeptide encoded immunogenic composition comprising an His gene, a polypeptide encoded protection against disease caused by Heemophilus strains in a susceptible host, preferably a human. An His protein is useful as an antigen, in immunogenic preparations including vaccines, as a carrier for corber immunogens, and in the generation of diagnostic reagents. His is useful for treating diseases caused by the infection of Haemophilus influenzae such as meningitis, epiglottitis, septicaemia and otitis media. Recombinant production of His favours high recovery of the protein compared to the low recovery of native protein from Haemophilus influenzae species. A truncated protein has a significantly higher amount of recovery than a full-length protein.
                                                                                                                                                                                                                                                                                                                                                                                                       1;
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from the non-typeable Haemophilus influenzae (NTHi) strain K9
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The present sequence represents a Haemophilus influenzae adhesin (Hia)

gene from the non-typeable Haemophilus influenzae (NTHI) strain K22.

His genes and proteins have antiinflammatory, auditory and antibocterial
activities, and can be used in the production of a vaccine. An
immunogenic composition comprising an Hia gene, a polypeptide encoded
by an Hia gene, or a recombinant Hia polypeptide is useful for Inducing
protection against disease caused by Haemophilus strains in a
susceptible host, preferably a human. An Hia protein is useful as an
antigen, in immunogens, and in the generation of diagnostic reagents. His
for other immunogens, and in the generation of diagnostic reagents. His
is useful for treating diseases caused by the infection of Haemophilus
influenzae such as mendingitis, epiglottitis, septicaemia and ottitis
media. Recombinant production of Hia favours high recovery of the
protein compared to the low recovery of native protein from Haemophilus
influenzae species.
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Best Local Similarity
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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                        APPLICANT: Loosmore, Sheena M.
APPLICANT: Sasaki, Ken
APPLICANT: Sasaki, Ken
APPLICANT: Hang, Yan Ping
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIG
TITLE OF INVENTION: PROTEIN OF MORAXELLA
FILE REPRENCE: 1038-921MIS: 1b
CURRENT APPLICATION NUMBER: US/09/361,619
CURRENT FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver
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                                                                                                                                                                        ; Score 6972; C; Pred. No. 0; 0; Mismatches
ALIGNMENTS
                                                                                                                                             catarrhalis
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GENERAL INFORMATION:
APPLICANT: SAGAKI, Ken
APPLICANT: HARKNESS, Robin E.
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER
TITLE OF INVENTION: MEMBRANE PROTEIN OF MORAXELLA
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US/08/483,855
FILING DATE: 07-UNV-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/431,718
FILING DATE: 01-MAy-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-503
TELECOMMUNICATION INFORMATION:
                                                                                                                          COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 6973 base pairs
TYPE: nucleic acid
ADDRESSEE: Sim & McBurn
STREET: Suite 701, 330
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                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 6972; Conserv
                                                         COUNTRY: Canada
ZIP: M5G 1R7
                                               Ontario
                            Toronto
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481 C	541 c 541 C	601 a   601 A	660 g   661 G	720 c     721 C	780 a     781 A	840 g	900 t 901 T	960 to	1020 a	1080 t	1140 g	1200	1260 1	1320 (	80	1440	1500	1560
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     APPLICANT: SASAKI, KEN
APPLICANT: HARKNESS, Robin E.
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER
TITLE OF INVENTION: MEMBRANE PROTEIN OF MORAXELLA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                             ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
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100.0%; Pred. No. 0;
ive 0; Mismatches
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REGISTRATION NUMBER: 24,973
REFENDE/DOCKET NUMBER: 1038-587
TELEPHONE: (416, 595-1153
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APPLICATION NUMBER: US 08/478,370
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/621,944
FILLING DATE: 26-MAR-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
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Best Local Similarity 100.
Matches 6972; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
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708..6683
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CITY: Toronto
STATE: Ontario
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US-08-621-944-1
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APPLICANT: HARKNESS, Robin E.
APPLICANT: HARKNESS, Robin E.
APPLICANT: LOCSWORE, Sheena M.
APPLICANT: LOCSWORE, Sheena M.
APPLICANT: HIGH MOLECULAR WEIGHT MAJOR OUTER
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER
TITLE OF INVENTION: MEMBRANE PROTEIN OF MORAXELLA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIM & MCBUTNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 6972; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           :: Sim & McBurney
Suite 701, 330 University Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,944A
FILING DATE: 26 WAR-1996
CLASSIFICATION NUMBER: US/08/621,944A
FILING DATE: 0.07-010-1995
CLASSIFICATION NUMBER: US 08/478,370
FILING DATE: 0.7-010-1995
GLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
RECISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-587
TELECOMMUNICATION INDER: 1038-587
FELECOMMUNICATION INFORMATION:
METEDIANE: 416,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UMBER: US/08/621,944A
26-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                        ; Sequence 1, Application US/08621944A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6973 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STATE: Ontario
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STRANDEDNESS:
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MOLECULE TYPE:
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; LOCATION:
US-08-621-944A-1
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Qy Db	1320	ctagctcgttgggagcgatagcccttggtgcaggtactcgtgctcagctacagggcagta 13 	379
Qy	1380	ttgccctaggtcaaggttctgttgtcactcagagtgataataattctagaccggcctata 14 	439
oy do	1440	caccaaatacccaggcactagaccccaagtttcaagccaccaataatacgaaggcggtc 14 	1499
Qy Db	1500	cactttccattggtagtaactctatcaaacgtaaaatcatcaatgtcggtgcaggtgtta 15 	1559
Qy	1560	ataaaaccgatycggtcaatgtggcacagctagaagcggtggtgaagtgggctaaggagc 16 	619
Qy	1620	gtagaattacttttcagggtgatgataacagtactgacgtaaaaataggtttggataata 16 	629
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QY	1740	taaaagaggctgataatagtggtctgaaagttaaacttgctaaaactttaaacaatctta 17 	1799
Qy	1800	ctgaggtgaatacaactacattaaatgccacaaccacagttaaggtaggt	1859
Qy Db	1860	gtactacagctgaattattgagtgatagtttaacctttacccagcccaatacaggcagtc 19 	1919
QV	1920	aaagcacaagcaaaacgtctatggcgttaatggggtgaagtttactaataatgcagaaa 19 	9261
Qy	1980 1981	caacagcagcaatcggcactactcgtattaccagagataaaattggctttgctcgagatg 20 	2039
QY Db	2040	gtgatgttgatgaaaaacaagcaccatatttggataaaaacaacttaaagtgggtagtg 20 	2099
Oy Db	2100	ttgcaattaccatagacaatggcattgatgcaggtaataaaaagatcagtaatcttgcca 21 	2159
Qy Db	2160	aaggtagcagtgctaacgatgcggttaccatcgaacagctcaaagccgccaagcctactt 22 	2219
Qy Db	2220	taaacgcaggcgctggcatcagtgtcacacctactgaaatatcagttgatgctaaggtg 22 	2279
οy	2280	gcaatgttaccgccccaacttacaacattggcgtgaaaccaccgagcttaacagtgatg 23	:339-

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                                                                                                                                                                                                                                                      APPLICANT: SASAKI, Ken
APPLICANT: HARKNESS, Robin E.
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER
TITLE OF INVENTION: MEMBRANE PROTEIN OF MORAXELLA
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/945,567 FILING DATE: 19-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATORNEY AGENT INFORMATION:
NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,933
REFERENCE/DOCKET NUMBER: 1038-745 MIS:JD
TELECOMMUNICATION INFORMATION:
TELEFRONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
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Pred. No. (
                                                                                                                                                                                                                                                                                                                                                              CITY: Tolu...
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
~~WPUTER: IBM PC compatible
~~WTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                         Sequence 1, Application US/08945567
GENERAL INFORMATION:
APPLICANT: SASAKI, Ken
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100.0%;
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Best Local Similarity
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; LOCATION:
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Sequence 1, Application US/08945567A

GENERAL INFORMATION:
APPLICANT: SASAKI, Robin E.
APPLICANT: HARKNESS, Robin E.
APPLICANT: HOSWORE, Sheena M.
APPLICANT: CHONG, Pele
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF
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TITLE OF INVENTION: HOR MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN DATE: 1998-03-19
CURRENT FILING DATE: 1998-03-19
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1996-03-26
PRIOR FILING DATE: 1996-03-26
PRIOR FILING DATE: 1996-03-26
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PALCATION NUMBER: 1996-03-26
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SOFTWARE: PALCATION NUMBER: 1996-03 1; OF. 6889 Gaps ccatggatatgggcaggtgtgctcgcctgccgtatgatggcgatgacaccccatttgccc 6541 GTATTGCCACCCACAACGGTCAAGGTGCGGTGGCAGTGGGACTGTCGAAGCTGTCGGATA tytyccattyaccaaaaaatyaccyatttatcccyaaaaatttctyattatyatccyttya Indels 0 DB ö Pred. No. 0; Mismatches Score 6961; 99.00, 100.08; Pre TYPE: DNA ORGANISM: Moraxella catarrhalis

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APPLICANT: HARKNESS, Robin E.
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: CONGY Pele
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR TITLE OF INVENTION: 1038-03-19
FRIOR REING DATE: 1995-05-01
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/478,370
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/621,944
PRIOR APPLICATION NUMBER: 08/621,944
PRIOR APPLICATION NUMBER: PCT/CA96/00264
PRIOR FILING DATE: 1996-04-29
NUMBER: OF SEQ ID NOS: 10
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SEQ ID NO 1
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Pred. No. 0;
0; Mismatches
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; APPLICANT: SASAKI, Ken
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ORGANISM: Moraxella catarrhalis
FEATURE:
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; LOCATION: (708)..(6683)
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APPLICANT: BARKNESS, Robin E.
APPLICANT: HARKNESS, Robin E.
APPLICANT: LOSMORE, Sheena M.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MA
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MA
FILE REFERENCE: 1038-745 MIS
CURRENT APPLICATION NUMBER: US/08/945,567D
CURRENT PILING DATE: 1996-04-29
PRIOR APPLICATION NUMBER: 08/431,718
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/21,944
PRIOR FILING DATE: 1996-04-29
PRIOR FILING DATE: 1996-04-29
NUMBER: PRIOR FILING DATE: 1996-04-29
NUMBER: PRIOR FILING DATE: 1996-04-29
NUMBER: PRIOR FILING DATE: 1996-04-29
NUMBER: PARCH FILING DATE: 1996-04-29 Score 6961; WEIGHT Sequence 1, Application US/08945567D; GENERAL INFORMATION: 99.88; 6972 ; NAME/KEY: CDS ; LOCATION: (708)..(6683) US-08-945-567D-1 ORGANISM: Moraxella Similarity cctdcaddtcdac cctgcaggtcgac Query Match Best Local Simi Matches 6972; 61 61 121 6781 6841 6901 0969 6961 6780 6840 0069 6721

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APPLICANT: LOOSMORE, Sheena M.
APPLICANT: Sasaki, Ken
APPLICANT: Sang, Yan Ping
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEI
TITLE OF INVENTION: PROTEIN OF MORAXELLA
FILE REFERENCE: 1038-921MIS:jb
CURRENT APPLICATION NUMBER: US/09/361,619
CURRENT FILING DATE: 1999-07-27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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                                                                                                                                                                                                                                            ADDRESSEE: Sim & MCBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M56 187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,718
FILING DATE: 01-MAY-1995
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100.0%; Pred. No. 0;
iive 0; Mismatches
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FILING DATE:
CLASSIFICATION: 44.
ATTORNEY/AGENT INFORMATION:
NAME: STEWART. Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-429
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
; INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6975 base pairs
"WPE: nucleic acid
"WPE: nucleic acid
"WPE: nucleic acid
                                                                                                                                    APPLICANT: Sasaki, Ken
APPLICANT: Harkness, Robin E
APPLICANT: Harkness, Robin E
TITLE OF INVENTION: HIGH MOLECULAR WEIG
TITLE OF INVENTION: MEMBRANE PROTEIN OF
NUMBER OF SEQUENCES:
ADDRESSEE: Sim & MCBULNEY
                                                                                                         Sequence 1, Application US/08431718 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 99.5
Best Local Similarity 100.
Matches 6972; Conservative
 6972
                 STRANDEDNESS: Sir
; TOPOLOGY: linear
US-08-431-718-1
6960 cctgcaggtcgac
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                                                                                                                                                                                  STREET: 6th Floor, 330 c...

STREET: Ontario
CITY: Toronto
COMPIRY: Canada
2IP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/431,718A
FILING DATE: 01-MAY-1995
CLASSIFICATION: 424
                                                                                             Sequence 1, Application US/08431718A
GENERAL INFORMATION:
APPLICANT: Sasaki, Ken
APPLICANT: Harkness, Robin E
APPLICANT: Klein, Michel H
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER
TITLE OF INVENTION: MEMBRANE PROTEIN OF MORAXELLA
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.5%; Score 6939; D
100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/COCKET NUMBER: 1038-429
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1165
TELEPHONE: (416) 595-1165
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6975 base pairs
                                  Matches 6972; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-431-718A-1
                                                                                        US-08-431-718A-1
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Local Similarity 100. les 6972; Conservative
                                 RESULT 12
US-08-431-718C-1
; Sequence 1, Application
; GENERAL INFORMATION:
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; ORGANISM: MOTAXELLA
US-08-431-718C-1
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APPLICANT: Robin, Harkness E.
APPLICANT: Robin, Harkness E.
APPLICANT: Loosmore, Sheena M.
APPLICANT: Loosmore, Sheena M.
APPLICANT: Liosmore, Sheena M.
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJ
TITLE OF INVENTION: MORAXELLA
FILE REFRENCE: 1034-429 MIS
CURRENT APPLICATION NUMBER: US/08/431,718C
CURRENT FILING DATE: 1995-05-01
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                99.5%; Score 6939; I
100.0%; Pred. No. 0;
Live 0; Mismatches
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APPLICANT: LOGSMORE, Sheena M.
APPLICANT: Sasaki, Ken
APPLICANT: Sasaki, Ken
APPLICANT: Tang, Yan Ping
APPLICANT: Tang, Yan Ping
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: RECOMBINANT HIGH MOLECU
TITLE REFERENCE: 1038-921MIS:1b
CURRENT APPLICATION NUMBER: US/09/361,619
CURRENT APPLICATION NUMBER: US/09/361,619
SOFTWARE: Patentin Ver: 2:1
SEG ID NOS: 32
SEG ID NOS: 32
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                                                                                                                  Mismatches
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Pred. No. 0
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ilarity 100.0%; Pr
Conservative 0;
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APPLICANT: HARKNESS, Robin E.
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OU
TITLE OF INVENTION: MEBBRANE PROTEIN OF MORAXELLA
NUMBER OF SEQUENCES: 10
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Suite 701, 330 University Avenue
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APPLICATION NUMBER: US/08/621,944
FILING DATE: 26-MAR-1996
CLASSTERICATION DATA:
APPLICATION NUMBER: US 08/478,370
FILING DATE: 07-JUN-1995
FILING DATE: 07-JUN-1995
FILING DATE: 07-JUN-1995
FILING SATE: 07-JUN-1995
FILING SATE: 07-JUN-1995
FILING SATE: 07-JUN-1995
FILING SATE: 07-JUN-1995
TELECOMUNICATION (416) 595-1155
FILECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                              Sequence 2, Application US/08621944 GENERAL INFORMATION:
                                                          STREET: Suite 701, 330 Uniter: Transcript Tr
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STRANDEDNESS: single
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Best Local Similarity
Matches 5976; Conserv
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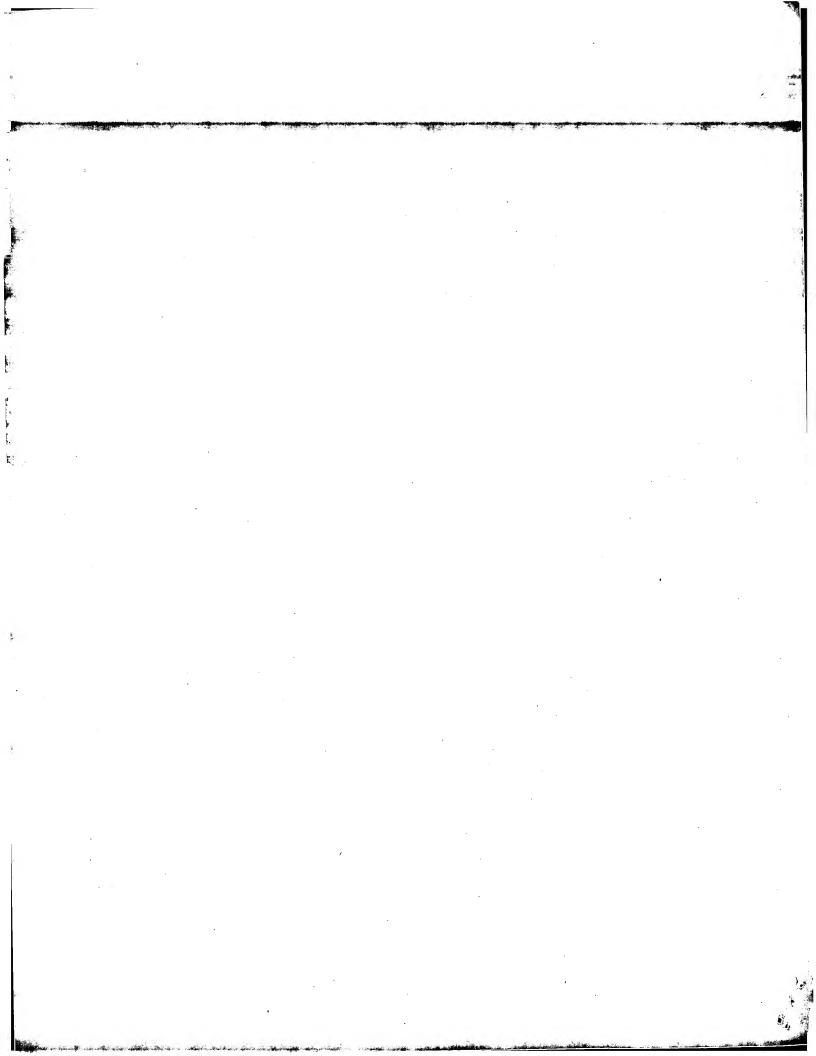
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   Sequence 1313, Ap Sequence 4611, Ap Sequence 2030, Ap Sequence 9, Applia APPLICANT: Sass Sequence 1269, Ap Sequence 1749, Ap Sequence 27947, A Sequence 2714, Ap Sequence 3, Appli Sequence 1359, Ap Sequence 1359, Ap Sequence 1599, Ap Sequence 94636, Ap Sequence 1599, Ap Sequence 1, Appli
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US-09-803-736-1313
US-09-821-710-4611
US-09-803-110-2030
US-09-788-657-12
US-09-803-110-1859
US-09-760-475-1749
US-09-760-475-1749
US-09-760-475-1749
US-09-760-475-1749
US-09-803-736-1375
US-09-803-736-1375
US-09-803-736-1321
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GENERAL INFORMATION:
APPLICANT: Peak, Ian
APPLICANT: Jennings, Michael
TITLE OF INVENTION: MODFIED SURFACE ANTIGEN
FILE REFERENCE: 8795-2401
CURRENT APPLICATION NUMBER: US/09/771,382
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 60/177,917
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.0
SEQ ID NO 18
LENGTH: 1797
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1088 cttatcgcggcgaagccggttacgccatcggctactccagtatttccgacggcggaatt 1147
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1559 acaacencategacaatgtgnaeggeaaegegegngegggnategeecaagegattgeaa 1618
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                                           6489 tggcgtccatgccacaagcctacattcctggcagatccatggttaccggggggtattgcca
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51.4%; Pred. No. 0.0005;
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GENERAL INFORMATION:
APPLICANT: Peak, Ian
APPLICANT: Jannings, Michael
TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
FILE REFERENCE: 8795-2401
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APPLICANT: Jennings, Michael
TILLE OF INVENTION: MODIFIED SURFACE ANTIGEN
FILLE REFERENCE: 8795-2401
CURRENT APPLICATION NUMBER: US/09/771,382
CORRENT FILLING DATE: 2001-01-25
PRIOR FILLING DATE: 2000-01-25
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US-09-771-382-30
Squence 30, Application US/09771382
; GENERAL INFORMATION:
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OTHER INFORMATION: "n" is any nucleotide, synonymous nucleotide or absent nucleotide
OTHER INFORMATION: at a corresponding position in any one of SEQ ID NOS:12-2
US-09-771-382-22
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APPLICANT: Jeanings, Michael
TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
FILE REFERENCE: 8795-2401
CURRENT APPLICATION NUMBER: US/09/771,382
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 60/177,917
PRIOR APPLICATION NUMBER: US 60/177,917
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.0
SEQ ID NO 22
                  APPLICANT: Peak, Ian
APPLICANT: Jennings, Michael
TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
FILE REFERENCE: 8795-2401
CURRENT APPLICATION NUMBER: US/09/771,382
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 60/177,917
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PATCHIN VETSION 3.0
SEQ ID NO 19
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, ORGANISM: Neisseria meningitidis
US-09-771-382-19
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Best Local Similarity 51.8%;
Matches 133; Conservative
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US-09-771-382-22
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APPLICANT: Dennings, Michael
TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
FILE REFERENCE: 8795-2401
CURRENT APPLICATION NUMBER: US/09/771,382
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 60/177,917
PRIOR PILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PATENTIN VERSION 3.0
SOFTWARE: PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                           Sequence 28, Application US/09771382;
GENERAL INFORMATION:
APPLICANT: Peak, Ian
TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
FILE REPERBENCE: 8795-2401
CURRENT APPLICATION NUMBER: US/09/771,382
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 60/177,917
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.0
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; ORGANISM: Neisseria meningitidis
US-09-771-382-28
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US-09-771-382-28
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US-09-771-382-14
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APPLICANT: Jennings, Michael
TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
FILE REFERNCE: 8795-2411
CURRENT APPLICATION NUMBER: US/09/771,382
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 60/177,917
PRIOR APPLICATION NUMBER: US 60/177,917
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
CURRENT APPLICATION NUMBER: US/09/771,382
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 60/177,917
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 52
SOFTWARE: atentin version 3.0
SEQ ID NO 31
LENGTH: 1302
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Sequence 32, Application US/09771382
GENERAL INFORMATION:
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US-09-771-382-31
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US-09-771-382-32
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Pred. No. 0.0006;
0; Mismatches 125; Indels
                                                                                                DB 5; Length 1770;
0.0006;
                                                                                                                                   0; Mismatches 125; Indels
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APPLICANT: Jennings, Michael
APPLICANT: Jennings, Michael
TITE OF INVENTION: MODIFIED SURFACE ANTIGEN
FILE REFERENCE: 8795-2401
CURRENT APPLICATION UNMER: US/09/71,382
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 60/177,917
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEC ID NOS: 52
SOFTWARE: PatentIn version 3.0
                                                                                                      Score 57;
Pred. No.
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US-09-771-382-12
                    ; TYPE: DNA
; ORGANISM: Neisseria meningitidis
US-09-771-382-14
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Best Local Similarity 51.4%;
Matches 132; Conservative (
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Best Local Similarity 51.4%;
Matches 132; Conservative
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US-09-771-382-12
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Pred. No. 0.0006;
0; Mismatches 125; Indels
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Pred. No. 0.0006;
0; Mismatches 125;
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APPLICANT: Peak, Ian
APPLICANT: Jennings, Michael
TITLE OF INVENTION: WODIFIED SURFACE ANTIGEN
FILE REFERENCE: 8795-2401
CURRENT APPLICATION NUMBER: US/09/771,382
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 60/177,917
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin Version 3.0
SEQ ID NO 21
                                                         APPLICANT: Peak, Ian
APPLICANT: Dennings, Michael
APPLICANT: Jennings, Michael
TITLE OF INVENTION: WODIFIED SURFACE ANTIGEN
FILE REFERENCE: 8795-2401
CURRENT APPLICATION NUMBER: US/09/771,382
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 60/177,917
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin Version 3.0
SEQ ID NO 16
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; GENERAL INFORMATION:
US-09-771-382-16
Sequence 16, Application US/09771382
GENERAL INFORMATION:
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, ORGANISM: Neisseria meningitidis
US-09-771-382-21
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Best Local Similarity 51.4%;
Matches 132; Conservative
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Best Local Similarity 51.49
Matches 132; Conservative
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US-09-771-382-21
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APPLICANT: Jennings, Michael
TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
FILE REFERENCE: 8795-2401
CURRENT APPLICATION NUMBER: US/09/771,382
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 60/177,917
PRIOR APPLICATION NUMBER: US 60/177,917
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.0
SEQ ID NO 20
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GENERAL INFORMATION:
APPLICANT: Peak, Ian
APPLICANT: Jennings, Michael
TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
FILE REFERENCE: 8795-2401
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 60/177,917
PRIOR FILING DATE: 2000-01-25
                                                                                                                                                                                                                                                                 TYPE: DNA
CRCANISM: Neisserla meningitidis
US-09-771-382-20
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; ORGANISM: Neisseria meningitidis
US-09-771-382-17
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Best Local Similarity 51.0%;
Matches 131; Conservative C
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SOFTWARE: PatentIn version 3.0
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Matches 131; Conservative
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Pred. No. 0.0015;
0; Mismatches 126; Indels
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APPLICANT: Jennings, Michael
TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
CURRENT APPLICATION NUMBER: US/09/771,382
CURRENT FILING DATE: 2001-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15, Application US/09771382 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Neisseria meningitidis US-09-771-382-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.0
SEQ ID NO 15
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                                                                                                                                                                                                      Sequence 29, Application US/09771382
GENERAL INFORMATION:
APPLICANT: Peak, Ian
APPLICANT: OF INTENTION:
TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
FILE REFERENCE: 8795-2401
CURRENT APPLICATION NUMBER: US/09/771,382
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 60/177,917
PRIOR PAPLICATION NUMBER: US 60/177,917
PRIOR PILING DATE: 2000-01-25
SOFTWARE: Patentin version 3.0
SEQ ID NO 29
LENGTH: 1542
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CRGANISM: Neisseria meningitidis
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Copyright (c) 1993 - 2000 Compugen Ltd.
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The present invention describes an isolated and purified nucleic acid (I) that encodes a 200 kDa outer membrane protein of Moraxella catarrhalis. The 200 kDa outer membrane protein of Moraxella catarrhalis. The 200 kDa outer membrane protein (II) has antibacterial activity and can be used in vaccines. (I), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarrhalis infections, particularly otitis media in humans. (II) is also used as antigen in immunoasays for detecting specific antibodies (Ab), and to generate Ab. (I) are used for recombinant production of (II) and its fragments are used as probes for identifying/cloning 200 kDa protein genes from other strains, and for diagnostic detection of M. catarrhalis. (I) makes possible production of large amount of recombinant immunogens. Expression of truncated versions of (II) reduces toxicity of the protein towards the Escherichia coll host. The present sequence represents the mannification of the account of the protein contains strains, and appendic 200kDa protein, which is given in the exemplification of the present invention. English 247pp; 3A-W; Claim 1; 

AA; 2047 Sequence

ó 120 120 180 180 240 240 300 300 360 360 420 420 480 480 540 540 900 720 Gaps. 9 9 NGHAVLKEIRSSKDNDVKYRRTTASGHASTAVGAMSYAQGHFSNAFGTRATAKSAYSLAV MNHIYKVIFNKATGTFMAVAEYAKSHSTGGGSCATGQVGSVCTLSFARIAALAVLVIGAT LSGSAYAQKKDTKHIAIGEQNQPRRSGTAKADGDRAIAIGENANAQGGQAIAIGSSNKTV GLAATAEGQSTIAIGSDATSSSLGAIALGAGTRAQLQGSIALGQGSVVTQSDNNSRPAYT PNTQALDPKFQATNNTKAGPLSIGSNSIKRKIINVGAGVNKTDAVNVAQLEAVVKWAKER TAAIGTTRITRDKIGFARDGDVDEKQAPYLDKKQLKVGSVAITIDNGIDAGNKKISNLAK GSSANDAVTIEQLKAAKPTLNAGAGISVTPTEISVDAKSGNVTAPTYNIGVKTTELNSDG RITFQGDDNSTDVKIGLDNTLTIKGGAETNALTDNNIGVVKEADNSGLKVKLAKTLNNLT EVNTTTLNATTTVKVGSSSSTTAELLSDSLTFTQPNTGSQSTSKTVYGVNGVKFTNNAET TSDKFSVKGSGTNNSLVTAEHLASYLNEVNRTADSALQSFTVKEEDDDDANAITVAKDTT KNAGAVSILKLKGKNGLTVATKKDGTVTFGLSQDSGLTIGKSTLNNDGLTVKDTNEQIQV ő 22; Length Indels ; DB Score 10303; Pred. No. 0; Mismatches ; 0 100.0%; Best Local Similarity 100. Matches 2047; Conservative Query Match 61 121 121 181 181 241 241 301 301 361 361 481 421 481 541 421 541 601 601 661 661 g qq ò á Db g g ò ò ò Db οy ò Dp ò g δ Q ò Ġ οy qq ò

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Moraxella catarrhalis strain 4223; major outer membrane protein;
200kDa outer membrane protein; antibacterial; immunogenic; infection;
otitis media; detection.
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N-PSDB; AAF59100, AAF59101.
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           Length 1992;
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           DB
  97.3%; Sco. 100.0%; Pred. No. v, 0, Mismatches
Score 10024;
                                     Conservative
                       Similarity
                         Best Local Sim
Matches 1992;
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immunogen; vaccine; otitis media;

kDa outer membrane protein

(first entry)

OMP;

membrane protein;

catarrhalis strain 4223

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Claim 14; Fig 6; 109pp; English.
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                                Moraxella 200
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01-MAY-1995;
07-JUN-1995;
                    25-JAN-1997
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                                AKTAQNSLHEFSVADEQGNNFTVSNPYSSYDTSKTSDVITFAGENGITTKVNKGVVRVGI
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An approx. 200 kDa outer membrane protein (AAW04505) can be isolated from Moraxella catarrhalis otitis media strain 4223 by electroclution, or expressed from a gene (see also AAT38740) obtd. Irom a strain 4223 genomic library. Natural or recombinant outer membrane protein is useful as an immunogen to protect against infection by Moraxella, esp. M. catarrhalis. It can also be used to detect antibodies, esp. for differential diagnosis between bacteria that cause similar symptoms, and also useful as a carrier for other antigens and used to raise antitumour antibodies for conjugation to therapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                 YSLAVGLAATAEGQSTIAIGSDATSSSLGAIALGAGTRAQLQGSIALGQGSVVTQSDNNS
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99.9%; Pred. No. 0;
iive 1; Mismatches
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AAW04505 standard; Protein; 1992 AA.

RESULT AAW04505 ID AAW04

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	LNNLTEVNTTTLNATTTVKVGSSSSTTAELLSDSLTFTQPNTGSQSTSKTVYGVNGVKFT	NNAETTAAIGTTRITRDKIGFARDGDVDEKQAPYLDKKQLKVGSVAITIDNGIDAGNKKI 	SNLAKGSSANDAVŢIEQLKAAKPTLNAGAGISVTPTEISVDAKSGNVTAPTYNIGVKTTE	LNSDGTSDKFSVKGSGTNNSLVTAEHLASYLNEVNRTADSALQSFTVKEEDDDDANAITV	AKDTTKNAGAVSILKLKGKNGLTVATKKDGTVTFGLSODSGLTIGKSTLNNDGLTVKDTN	EQIQVCANGIKFTNVNGSNPGTGIANTARITFBKIGFAGSDGAVDTNKPYLDQDKLQVGN 	VKITNTGINAGGKAITGLSPTLPSIADQSSRNIELGNTIQDKDKSNAASINDILNTGFNL 	KNNNNPIDFVSTYDIVDFANGNATTATVTHDTANKTSKVVYDVNVDDTTIHLTGTDDNKK 	LGVKTTKLNKTSANGNTATNFNVNSSDEDALVNAKDIAENLMTLAKETHTTKGTADTALQ 	TFTVKKVDENNNADDANAITVGOKNANNQVNTLTLKCENGLNIKTDKNGTVTFGINTTSG 	LKAGKSTLNDGGLSIKNPTGSEDIQVGADGVKFAKVNNNGVVGAGIDGTTRITRDEIGFT 	GTNGSLDKSKPHLSKDGINAGGKKITNIQSGEIAQNSHDAVTGGKIYDLKTELENKISST 	AKTAQNSLHEFSVADEOGNNFTVSNPVSSYDTSKTSDVITFAGENGITTKVNKGVVRVGI 	DOTKGLTTPKLTVGNNNGKGIVIDSONGONTITGLSNTLANVTNDKGSVRTTEGGNIIKD	EDKTRAASIVDVLSAGENLQGNGEAVDEVSTYDTVNFADGNATTAKVTYDDTSKTSKVVY	DVNVDDTTIEVKDKKLGVKTTTLTSTGTGANKFALSNQATGDALVKASDIVAHLNTLSGD 	IOFAKGASQANNSAGYVDADGNKVIYDSTDNKYYQAKNDGTVDKTKEVAKDKIVAQAQTP 	DGTLAQMNVKSVINKEQVNDANKKQGINEDNAFVKGLEKAASDNKTKNAAVTVGDLNAVA
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GGIQVGVDKDGNANGDLSNVWVKTQKDGSKKALLATYNAAGQTNYLTNNPAEAIDRINEQ 1735
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200kDa outer membrane protein; antibacterial; immunogenic; infection;
otitis media; detection.
                                                          1556 VNAGGTKIDDKGVSFVDSSGQAKANTPVLSANGLDLGGKVISNVGKGTKDTDAANVQQLN
                                                                                                                  1616 EVRNILGLGNAGNDNADGNQVNIADIKKDPNSGSSSNRTVIKAGTVLGGKGNNDTEKLAT
                                                                                                                                                                                          1916 VSVGASGAERRIQNVAAGEVSATSTDAVNGSQLYKATQSIANATNELDHRIHQNENKANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1976 GISSAMAMASMPQAYIPGRSMVTGGIATHNGQGAVAVGLSKLSDNGQWVFKINGSADTQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M. catarrhalis M56 200kDa protein in pKS348 SEQ ID NO:13.
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N-PSDB; AAF59106.
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protein,

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The present invention describes an isolated and purified nucleic acid (I) that encodes a 200 kba outer membrane protein of Moraxella catarrhalis. The 200 kba outer membrane protein of Moraxella catarrhalis. The can be used in vaccines. [II], and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarrhalis infections, particularly offitis media in humans. [II] is also used as antigen in immunoassays for detecting specific antibodies (Ab), and to generate Ab. (I) are used for recombinant production of (II) and its fragments are used as probes for identifying/Clouning 200 kba protein genes from other strains, and for idagnostic detection of M. catarrhalis. (I) makes possible production of large amount of recombinant immunogens. Expression of truncated versions of (II) reduces toxicity of the protein towards the Escherichia coli host. The present sequence represents the M. catarrhalis MSG 200kba protein in pKS348, which is given in the exemplification of the present invention. Heic acid encoding Moraxella catarrhalis in protective vaccines and for diagnosis Claim 1; Fig 8A-V; 247pp; English. nucleic useful 

AA; 1992 Seguence

ö 595 540 420 480 600 115 SNKTVNGSSLDKIGTDATGQESIAIGGDVKASGDASIAIGSDDLHLLDQHGNPKHPKGTL 175 355 300 415 360 475 235 180 295 Gaps RPAYTPNTQALDPKFQATNNTKAGPLSIGSNSIKRKIINVGAGVNKTDAVNVAQLEAVVK SNLAKGSSANDAVTIEQLKAAKPTLNAGAGISVTPTEISVDAKSGNVTAPTYNIGVKTTE AKDTTKNAGAVSILKLKGKNGLTVATKKDGTVTFGLSQDSGLTIGKSTLNNDGLTVKDTN INDLINGHAVLKEIRSSKDNDVKYRRTTASGHASTAVGAMSYAQGHFSNAFGTRATAKSA YSLAVGLAATAEGQSTIAIGSDATSSSLGAIALGAGTRAQLQGSIALGQGSVVTQSDNNS WAKERRITFQGDDNSTDVKIGLDNTLTIKGGAETNALTDNNIGVVKEADNSGLKVKLAKT LNNLTEVNTTTLNATTTVKVGSSSSTTAELLSDSLTFTQPNTGSQSTSKTVYGVNGVKFT NNAETTAAIGTTRITRDKIGFARDGDVDEKQAPYLDKKQLKVGSVAITIDNGIDAGNKKI Length 1992; ő Indels 22; ó, DB Score 10021; I Pred. No. 0; 1; Mismatches Query Match Best Local Similarity 99.9%; Matches 1991; Conservative 1 26 236 181 356 301 116 361 476 536 969 541 959 501 116 61 176 121 296 241 121 481 qq ò g ò q ö q ò g ò g δ g ò q ò g οğ g ò ò

1320 1435 1380 1495 1440 1500 1615 1735 1135 1080 1195 1255 1260 IGDNAQATGDQSIAIGTGNVVAGKHSGAIGDPSTVKADNSYSVGNNNQFTDATQTDVFGV 1855 1015 1075 960 GIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGRQTQAGNQSIA VNAGGTKIDDKGVSFVDSSGQAKANTPVLSANGLDLGGKVISNVGKGTKDTDAANVQQLN **DGTLAQMNVKSVINKEQVNDANKKQGINEDNAFVKGLEKAASDNKTKNAAVTVGDLNAVA QTPLTFAGDTGTTAKKLGETLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNS** GGIQVGVDKDGNANGDLSNVWVKTQKDGSKKALLATYNAAGQTNYLTNNPAEAIDRINEQ TFTVKKVDENNNADDANAITVGQKNANNQVNTLTLKGENGLNIKTDKNGTVTFGINTTSG LKAGKSTLNDGGLSIKNPTGSEQIQVGADGVKFAKVNNNGVVGAGIDGTTRITRDEIGFT DQTKGLTTPKLTVGNNNGKGIVIDSQNCQNTITGLSNTLANVTNDKGSVRTTEQGNIIKD EDKTRAASIVDVLSAGFNLQGNGEAVDFVSTYDTVNFADGNATTAKVTYDDTSKTSKVVY EQIQVGANGIKFTNVNGSNPGTGIANTARITRDKIGFAGSDGAVDTNKPYLDQDKLQVGN KNNNNPIDEVSTYDIVDFANGNATTATVTHDTANKTSKVVYDVNVDDTTIHLTGTDDNKK LGVKTTKLNKTSANGNTATNFNVNSSDEDALVNAKDIAENLNTLAKEIHTTKGTADTALQ GINGSLDKSKPHLSKDGINAGGKKITNIQSGEIAQNSHDAVTGGKIYDLKTELENKISST 1796 1556 1616 1561 1681 1316 1261 1381 1496 1501 1676 1021 1141 1256 1201 1436 1736 1016 196 1076 1136 1196 836 781 841 926 1081 716 176 721 968 901 661 QQ g ò Ω ò g ô g QQ qq g Op δ q ò qq ò QQ οχ g ò Q δ Op οy а Q g ολ q ò ò ò Qγ ò à

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The 200 kbs outer membrane protein of Moraxella catarrhalis.

The 200 kbs outer membrane protein (II) has antibacterial activity and can be used in vaccines. (II), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarrhalis infections, particularly otitis media in humans. (II) is also used as infugen in immunoassays for detecting specific antibodies (Ab), and to generate Ab. (I) are used for recombinant production of (II) and its fragments are used as probes for identifying/cloning 200 kba protein genes from other strains, and for diagnostic detection of M. catarrhalis.

(I) makes possible production of large amount of recombinant immunogens. Expression of truncated versions of (II) reduces toxicity of the protein towards the Escherichia coll host. The present sequence represents the m. catarrhalis strain Q8 200kba protein, which is given in the exemplification of the present invention.
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                                                                                                                                                    Moraxella catarrhalis strain Q8; major outer membrane protein;
200kDa outer membrane protein; antibacterial; immunogenic; infection;
GNNITVTESNSVALGSNSAISAGTHAGTQAKKSDGTAGTTTTAGATGTVKGFAGQTAVGA
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The present invention describes an isolated and purified nucleic acid (I) that encodes a 200 kDa outer membrane protein of Moraxella catarrhalis.

The 200 kDa outer membrane protein (II) has antibacterial activity and can be used in vaccines. (II), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarrhalis infections, particularly otitis media in humanas (II) is also used as antigen in immunoassays for detecting specific antibodies (Ab), and to generate Ab. (I) are used for recombinant production of (II) and its fragments are used as probes for identifying/Coloning 200 kDa protein generate Ab. (I) are used for recombinant production of (II) and its genes from other strains, and for idenostic detection of M. catarrhalis.

(I) makes possible production of large amount of recombinant immunogens. Expression of truncated versions of (II) reduces toxicity of the protein towards the Escherichia coli host. The present sequence represents the M. catarrhalis less 200 kDa protein, which is given in the exemplification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSGSAYAQKKDTKHIAIGEQNQPRRSGTAKADGDRAIAIGENANAQGGQAIAIGSSNKTV 120
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                                                                                                                                                                                                                            lla catarrhalis strain Q8; major outer membrane protein;
outer membrane protein; antibacterial; immunogenic; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MNHIYKVIFNKATGTFMAVAEYAKSHSTGGGGSCATGQVGSVCTLSFARIAALAVLVIGAT
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64.0%; Score 6593.5; DB 22
Best Local Similarity 60.7%; Pred. No. 2.3e-282;
Matches 1466; Conservative 149; Mismatches 330;
NGQGAVAVGLSKLSDNGQWVFKINGSADTQGHVGAAVGAGFHF
              New nucleic acid encoding Moraxella catarrhalis useful in protective vaccines and for diagnosis
                                                                                                                                                                                                  NO:11
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                                                                                                         AAB69136 standard; Protein; 2314
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                                                                                                                                                                                                                                                                                                                                                                                     2000WO-CA00870.
                                                                                                                                                                                                  catarrhalis les1 200kDa
                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sasaki K,
                                                                                                                                                                                                                                                                otitis media; detection.
                                                                                                                                                                                                                                                                                           Moraxella catarrhalis
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N-PSDB; AAF59105.
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                                                                                                                                                                                                                                                                                                                                                                                      26-JUL-2000;
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200kDa out
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AAB69136
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dtsktsdvitfagengittkvnkgvvrvgidqtkglttpkltvgnnngkgivids 1163

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1104 pyssyd	1221 QNGQNT ::     1164 kdgqnt	1281 VDFVST         1222 vdfvst		1282 ktsang		1458 KKQGIN         1399 kkqgin	1518 IKGGQT         1459 ikggqt	1578 KANTPV	_	1592 1579 vtdang	1592 1639 daghqv	1592 1699 dvlnvq		1759 gnvlik			1612 QQLNEV        1879 qqlnev	1672 KLATGG         1939 klatgg	1732 INEQGI		1792 QSIAIG         2059 qsiaig			1912 AVGAVS         2179 avgavs
qq	Qy Dp	Qy	Oy	a a	<b>3</b> 8	Qy	Oy Dp	Qy	qo ,	oy Op	Oy Op	QY	ò	qq	Oy d	g :	da Dp	Oy Dp	QY	qa .	Oy Dp	Ογ	අු	Oy Dp
::   		29	innnnka 293 JEAVVKWA 357	:      kavenla 350	3LKVKLAK 414          31kvklak 407	4		JILVANTI 322 SGNVTAPT 586	: spyldkkg 581	ALQSFTVK 643       ::: alqsfsir 637				3NTI-QDK 817       : antitsde 752	- σ	:        qtskvtyd 812	NAKDIAEN 935           akdiaen 868		SVKFAKVN 1052		INAGGKKI 1100	116	:       	3KGIVIDS 1220
::    :    :    :	INGHAVLKEIRSSKDNDVKYRRTTASGHASTAVGAMSYAQCHFSNAFGTRATAKSAYSLA				RERRITFQGDDNSTDVKIGLDNTLTIKGGAETNAL/TD-NNIGVVKEADNSGLKVKLAK					587 YNI-GVKTTELNSDGTSDKFSVKGSGTNNSLVTAEHLASYLNEVNRTADSALQSFTVK :           :     :			5 ltvgsdkdgktqlvieqvasgndtkni	DINKPYLDQDKLQVGNVKITNTGINAGGKAITGLSPTLPSIADQSS-RNIELGNTI-QDK			3 VNVDDTTIHLTGTDDNKKLGVKTTKLNKTSANGNTATNFNVNSSDEDALVNAKDIAEN				NNGVVGAGIDGTTRITRDEIGFTGTNGSLDKSKPHLSKDGINAGGKKI   A		:	1 PYSSYDTSKTSDVITFAGENGITTKVNKGVVRVGIDQTKGLTPRLTVGNNNGKGIVIDS
116	180	240	299	294	358	415	408	529	523	587	644	702	969	760	818	753	878	936	994	925	1053	1101	1044	1161
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1397 1517 1458 2118 vlsangldlggkrisnigaavddndavnfkqfnevaktvnnlnngsnsgaslpfv 1578 gkpingtdgkpqkaikgadgkyyhanangvpvdkdgkpitdadklanlaahgkpl 1638 gfnlgtnhngvdfvkaydtvnfvngtgaditsvrsadgtmsnitvntalaatddd 1758 STDNKYYQAKNDGTVDKTKEVAKDKLVAQAQTPDGTLAQMNVKSVINKEQVNDAN 1457 SVGASGAERRIQNVAAGEVSATSTDAVNGSQLYKATQSIANATNELDHRIHQNEN 1971 NEDNAFVKGLEKAASDNKTKNAAVTVGDLNAVAQTPLTFAGDTGTTAKKLGETLT vvaslggnsdaitltnikstlpqidtpntgnanagqaqslpslsaaqqsnaasvk VRNLLGLGNAGNDNADGNQVNIADIKKDPNSGSSSNRTVIKAGTVLGGKGNNDTE GDNAQATGDQSIAIGTGNVVAGKHSGAIGDPSTVKADNSYSVGNNNQFTDATQTD TITGLSNTLANVTNDKGSVRTTEQGNIIKDEDKTRAASIVDVLSAGFNLQGNGEA TYDTVNFADGNATTAKVTYDDTSKTSKVVYDVNVDDTTIEV-KDKKLGVKTTTLT AN -- KFALSNQATGDALVKASDIVAHLNTLSGDIQTAKGASQANNSAGYVDADGN -----GGKVISNVGKGTKDTDAANV IRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGRQTQAGN NNITVTESNSVALGSNSAISAGTHAGTQAKKSDGTAGTTTTAGATGTVKGFAGQT VLSANGLDL-----

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Gaps 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 AQGGQAIAIGSSNKTVNGS----SLDKIGTDAT--GQESIAIGGDVKASGD-ASIAIGSD 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 -LVIGATLSGSAYAQKKDTKHIALGEQNQPRRS-----GTAKADGDRAIAIGENAN 104
54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus adhesion protein HA2 (AAR99393) is associated with the formation of surface fibrils involved in adhesion to various host cells; it is also referred to haf (Haemophilus surface fibrila). Its amino acid sequence was deduced from a genomic DNA clone (AAT41476) derived from Haemophilus influenzae type b strain C65. Itage quantities of recombinant HA2 can be produced in transformed prokaryotic or eukaryotic host cells, for use in vaccines against H. influenzae infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant Haemophilus adhesion proteins HAl and HA2 - for use in vaccines against H. influenzae infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MNHIYKVIFNKATGTFMAVAEYAKSHSTGGGGSCATGQVGSVCTLSFARIAALAV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.9%, Score 1123, DB 17, Length 2353; 23.0%, Pred. No. 1.6e-41;
                                                                                                                                                                                                                                                    Haemophilus adhesion protein; HA2; hsf protein; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
10.9%; Score 1123; DB 17;
Best Local Similarity 23.0%; Pred. No. 1.6e-41;
Matches 607; Conservative 318; Mismatches 838;
                                                                                                                                                                                                                                                                             наеморhilus influenzae type b strain C54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 66-73; 120pp; English.
                                                                                                                                                AAR99393 standard; Protein; 2353 AA.
                                                                                                                                                                                                                              Haemophilus adhesion protein HA2.
                                                                                                                                                                                                                                                                                                                                                             96WO-US04031
                                                                                                                                                                                                                                                                                                                                                                                      95US-0409995
                                                                     Barenkamp SJ, St Geme JW;
                                                        2032 DTQGHVGAAVGAGFHF 2047
                                                                                                                                                                                                     (first entry)
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(UNIW ) UNIV WASHINGTON.
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                                                                                                                                                                                                                                                                                                           WO9630519-A1
                                                                                                                                                                                                                                                                                                                                                             22-MAR-1996;
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Qy Db	INGHAVLKEIRSSKDNDVKYRRT	
Qy	203TASGHASTAVGAMSYAQGHFSNAFGTRATAKSAYSLAVGLAATAEGOSTIAIGSDA 258	
م م	TSSSLGAIALGAGTRAQLQGSIALGQGSVVTQSDNNSRPAYTPNTQP	യയ
oy oy	GPLSIGSNSIKKKIINVGAGVNKTDAVNVAQLEAVVKWAKERRITFQGDDNST	н
Dp	takavidavnkagwrvktitanggngdfatvasgtnvtfesgdgttasvtkdt 36	4
δλ	72 DVKIGLDNT-LTIKGG	9 5
QQ	65 ngngitukydakugdglkfdsdkkivadttaltutggkuaelakeddkKkIunagdIVta 42.	φ α
90 ج	AETNALTDNNI-GVVKEADNSGLKVKLANTLNN 4 	0 4
6 6 6	19 LIEVNITILNATITVKVGSSSSTTAELLSDSLFFTQPNTGSQSTSKTV-YGVNGVKFTNN 47	7.1
qq		37
ΟŸ	78 AETTAAIGTTRITRDKIGFARDGDVDEKQAPYLDKKOLKVGSV 52	50
q	rayddanfdvlnnsatdlnr-hvedaykglinineknankqpivlusl 39	
ο d	GIDAGNKKISNLAKGSSANDAVTIEQLKAAKPTLNAGAGISVTPTE 57	34
č.	73 ISVDAKSGNVTAPTYNIGVKTTELNSDGTSDKFSVKGSGTNNSLVTAEHLASYLNE 62	88
qq	:  :	84
δy	ALQSFTVKE-EDDDDANALTVAKDTTKNAGAVSILKLKGKNGLTVATKKDGTV 6	8.7
qq	gtavtkggfetvktgatdadrgkvtv-kdatandadkkvatvkdvatainsaa 7	37
οy	72GLSQDSGLTIGKSTLNNDGLTVKDTNEQIQVGANGIKFT 72	0
QQ	tenlttsidednptdngkdaalkagdtltfkagknlkvkrdgknitfdlakn 79	
Qý	NGSNPGTGIANTARITRDKIGFAGSDGAVDTNKPYLDQDKLQ 77	72
qq	dtltiggntptggttatpkvnitstadginfa	m
QY	NVKITNTGINAGGKAITGLSPTLPSIADQSSRNIELGNTIQDKDKSNAASINDI 82	C
qq	gsknvylkgiattltepsagakss-hvdlnvdatkksnaas	00
οy	FULKNINNPIDEVSTYDIVDEANGNATTATVTHDTANKTSKVVYDVNVDDTIHLT 8	8
Dp	iggngnnvdyvatydtvnftddstgtttvtvtqkad 9	72
Qy	DDNKKLGVKTTKLNKTSANGNTATNENVNSSDEDALVNAKDIAEN 9	m
qq	dhngklftgkdlkdanngatvseddgkdtgtgivtaktvida 9	œ
٥y	LAKEIHTTKGTADTALQTFTVKKVDENNNADDANAITVGOKNANNQVNTLTLK 9	6
qq	aetgatavnagnaetvtsgtsvnfkngnattatvs l	93
Qy	92 GENG-LNIKTDKNGTVTFGINTTSGLKAGKSTLNDGGLSIKNPTGSEQIQ 1:	1040
QQ	vnvgdglkigddkkivadtttltvtggkvsvpagansviiii i	
Óý	1041VGADGVKFAKVNN	1053

us-09-361-619-7.rag

2085 nahdkvrfanglntkv---saatvestdangdkvtttfvktdvelpltgiy---ntdang 2138

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1145	1089	1205	1137 1264	1169	1324	1202	1307	1444	1254	1503	1305	1355	1607	1403	1666	1452	1711	1512	1757	1563	0000	1868	1649	1928	1681	1988	1724	2042	1774	2084	1825
kklvnaeglata-lnnlswtakadkyadgesegetdqevkagdkvtfkagknlkvkqsek	NGVVGAGIDGTTRIIRDEIGFIGTNGSLDKSKPHLS	dftyslqdtltgltsitlggtangrndtgtvinkdgltitlangaaagtdasngntisvt	KDGINACGKKITNIQSGSIAQNSHDAVTGGKIYDLKTELENKISSTAK	TAQNSLHEPSVADEQGNNFTVSNPYSSYDTSK	tdnigkhtvtidvaeakvgdglekdtdgkiklkvdntdgnnlltvdatkgasvakgefna	-TSDVITFAGENGITTKVNKGVVRVGIDQTKGLT	E-IMGE	:    : :    : :    : :    : :    : :  : :  : :  : : :  : :  : :  : : :  : : :  : : :  : : :  : : :  : : : :  : : :  : : : :  : : : : :  : : : : :  : : : : : :  : : : : : :  : : : : : :  : : : : : : : :  : : : : : :  : : : : : :  : : : : : :  : : : : : : : : : : :  :	VGNNNGKGIVIDSONGONTITGLSNTLANVTNDKGSVRTTEQGNIIK	lgtngnkvnitsdtkglnfakdsktgddanihlngiastltdtllnsgat-tnlggngit	DEDKTRAASIVDVLSAGFNLQGNGEAVDFVSTYDTVNFADGNATTAKVTYD-   :	-DTSKTSKVVYDVNVDDTTIEVKDKKLGVKTTTLFSTGTGAN-KFALSNQAT		GDALVKASDIVAHLNTLSGDIOTAKGASOANNSAGYVDADGNKVIYDS	:      :: :  ::  dgkdegnglvtakavldavnkagwrvktt-gangqnddfatvasgtnvtfadgngttaev	TDNKYYQAKNDGTVDKTKEVAKDKLVAQAQTPDGTLAQMNVKSVINKEQ		VNDANKKQGINEDNAFVKGLEKAASDNKTKNAAVTVGDLNAVAQTPLTFAGDTGTTAKKL	-ngdgkkfvdasgladainklswta-tagkegtgevdpansaggevka	GETLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGTKI  : :      :  :	DINKARGENING CONTRACTIVATION CONTRACTION C	the state of the s	NVQQLNEVRNLLGLGNAGNDNADGNQVNIADIKKDPNSGS	: :   ::    ::	SSNRTVIKAGTVLGGKGNNDTEKLATGGIQVG	qvrnanevkfksgnginvsgktlngtrvitfelakgevvksneftvknadgsetnlvkvg	VDKDGNANGDLSNVWVKTQKDGSKKALLATYNAAGQTNYLTNN	dmyyskedidpatskpmtgktekykvengkvvsangsktevtltnkgsgyvtgn	PAEAIDRINEQGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAK	qvadalaksgfelgladaaeaekafaesakdkqlskdkaetv	-ADGEAAVAIGRQTQAGNQSIAIGDNAQATGDQSIAIGTGNVVAGKHSGAIG
1087	1054	1146	1090	1138	1265	1170	1203	1385	1208	1445	1255	1306	1564	1356	1608	1404	1667	1453	1712	1513	18.6	1809	1610	1869	1650	1929	1682	1989	1725	2043	1775
qq	Qy	q	Qy Db	Οy	qq	۶ و م	3 8	연	οy	g G	8 8	ò	g	ò	- qa	Qγ	qq	οy	οp	oy O	3 8	g G	Oγ	QΩ	ΟŊ	QQ	δy	οp	οy	qq	ΟŸ

The present sequence represents a Haemophilus influenzae adhesin

(Hia) protein from the type c Haemophilus influenzae strain API.

Hia genes and proteins have antiinflammatory, auditory and antibacterial

cutivities, and can be used in the production of a vaccine. An

immunogenic composition comprising an Hia gene, a polypeptide encoded

by an Hia gene, or a recombinant Hia polypeptide is useful for inducing

protection against disease caused by Haemophilus strains in a

susceptible host, preferably a human. An Hia protein is useful as an

antigen, in immunogenic preparations including vaccines, as a carrier

for other immunogenic preparations including vaccines, as a carrier

for other immunogenic acused by the infection of Haemophilus

influenzae such as meningitis, epiglottitis, septicaemia and otitis

media. Recombinant production of Hia favours high recovery of the

protein compared to the low recovery of native protein from Haemophilus

influenzae species. A truncated protein has a significantly higher

amount of recovery than a full-length protein. Hia; adhesin; Haemophilus influenzae adhesin; NTH1; infection; vaccine; non-typeable Haemophilus influenzae; antiinflammatory; auditory; antibacterial; meningitis; epiglottitis; septicaemia; otitis media; diagnosis; immunogenic; antigen. 1826 DPSTVKADNSYSVGNNNQFTDATQTDVFGVGNNITVTESNSVALGSNSAISAGTHAGTQA 1885 nkivkkadgkw-----yelnadgtasnkevtlgnvdangkk----vv 2176 1886 KKSDGTAGTTTTAGATGTVKGFAGQTAVGAVSVG------ASGAERRIQNVAAG 1933 1934 EVSATSTDAVNGSQLY---KATQSIANATNELDHRIHQNENKANAGISSAMAMASMPQAY 1990 Novel nucleic acid encoding Hemophilus influenzae adhesin protein, for use as antigens and vaccines and for treating Hemophilus influenzae Haemophilus influenzae adhesin (Hia) protein from type c strain API. AAB23860 standard; Protein; 2411 AA. Klein MH; Claim 1; Fig 24; 275pp; English. 99US-0268347. 16-MAR-2000; 2000WO-CA00289. (first entry) (CONN-) CONNAUGHT LAB LID. Haemophilus influenzae. Loosmore SM, Yang Y, WPI; 2000-618897/59. N-PSDB; AAA92499 WO200055191-A2. 16-MAR-1999; 17-JAN-2001 21-SEP-2000. infection AAB23860; œ 2139 AAB23860 셤 ŏ q ò g ò

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Sequence 2411 AA;		
,	٥y	853 F
10.8%; Score 1109; DB 21; Length 2411; 23.2%; Pred. No. 6.8e-41;	qa	3 806
l e	δλ	855
ro i	qa	968 k
vlatllfatvqanatdedeel	Qy	B60 T
	qa	1028
	٥٧	X 898 ×
	qa -	1086
gdkvaltsdangiki	δλ	925
	qu	1145
	QY	941
203 TASCHASTAVGAMSYAQGHFSNAFGTRATAKSAYSLAVGLAATAEGGSTTAIGSDATSSS 262	qa	1205
	δλ	970
DPKFQATNNTKAGPLS	qa	1265
tdntdegngl	QY	666
	qa	1321
tkdtngng	0y	1051
DNNIGVVKEADNSGL	QO	1378
	Oy	1105
SSTTAELLSDSLTFTQPNT :::	qq	1423
	- Oy	1165
	qq	1457
	0y	1215
518GSVAITIDNGIDAGNKKISNLAKGSSANDAVTIEQLKAAKPTLN 561	අ <u>ය</u>	1516
	QY	1268
	qa	1575
	Qy	1318
FTVKEEDDDDANAITVAKDTT       :	qa	1631
klkvdngnt	οy	1364
	qa	1679
æ	0у	1416
	qa	1732
gdtltfkagknlkvkrdgknitidl	Qy	1466
770KLOVGNVKITNTGINAGGKALTGLSPTLPSIADOS-SRNIELG 811	qa	1776
789 aknlevktakvsdt-ltiggntptggttatpkvnitstadginiaketadasgsknvyik 64/		

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1525 NKLTDNNIGVVAGTDGFTVKLAKDLTNLNSV----NAG----GTKIDDKGVSFVDSSGQ 1576 1678 DIVAHLNTLSGDIQTAKGASQANNSAGYVD-----ADGNKVIYDSTDNKYYQAKNDG- 1415 1731 -TVDKTKEVAK-----DKLVAQA---QTPDGTLAQMNVKSVINKEQVNDANKKQGINED 1465 ----GIVIDSQNGQNT---ITGLSNTLANVTNDKGSVRTTEQGNIIKDEDKTRAASIVDV 1267 LSAGFNLQG------NGEAVDFVSTYDTVNFADGNATTAKVTYD--DTSKTSKVYDV 1317 NVDDTIIEVKDKKLGVKTTTLTSTG----TGAN-KFALSNQAT------GDALVKAS 1363 YDTSKTSDVITF-AGENGITTKVNKGV---VRVGIDQTKGLTTPKLTVGNNNGK----- 1214 -KIDKNGTVTFGINTTSGLKAG----KSTLNDGGLSIK--NPTGSEQIQVGA-DGVKFAK 1050 VNNNGVV--GAGIDGTTRITRDEIGFTGTNGS----LDKSKPHLSKDGINAGGKKITNIQ 1104 SGEIAQNSHDAVTGGKIYDLKTELENKISSTAKTAQNSLHEFSVADEQGNNFTVSNPYSS 1164 klvnaegl-atalnnlswtakadkyadgesegetdqevkagdkvtfkagknlkvkqsekd 1144 ftyslądiltgitsitlggtangrndtgtvinkdgititlangaaagtdasngntisvtk 1204 dgisagnkeltnvksalktykdtgntagatgpaantaevakqdlvdltkpatgaagngad 1264 ||||| kdtgtglvtaktvidavnksgwrvtgegataetgatavnagnaetvtsgtsvnfkngnat 1027 ALVNAKDI----AENLNTLA--- 940 KL----GVKTTKLNKTS------ANGNT------ATNFNVNSSDED 924 ----- NGNAT 859 NAFVKGLEKAASDNKTKNAAVTVGDLNAVAQTPLTFAGDTGTTAKKLGETLTIKGGQTDT -----KEIHTTKGTADTALQTFTVKKVD-------ENNNAD ----KNANNQVNTLTLKGENGLNI-ftddstgtttvtvtqkadgkgadvkigaktsvikdhngklftgkdlkdanngatvseddg TATVTHDTANKTSKVVYDVNV------TDDTTIHLTG-------TDDNK ----DANAITVGQ----

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----dnlkikqsgkdftyslkkelkdltsvefkdanggtgsestkitkdgltitpanga 1879
                              --SSNRTVIKAG 1659
                                                                               1940 tnldekgadnnptvadntaatvgdlrglgwvisadkttgepngeynagvrnanevkfksg 1999
                                                                                                    T-----VLGG-----VDKDGNNDTEKLATGG----IQVG----VDKDGNA 1688
                                                                                                                        2000 nginvsgktlngtrvitfelakgevvksneftvknadgsetnlvkvgdmyyskedidpat 2059
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                                                                                                                                                                                                                                                                                                                              NGDLSNVWVKTQK-------DGSKKALLATYNAAGQTNYLTNNPAEAIDRINEQGI 1737
                                                                                                                                                                 skpmtg---ktekykvengkvvsangsktevtltnkgsg---yvtgn--qvadalaksgf 2111
                                                                                                                                                                                     1738 RFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAK------ADGEAAVAIGRQ 1786
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                   1577 A-----KANTPVLSANGLDLGGKVISNVGKGTK------DTDAANVQQL--NEVRNL
                                                                                                                                                                                                                               TQAGNQSIAIGDNAQATGDQ----SIAIGTGNVVAGKHSGAIGDPSTVKADNSYSV
                                                                                                                                                                                                                                                    2156 tkv---saatvestdangdkvtttfvktdvelpltgiy---ntdangnkivkkadgkw--
                                                                                                                                                                                                                                                                                             ---vvkvtengadkwyyt
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The present sequence represents a Haemophilus influenzae adhesin (Hia) protein from the non-typeable Haemophilus influenzae (NTHi) strain 29. Hia genes and proteins have antinflammatory, auditory and antibacterial activities, and can be used in the production of a vaccine. An immunogenic composition comprising an Hia gene, a polypeptide encoded by misa gene, or a recombinant Hia polypeptide is useful as an susceptible host, preferably a human. An Hia protein is useful as an unique, in immunogenic preparations including vaccines, as a carrier for other immunogens, and in the generation of diagnostic reagents. Hia is useful for treating diseases caused by the infection of Haemophilus influenzae such as meningitis, epiglottitis, septicaemia and otitis medium compared to the low recovery of native protein from Haemophilus influenzae species. A truncated protein has a significantly higher amount of recovery than a full-length protein.
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Novel nucleic acid encoding Hemophilus influenzae adhesin protein, for use as antigens and vaccines and for treating Hemophilus influenzae
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.larity 27.9%; Pred. No. 3.4e-37;
Conservative 166; Mismatches 405;
                                                                                                                                                             Claim 1; Fig 20; 275pp; English
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for

Novel nucleic acid encoding Hemophilus influenzae adhesin protein, fuse as antigens and vaccines and for treating Hemophilus Influenzae infection

MH.

Klein

Yang Y,

Loosmore SM,

2000-618897/59

N-PSDB; AAA92498

CONN-) CONNAUGHT LAB LTD.

16-MAR-1999;

16-MAR-2000; 2000WO-CA00289.

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Hia; adhesin; Haemophilus influenzae adhesin; NTH1; infection; vaccine; non-typeable Haemophilus influenzae; antiinflammatory; auditory; antibacterial; meningitis; epiglottitis; septicaemia; otitis media; diagnosis; immunogenic; antigen.
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The present sequence represents a Haemophilus influenzae adhesin (Hia) protein from the non-typeable Haemophilus influenzae (NTH1) strain K22. His genes and proteins have antlinflammatory, auditory and antibacterial activities, and proteins have antlinflammatory, auditory and antibacterial activities, and can be used in the production of a vaccine. An immunogenic composition comprising an Hia gene, a polypeptide encoded by an Hia gene, or a recombinant Hia polypeptide is useful for inducing protection against disease caused by Haemophilus strains in a susceptible host, preferably a human. An Hia protein is useful as an antigen, in immunogenic preparations including vaccines, as a carrier for or other immunogens, and in the generation of dispnostic reagents. His is useful for treating diseases caused by the infection of Haemophilus influenzae such as meningitis, epiglottitis, septicaemia and otitis media. Recombinant production of His favours high recovery of the cortein compared to the low recovery of native protein from Haemophilus influenzae species. A truncated protein negation is a significantly higher amount of recovery than a full-length protein.
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Hia; adhesin; Haemophilus Influenzae adhesin; NTH1; infection; vaccine; non-typeable Haemophilus, influenzae; antiinflammatory; auditory;
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                                                                                                                        GYVDADGNKVI-----YDSTDNKYYQAK--ND-----GTVDKTKEVAKDKLV 1429
                                                                                                                                                                                     1430 AQAQTPDGTLAQMNVKSVINKEQVNDANKKQGINEDNAFVKGLEKAASDNKTKNAAVTVG 1489
                                                                                                                                                                                                                                                 DLNAVAQTPLTFAGDTGTTAKKLGETLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKD 1549
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                           393 nvnvttdtahkkttvrvdvtglpvqyvtedgktvvkvdnkyyeakqdgsadmdkkvenge 452
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ngtkttdglveasel----veslnklgwkvgvdkdgs----
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The present sequence represents a Haemophilus influenzae adhesin (Hia) protein from the non-typeable Haemophilus influenzae (NTHi) strain M407. Hia genes and proteins have antlinflammatory, auditory and antibacterial activities, and can be used in the production of a vaccine. An immunogenic composition comprising an Hia gene, a polypeptide encoded by an Hia gene, or a recombinant Hia polypeptide is useful for inducing protection against disease caused by Haemophilus strains in a susceptible host, preferably a human. An Hia protein is useful as an antigen, in immunogenic preparations including vaccines, as a carrier for other immunogenic preparations including vaccines, as a carrier for other immunogenic preparations including vaccines, as a carrier for useful for treating diseases caused by the infection of Haemophilus influenzae such as meningitis, epiglottitis, septicaemia and otitis medium Recombinant production of Hia favours high recovery of the protein compared to the low recovery of native protein from Haemophilus influenzae species. A truncated protein has a significantly higher amount of recovery than a full-length protein. for 979 KNANNQVNTLTLKGENGLNIKTDKNGTVTFGINTTSGLKAGKSTLNDGGLSIKNPTGSEQ 1038 1039 IQVGADGVKFAKVNNNGVVGAGIDGTTRITRDEIGFTGT-NGSLDKSKPHLSKDGINAGG 1097 1158 VSNPYSSYDTSKTSD---VITFAGENGITTKVNKGVVRVGIDQTKGLTTPKLTVGNN--- 1211 Novel nucleic acid encoding Hemophilus influenzae adhesin protein, f use as antigens and vaccines and for treating Hemophilus influenzae epiglottitis; septicaemia; otitis media; 1098 KKITNIQSGEIAQNSHDAVTGGKIYDLKTELENKISSTAKTAQNSLHEFSVADEQGNNFT v-----tsksengkhtvtftlekdlnvk------natvsdklslgangnk ----NGKGIVIDSQNGQN---TITGLSNTLANVTNDKGSVRTTEQGNIIKDEDKTRA 194 vditsdtnglkfakpstnggngnvhlngiastltdtit--gttksatng--vdvqnhnra 28 krasatvatavi----atilsttvgatttggttstnglkaygst-------Indels 386; Length 1004; Ouery Match 9.4%; Score 970; DB 21; I Best Local Similarity 28.1%; Pred. No. 3.2e-35; Matches 341; Conservative 146; Mismatches 341; Klein MH; Claim 1; Fig 21; 275pp; English. antibacterial; meningitis; epigidiagnosis; immunogenic; antigen 16-MAR-2000; 2000WO-CA00289 99US-0268347 (CONN-) CONNAUGHT LAB LTD. Haemophilus influenzae Yang Y, 2000-618897/59 1004 AA; N-PSDB; AAA92496 WO200055191-A2 Loosmore SM, 16-MAR-1999; 21-SEP-2000 Sequence 1212 ---89 155 g ð δ q δ a ò q δ q

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ASIVDVLSAGFNLQGNGEAVDFVSTYDTVNFADGNATTAKVTYDDTSKTSKVVYDVNVDD 1321

1262 250

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Hia; adhesin; Haemophilus influenzae adhesin; NTHi; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAVSVGASGAERRIQNVAAGEVSATSTDAVNGSQLYKATQSIANATNELDHRIHQNENKA 1973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1974 NAGISSAMAMASMPQAYIPGRSMVTGGIATHNGQGAVAVGLSKLSDNGQWVFKINGSADT 2033
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                                                                                   -----yvtedgetvv--kvgneyyeakqdgsadmdkkvengklaktkvklvsangt 361
                                                                                                                                   DPSTV--KADNSYSVGNNNQFTDATQTDVFGVGNNI------TVTESNSV-----
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                                                                                                                                                                                                                             -LNAVAQTPLTFAGDTGTTAKKLGETLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKD
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                                                          1382 ASQANNSAGYVDADGNKVIYDSTDNKYYQAKNDGTVDKTKEVAKDKL--
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The present sequence represents a Haemophilus influenzae adhesin (Hia)

protein from the non-typeable Haemophilus influenzae (NTH1) strain 33.

Hia genes and proteins have antiinflammatory, auditory and antibacterial

activities, and can be used in the production of a vaccine. An

activities, and can be used in the production of a vaccine. An

muniogenic composition comprising an Hia gene, a polypeptide encoded

yan Hia gene, or a recombinant Hia polypeptide is useful for inducing

protection against disease caused by Hemophilus strains in a

protection against disease caused by Hemophilus strains in a

protection against disease caused by themophilus strains in a

susceptible host, preferably a human. An Hia protein is useful as an

antigen, in immunogenic preparations including vaccines, as a carrier

for other immunogenic acused by the infection of Haemophilus

is useful for treating diseases caused by the infection of Haemophilus

influenzae such as meningitis, epiglottitis, septicaemia and otitis

media. Recombinant production of Hia favours high recovery of the

protein compared to the low recovery of native protein from Haemophilus

influenzae species. A truncated protein has a significantly higher

amount of recovery than a full-length protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      si nucleic acid encoding Hemophilus influenzae adhesin protein, f
as antigens and vaccines and for treating Hemophilus influenzae
non-typeable Haemophilus influenzae; antiinflammatory; auditory; antibacterial; meningitis; epiglottitis; septicaemia; otitis media; diagnosis; immunogenic; antigen.
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9.0%; Score 927.5; DB 21;
Best Local Similarity 28.2%; Pred. No. 2.4e.33;
Matches 322; Conservative 136; Mismatches 321;
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                                                                                                                                                                                                                                                                                                                                            Klein
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                                                                                           Haemophilus influenzae
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                                                     --NKKQGINEDNAFVKGLEKAASDNKTKNAAVTVG-DLNAVAQTP 1498
                                                                                        -----LTFAGDTGTTAKKLGET-----LTIKGGQTDTNKLTD------NNIGVVA 1537
                                                                                                                                                                    ----NAGGTKIDDKGVSFV---DSSGQA--KANTPVLSANGLDLGGKVISNVGKGTKDT 1606
                                                                                                                                                                                                          DAANVQQLNEVRNLLGLGNAGN-----DNADGNQVNIADIKKDPNSGSSSNRTVIKAGTV 1661
                                                                                                                                                                                                                                               1662 LGGKGNNDTEKLATGGIQVGVDKDGNANGDLSNV-WV--KTQKDGSKKALLATYNAAGQT 1718
                                                                                                                                                                                                                                                                                   1719 NYLTNNPAEAIDRINEQGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGE 1778
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                                                                                                                                                                                 tengangastk1tkdgltitpandangaaatdadkikvasdqisaqnkavknvvsqlkf
                                                                      gtedtdavsfkqlkalqdkqvtlsasnayang----gsdadggkatqtlgndlnfkfkst
                                                                                                                                            ----gdlrglgwvisadkttgeskeysaqvrnanev
                                                                                                                                                                                                                                                                                                                                   --FTVKLAKDLTNLNSV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents an antigenic protein derived from Haemophilus paragallinarum strain A-221. The antigenic protein stimulates the production of HI antibodies in fowl. The protein and DNA coding for it can be used in the preparation of vaccines for the prevention of chicken infectious coryza (CIC). The protein and its antibodies can be used in the diagnosis and treatment of CIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antigenic polypeptide from Haemophilus paragallinarum induces HI antibody production - and is useful for diagnosis of and preparation of vaccines for chicken infectious coryza
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 mglnaytqldpr--gtsketrqgsvvigenaksagnqsvslgqnswsktnsisigagtfa
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(KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
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Location/Qualifiers
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                                         /label= signal
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Haemophilus paragallinarum; antigenic protein; HI antibody; diagnosis; vaccine; chicken infectious coryza; CIC; fowl.
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                                                                                                           1591 ---LGGKVISNVGKGTKDTDAANVQ-----QLN-EVRNLLGLGNAGNDNA-----DGNQV 1636
                                                                                                                                                                                                                                   1637 NIADIKKDPNS----GSSSNRTVI----KAGTVLGGK-----GNNDTEKLATGGIOV 1680
                                                                                                                                                                                                                                                                                   1681 GVDKDGNANGDLSNVWVKTQKDGSKKALLATYNAAGQTNYLTNNPAEAIDRINEQGIRFF 1740
                                                                                                                                                                                                                                                                                                   1741 HVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGRQTQAGNQSIAIGDNA 1800
             1543 sktevdaeigkskvtl---tpdsgl-----ifatkqagsgn-nagidagnkkisnv-- 1589
                                                                                            1475 AASD-NKTKNAAVTVGDLNAVAQTPLTFAGDTGTTAKKLGETLTIKGGQTDTNKLTDNNI 1533
                                                                                                                                                                                                     1418 DKTK---EVAKDKLVAQAQTPDGTLAQMNVKSVINKEQVNDANKKQGINEDNAFVKGLEK 1474
                                                                                                                                                       1364 DIVAHLNTLSGDI-----QTAKGASQANNSAGYVDADGNKVIYDSTDNKYYQAKNDGTV 1417
                                                                                                                                        1534 GVVAGTDGFTVKLAKDLTNLNSVNAGGTKIDDKGVSFVDSSGQAKANTPVLSANGLD---
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1..70
/label= signal
71..2039
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2036 msvgfsf 2042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TKHIAIG----EQNQPRRSGTAKADGDRAIAIGENANAQGGQAIAIGSS--NKTVNGSSL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 siwdifselymgkktngtdydakkndrdpnkpeafytysdfksryvnnpstsptyaaklg 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 ALDPKFQATNNTKAGPLSIGSNSIKRKIINVGAGVNKTDAVNVAQLEAVVKWAKERRITF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365 QGDDNSTDVKIGLDNTLTIKGGAETNALTDNNIGVVKEADNSGL-KVKLAKTLNNLT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKIGTDATGQESIAIGGDVKASGDASIAIGSDDLHLLDQHGNPKHPKGT------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.8%; Score 804; DB 19;
ilarity 21.8%; Pred. No. 1.5e-27;
Conservative 298; Mismatches 778;
                                                                                                                                                                                             Sakaguchi M, Tokiyoshi
                                                                                                                                               (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
(KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
 protein"
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                                                         26-MAR-1998
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Matches 514;
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Klein MH;

Yang Y,

Loosmore SM,

WPI; 2000-618897/59. N-PSDB; AAA92497.

99US-0268347.

16-MAR-1999;

(CONN-) CONNAUGHT LAB LTD.

16-MAR-2000; 2000WO-CA00289.

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Hia; adhesin; Haemophilus influenzae adhesin; NTHi; infection; vaccine; non-typeable Haemophilus influenzae; antiinflammatory; auditory; antibacterial; meningitis; epiglottitis; septicaemia; otitis media; diagnosis; immunogenic; antigen.
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                                                                                                                                       1443 NVKSVINKEQVNDANKKQGI---NEDNAFVKGLEKAASDNKTKNAAVTVGDLNAVAQTPL
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                                1530 ----lg--ttdlavt-knpnqtsifnpingtapttfkdavdkltta---vntgwgskv
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                                                                                             AAB23858 standard; Protein; 1094 AA
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The present sequence represents a Haemophilus influenzae adhesin (Hia)

protein from the non-typeable Haemophilus influenzae (NTH1) strain K9.

His agenes and proteins have antiinflammatory, auditory and antibacterial

crivities, and can be used in the production of a vaccine. An

cutivities, and can be used in the production of a vaccine. An

immunogenic composition comprising an His gene, a polypeptide encoded

by an His gene, or a recombinant His polypeptide is useful for inducing

protection against disease caused by Haemophilus strains in a

susceptible host, preferably a human. An His protein is useful as an

antigen, in immunogenic preparations including vaccines, as a carrier

for other immunogenic acused by the infection of Haemophilus

influenzae such as meningitis, epiglottitis, septicaemia and otitis

media. Recombinant production of His favours high recovery of the

protein compared to the low recovery of native protein from Haemophilus

influenzae species. A truncated protein has a significantly higher

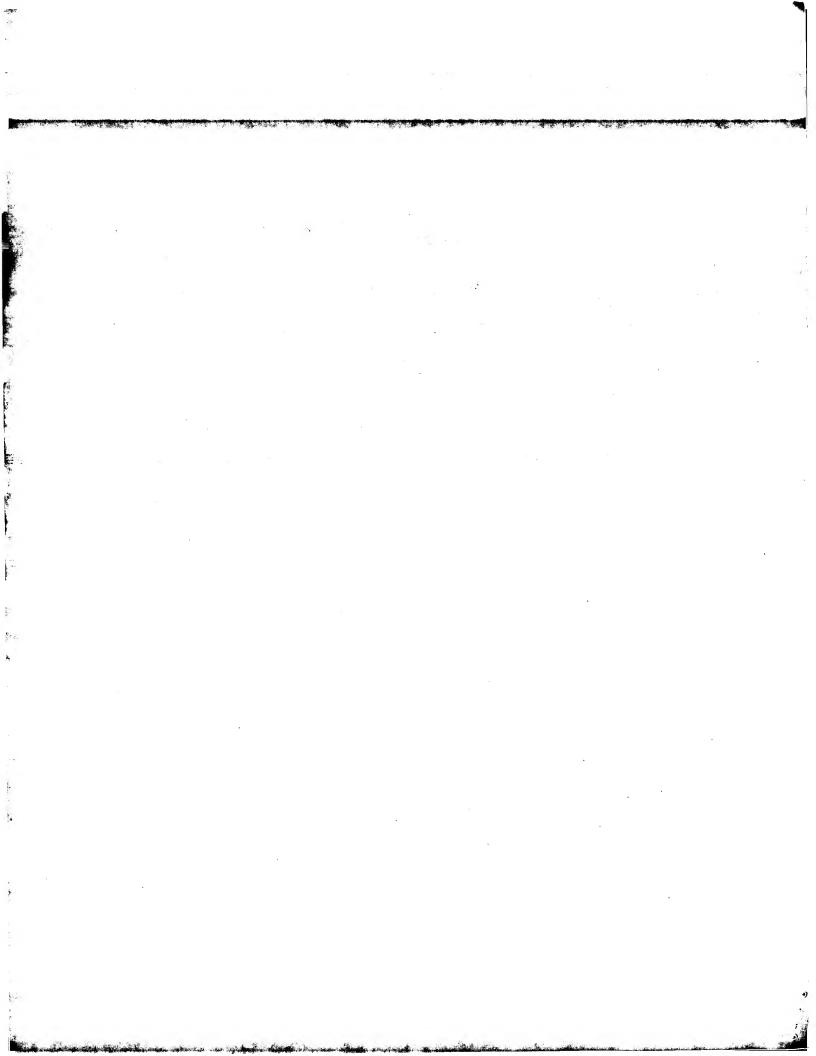
amount of recovery than a full-length protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58;
                                                                                                                                                                                                                           Novel nucleic acid encoding Hemophilus influenzae adhesin protein, for use as antigens and vaccines and for treating Hemophilus influenzae infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 vhdgllnlnengankkllvddntaatvgdlrklgwvvstkng-----
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Search completed: September 13, 2001, 12:37:02 Job time: 82058 sec



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                                                                                                                                                                                                                                                                                                                                                                        10303
1 MNHIYKVIFNKATGTFMAVA.....NGSADTQGHVGAAVGAGFHF 2047
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Sequence 32,
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/FB_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-377-155-33
US-08-91942-4
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US-08-685-467-4
US-08-685-467-2
US-08-913-942-2
US-08-913-942-1
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Gapop 10.0 , Gapext 0.5
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PROTEIN-106 POLYPEPTIDE, GENE SEQUENCE AND USES THEREOF
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                                                                                                                                                                                Sequence 13, Sequence 19, Sequence 17, A Sequence 2, A Sequence 11, Sequence 11, Sequence 5, A
                                                                                                        Sequence 15, Sequence 9, 7
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence Sequence
                              Sequence S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 71.6%; Score 7380; DB 4; I Best Local Similarity 68.3%; Pred. No. 0; Matches 1555; Conservative 118; Mismatches 219;
                                              US-08-617-697-4

US-08-171-611-4

US-09-377-155-15

US-09-377-155-15

US-09-377-155-13

US-09-377-155-13

US-09-377-155-17

US-08-137-155-17

US-08-137-155-17

US-08-137-155-17

US-08-185-467-5

US-08-185-467-5
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FILING DATE: No. 6214981ember 12, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Baldwin, Geraldine F.
REGISTRATION NUMBER: 31,232
REFERENCE/DOCKET NUMBER: 7969-060
TELECHONONICATION INFORMATION:
TELECHONONICATION:
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-968-685A-10; Sequence 10, Application US/08968685A; Patent No. 6214981; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: TUCKER, KENNETH
APPLICANT: PLOSILA, LAURA
TITLE OF INVENTION: PROARAEL
TITLE OF INVENTION: PROTEIN-
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 2123 amino acids
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1155 Aven
CITY: New York
STATE: New York
COUNTRY: USA
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1809 1749 1825 1885 1945 1929 1989 2065 1449 1525 1509 1585 1569 1645 1705 1689 1765 1269 1405 1465 GSNSAISAGTHAGTQAKKSDGTAGTTTTAGATGTVKGFAGQTAVGAVSASGAERRIQN AGFNLQGNGEAVDFVSTYDTVNFADGNATTAKVTYDDTSKTSKVVYDVNVDDTTIEVKDK KKLGETLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGTKIDDKGVS KKLGETLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGTKIDDKGVS FVDSSGQAKANTPVLSANGLDLGGKVISNVGKGTKDTDAANVQQLNEVRNLLGLGNAGND FVDSSGQAKANTPVLSANGLDLGGKVISNVGKGTKDTDAANVQQLNEVRNLLGLGNAGND VVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGRQTQAGNQSIAIGDNAQATGDQSIA 1826 VVQGRNGIDSSASGKHSVAIGFQARADGEAAVAIGRQTQAGRQSIAIGDNAQATGDQSIA IGTGNVVACKHSGAIGDPSTVKADNSYSVGNNNQFTDATQTDVFGVGNNITVTESNSVAL GSNSAISAGTHAGTQAKKSDGTAGTTTTAGATGTVKGFAGQTAVGAVSVGASGAERRIQN KLGVKTTTLTSTGTGANKFALSNQATGDALVKASDIVAHLNTLSGDIQTAKGASQANNSA GYVDADGNKVIYDSTDNKYYQAKNDGTVDKTKEVAKDKLVAQAQTPDGTLAQMNVKSVIN NADGNQVNIADIKKDPNSGSSSNRTVIKAGTVLGGKGNNDTEKLATGGIQVGVDKDGNAN TATNENVNSSDEDALVNAKDIAENLNTLAKEIHTTKGTADTALQTFTVKKVDENNNAD-D ANAITVGQKNANNQVNTLTLKGENGLNIKTDKNGTVTFGINTTSGLKAG-KSTLNDGGLS IKNPTGSEQIQVGADGVKFAKVNNNGVVGAGIDGTTRITRDEIGFTGTNGSLDKSKPHLS KDGINAGGKKITNIQSGEIAQNSHDAVTGGKIYDLKTELENKISSTAKTAQNSLHEFSVA DEQGNNFTVSNPYSSYDTSKTSDVITFAGENGITTKVNKGVVRVGIDQTKGLTTPKLTVG NNNGKGIVIDSQNGQNTITGLSNTLANVTNDKGSVRTTEQGNIIKDEDKTRAASIVDVLS 1750 1810 1886 1870 1946 1930 2006 1646 1630 1690 1766 1346 1330 1406 1466 1450 1526 1510 1586 1570 1706 1210 1270 1390 1047 1030 1107 1090 1166 1150 1226 1286 987 912 971 Q g 8 qq g g ò ò g g ŏ g οy g οy QQ οy Ω δ Ωp δý a οý g οy g ò ò Qγ ò QQ qq ΟŽ á ·δ

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221 KGAKTAGGNVESVDLVSAYNNVEFIT--GDKNT-----LDVVLTAKENGKTTEVKFTPK 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -LVIGATLSGSAYAQKKDTKHIAIGEQNQPRRS------GTAKADGDRAIAIGENAN 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 AQGGQAIAIGSSNKTVNGS----SLDKIGTDAT--GQESIAIGGDVKASGD-ASIAIGSD 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 IK-----QNTDESTNASSFTYSLKKDLTDLTSVATEKLSFG----ANGDKVDITSDAN 161
1 MNHIYKVIFNKATGTFMAVAEYAKSHSTGGGSCATGQVGSVCTLSFARIAALAV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLHLLDQHGNPKHPKG--TLINDLINGHAVLKEIRSSKDNDVKYRRT-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 874;
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                                                                                                                                                                                                             APPLICANT: PEAK, Ian Richard Anselm APPLICANT: DENNINGS, Michael Paul APPLICANT: DENNINGS, Michael Paul TITLE OF INVENTION: NOVEL SURFACE ANTIGEN FILE REFERENCE: 65564/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR APPLICATION NUMBER: GB 9726398.2
NUMBER: OF SEQ ID NOS: 33
SCOTWARE: PALENTIN Ver: 2.0
                                                                                                                                                   Sequence 33, Application US/09377155
Patent No. 6197312
GENERAL INFORMATION:
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                                                                                                                             -09-377-155-33
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Gaps 119; 307 GNGLVTAKAVIDAVNKAGWRVKTTTANGQNGDFATV--ASGTNVTFESGDGTTASVTKDT 364 | || || || || || 365 NGNGITVKYDAKVGDGLKFDSDKKIVADTTALTVTGGKVAEIAKEDDKKKLVNAGDLVTA 424 259 TSSSLGAIALGAGTRAQLQGSIALGQGSVVTQSDNNSRPAYTPNTQALDPKFQATNNTKA 318 -----VIKEKDGKLFTGKENNDTNKVTSNT-----ATDNTDE 306 LIEVNTTTLNATITVKVGSSSSTTAELLSDSLTFTQPNTGSQSTSKTV-YGVNGVKFTNN 477 319 GPLSIGSNSIKRKIINVGAGVNKTDAVNVAQLEAVVKWAKERRITFQGDDNST----------AETINALTDNNI -GVVKEAD------NSGLKVK-------DVKIGLDNT-LTIKGG----273 TS-----387 419 485 372

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GSV 520   DST 593	PTE 572	LNE 628	GTV 687 SAA 737	728 AKN 793	KLQ 772	NDI 828  : EDV 885	THLT 888 QKAD 927	AEN 935 : IDA 985	TLK 991  : TVS 1034	Q 1040 NNN 1086	1053 SEK 1145	108	-SSTAK 1137 ::   ATVSAK 1264	1169 FNA 1324	1202 NDD 1384	TPKLT 1207 : 11: SDKLS 1444	125
YLDKKQLKVGSV : :     NKQPLVTDST	AGAGISVT	TAEHLASY	SLTVATKKDGTV    : DVATAINSAA	GIKET         GKNITEDL	NKPYLDQD	TIQDKDKSNAASINDI :        : NVDATKKSNAASIEDV	TTTGGVNVC	ALVNAKDIAEN       : :  GLVTAKTVIDA	KNANNQVNTLTLK 	CNPTGSEQI    : : SVPAGANSV	OKALKAKO	LDKSKPH   : : TDASNGNTI	: : :VGKNGATV	SSYDTSK :  :GASVAKGE	)AATFVKVE	:	SVRTTEQGN
Δ	EQLKAAKPTLNAGAGIS  :        : -QVKQADEVLFTGAGAA	-LNSDGTSDKFSVKGSGTNNSLVTAEHLASYLNE                       SLEKDGDTIKLKVDNQNTDNVLTVGN	SILKLKGKNC : : ! :VATVK	NNDGLTVKDTNBQIQVGANGIKFT 	TRDKIGFAGSDGAVDTNKPYLDQDKLQ       :     TADGLNFA	-PSIADQSSRNIELGNTIQDKDKSNAASINDI    :   ::  : EPSAGAKSS-HVDLNVDATKKSNAASIEDV	ANKTSKVVYI	SDED  ::  SEDDGKDTG	SVNF	STLNDGGLSIKNPTGSEQIQ :     :    : TTLTVTGGKVSVPAGANSVN	CAGDKVTFK	rgtngs]     :  LANGAAAG	TELENKI - : :   :: \VKNANEVE	-EFSVADEQGNNFTVSNPYSSYDTSK :-  -  -  -  -  -  -  -  -  -  -  -  -  -	/GDVAKAIN	TONETANDI	ITGLSNTLANVTNDKGSVRTTEQGNIIK :  :::   : :       LNGIASTLTDTLLNSGAT-TNLGGNGIT
IGFARDG :	ANDAVTIEC	GTSDKFSVF   :     GDTIKLKVI	TTKNAGAVS      ATANDADKE	VKDT     AGDTLTFK	TRDKIGE     :  TSTADGLNE	TADQSSRNI :  ::	TATVTHDT?            TTTVT	NFNVNSSDED      ::   CDANNGATVSEDD	INADDANAIT    :  :   NAGNAETVT	:    :  XKIVADTT	SEGETDOEVI	TRITRDEIGFTGTNGS     :  :     : TVINKDGLTITLANGA	TGGKIYDLI   : TQDKEFHAA	FSVADEQGI   :  -  LKVDNTDGI	IDQTKGLT	N X C C C X X X X	-ITGLSNT] :  :::  :HLNGIAST]
AETTAAIGTTRITRDKIGFARDGDVDEKQA 	GIDÄGNKKISNLAKGSSANDAVTIEQLKAAKPTLNAGAGISVTPTE 	ADC	VNRTADSALQSFTVKE-EDDDDANAITVAKDTTKNAGAVSILKLKGKNGLTVATKKDGTV 	GLSQDSGLTIGKSTLNNDGLTVKDT ::: :       SIDEDNPTDNGKDDALKAGDT	NVNGSNPGTGIANTARITRDKIGFA 	TNTGINAGGKAITGLSPTLPSIADQSS     :   :    :     :   KETADASGSKNVYLKGIATTLTEPSAGAKSS	LNTGFNLKNNNNPIDFVSTYDIVDFANGNATTATVTHDTANKTSKVVYDVNVDDTTIHLT    : ::    : :    :      LRAGWNIQGNGNNVDYVATYDTVNFTDDSTGTTTVTVTQKAD	TSANGNTATNENVNSSDEDALVNAKDIAEN	LNTLAKEIHTTKGTADTALQTFTVKKVDENNNADDANAITVGQ :	INTTSGLKAGKSTLNDGGLSIKNPTGSEQ1Q	-VGADGVKFAKVNN   1   1:	NGVVGAGIDGTTRITRDEIGFTGTNGSLDKSKPHLS	KDGINAGGKKITNIQSGEIAQNSHDAVTGGKIYDLKTELENKISSTAK 	TAQNSLH	-TSDVITFAGENGITTKVNKGVVRVGIDQTKGLT	TUDESPINGANDALKACHTITIKACKNI KVKRNGKNTWBALANDI SVKGATVCKKIT	VGNNNGKGIVIDSQNGQNTITGLSNTLANVTNDKGSVRTTEQGNIIK
DANEDVLNN	-GIDAGNKK    : VSTKNGTKE	TYNIGVKTT   :     TITVSVAET	VKE-EDDDD          VKTGATDAD	DDSGLTIGK :   :       EDNPTDNGK	NVNGSNPGTGIANTARI :	GGKAITG 	IDFVSTYDI : : :   VDYVATYDT	KLNKTSANG :    VIKDHNG	TADTALQTF   :  TAETGATAV	GTVTFGINT :	VNN :- -  I,NNI,SWTAK	-NGVVGAGIDGT-  :    LTGLTSITLGGTA	IQSGE ::	AEAKVGDGL	ITTK :   NERGKVVVK	ECS A STORY	GIVID      TKGLNFAKD
AAIG     VASGLRAYD	AITIDNGIDAGNKKISN     : :     :     AATVGDLRKLGWVVSTKNGTKEESN	ISVDAKSGNVTAPTYNIGVKTTE :	VNRTADSALQSFTVKE       :      - -NGTAVTKGGFETVKT	GLSQDSGLTIGK : : : KTENLTTSIDEDNPTDNGK	TAKVSDTLT	VGNVKITNTGINAGGKAI   :  : KETADASGSKNV	FNLKNNNP : ::   WNIQGNGNN	GTDDNKKLGVKTTKLNKTSANGNTAT    :     :  GKGADVKIGAKTSVIKDHNGKLFT	LNTLAKEIHTTKGTADTALQTF :  VNKSGWRVTGEGATAETGATAV	GENG-LNIKTDKNGTVTFGINTTSGLKAG 	VGADGVKFAKVNN    : :   :   VNAEGLATA-LNN	SLQDTLTGL	KDGINAGGKKITNIQSG     :     :   KDGISAGNKEITNVKSA	SLH    SKHTVTIDV	-TSDVITFAGENG  :        VTTDATTAQGTNA	ODSPTDDGA	NGK      SNKVNITSD
AETTA     AITN	AITIDN    ::   AATVGD	ISVD/ :: -TVT:	VNRT	TF     TFVK	LEVK	VGNV	LNTG     LRAG	GTDDI   GKGAI	LNTL. : I VNKS	GENG : I   KDNG!	V(	FTY	KDGII 	TAQNSLH 	-TSD  :  VITIV	SATT	VGNNNGK- :      LGTNGNKV
478	521	573 635	629	688	729	773	829	989	936	992	1041	1054	1090	1138	1170	1203	1208
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COUNTRY: United States ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                  NAME: Vance, Dolly A. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
          CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr Hohb,
STREET: Four Embarcad
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-913-942-4
                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               al Similarity
607; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         273 TS----
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Matches 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1929 OVRNANEVKFKSGNGINVSGKTLNGTRVITFELAKGEVVKSNEFTVKNADGSETNLVKVG 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DMYYSKEDIDPATSKPMTG---KTEKYKVENGKVVSANGSKTEVTLTNKGSG---YVTGN 2042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -ADGEAAVAIGRQTQAGNQSIAIGDNAQATGDQ-----SIAIGTGNVVAGKHSGAIG 1825
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                                                                                                                    ----GDALVKASDIVAHLNTLSGDIQTAKGASQANNSAGYVD-----ADGNKVIYDS 1403
                                                                                                                                        TDNKYYQAKNDG--TVDKTKEVAK-----DKLVAQA--QTPDGTLAQMNVKSVINKEQ 1452
                                                                                                                                                                                                                                      1453 VNDANKKQGINEDNAFVKGLEKAASDNKTKNAAVTVGDLNAVAQTPLTFAGDTGTTAKKL 1512
                                                                                                                                                                                                                                                                                                                          1758 GDKVTFKAG------DNLKIKQSGKDFTYSLKKELKDLTSVEFKDANGGTGSESTKI 1808
                                                                                                                                                                                                                                                         DEDKTRAASIVDVLSAGFNLQG-----NGEAVDFVSTYDTVNFADGNATTAKVTYD- 1305
                     -----KIGAKTSVIKDHNGKLFTGKELKDANNNGVTVTET 1607
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ---SSNRTVIKAGT-----VLGG-------KGNNDTEKLATGG----IQVG
                                                                                                                                                                                                          1667 T-----KANDGSITVKYNVKVADGLKLDGDKIVADTTVLTVADGKVTAPN-----
                                                                                                                                                                                                                                                                                               1513 GETLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSV-----NAG----GTKI
                                                                                                                                                                                                                                                                                                                                                          1564 DDKGVSFVDSSGQA-----DTDAA
                                                             1306 -DISKTSKVVYDVNVDDTTIEVKDKKLGVKTTTLTSTG----TGAN-KFALSNQAT----
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; Sequence 4, Application US/08913942
; Sequence 4, Calo578
; GENERAL INFORMATION:
; APPLICANT: St. Geme, Joseph
APPLICANT: Bt-enchamp, Stephen J.
TITLE OF INVENTION: HAEMOPHILUS ADHESION PROTEINS
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KDNGKRTEV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----VIKEKDGKLFTGKENNDTNKVTSNT------ATDNTDE 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GNGLVTAKAVIDAVNKAGWRVKTTTANGONGDFATV--ASGINVTFESGDGTTASVTKDT 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 -LVIGATLSGSAYAQKKDTKHIAIGEQNQPRRS------GTAKADGDRAIAIGENAN 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 KGAKTAGGNVESVDLVSAYNNVEFIT--GDKNT-----LDVVLTAKENGKTTEVKFTPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MNHIYKVIFNKATGTFMAVAEYAKSHSTGGGSCATGQVGSVCTLSFARIAALAV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 AQGGQAIAIGSSNKTVNGS----SLDKIGTDAT--GQESIAIGGDVKASGD-ASIAIGSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 DLHLLDQHGNPKHPKG--TLINDLINGHAVLKEIRSSKDNDVKYRRT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----TASGHASTAVGAMSYAQGHFSNAFGTRATAKSAYSLAVGLAATAEGQSTIAIGSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         319 GPLSIGSNSIKRKIINVGAGVNKTDAVNVAQLEAVVKWAKERRITFQGDDNST----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2353;
Test Albritton & Herbert LLP
Center, Suite 3400
                                                                                                                                                                                                 OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: A 61053-1/RFT/RMS/DAV TELECOMMUNICATION: TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --DVKIGLDNT-LTIKGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.9%; Score 1123; DB 4; 23.0%; Pred. No. 1.5e-60;
                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,995
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/4031
FILING DATE: 22-MAR-1996
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/913,942
FILING DATE: 29-DEC-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative 318;
                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39,054
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 4:
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    : Flehr Hobbach
Four Embarcadero
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424	418	477	520	572 634	628 684	687 737	728	772	828 885	927	935	991 1034	1040	1053	1145	1089	1137	1264	1169	1202
	AETNALTDNNI-GVVKEADNSGLKVKLAKTLNN		AETTAAIGTTRITTEDKIGFARDGDVDEKQAPYLDKKQLKVGSV 	AITIDNGIDAGNKKISNLAKGSSANDAVTIEQLKAAKPTLNAGAGISVTPTE   1	ISVDAKSGNVTAPTYNIGVKTTELNSDGTSDKFSVKGSGTNNSLVTAEHLASYLNE :	VNRTADSALQSFTVKE-EDDDANAITVAKDTTKNAGAVSILKLKGKNGLTVATKKDGTV 	TFGLSQDSGLTIGKSTLNNDGLTVKDTNEQIQVGANGIKFT	NVNGSNPGTGIANTARITRDKIGFAGSDGAVDTNKPYLDQDKLQ 	VGNVKITNTGINAGGKAITGLSPTLPSIADQSSRNIELGNTIQDKDKSNAASINDI 	LNTGENLKNNNNPIDEVSTYDIVDEANGNATTATVTHDTANKTSKVVYDVNVDDTTIHLT 	GTDDNKKLGVKTTKLNKTSANGNTATNFNVNSSDEDALVNAKDIAEN   :  :      :	LNTLAKEIHTTKGTADTALQTFTVKKVDENNNADDANAITVGQKNANNQVNTLTLK :	GENG-LNIKTDKNGTVTFGINTTSGLKAGKSTLNDGGLSIKNPTGSEQIQ :   :		KKLVNAEGLATA-LNNLSWTAKADKYADGESEGETDQEVKAGDKVTFKAGKNLKVKQSEK	NGVVGAGIDGTTRITRDEIGFTGTNGSLDKSKPHLS		KDGISAGNKEITNVKSALKTYKDTQNTAD	TAQNSLHTAQNSLH	-TSDVITEAGENGITTKVNKGVVRVGIDQTKGLT
365	387	419	478 538	521 594	573 635	629	688 738	729	773 835	829	928	936	992	1041	1087	1054	1090	1206	1138	1170
QQ	oy Op	Qy Db	QY	Qy Dp	Qy Dp	Oy Dp	o d	QY	Oy Db	OY Db	Qy Dp	oy Og	Sp G	Qy	g	Qy Db	δō	QQ	Ογ Dp	ογ

2176 DEDKTRAASIVDVLSAGFNLQG-----NGEAVDFVSTYDTVNFADGNATTAKVTYD- 1305 1608 DGKDEGNGLVTAKAVIDAVNKAGWRVKTT-GANCQNDDFATVASGTNVTFADGNGTTAEV 1666 TDNKYYQAKNDG--TVDKTKEVAK-----DKLVAQA---QTPDGTLAQMNVKSVINKEQ 1452 1453 VNDANKKQGINEDNAFVKGLEKAASDNKTKNAAVTVGDLNAVAQTPLTFAGDTGTTAKKL 1512 1564 DDKGVSFVDSSGQA-----KANTPVLSANGLDLGGKVISNVGKGTK------DTDAA 1609 2085 NAHDKVRFANGLNTKV---SAATVESTDANGDKVTTTFVKTDVELPLTQIY---NTDANG 2138 1886 KKSDGTAGTTTTAGATGTVKGFAGQTAVGAVSVG------ASGAERRIQNVAAG 1933 2177 KVTENGADKWYYINADGAADKTKGEVSNDKVSTDEKHVVRLDPNNQSNGKGVVIDNVANG 2236 EVSATSTDAVNGSQLY---KATQSIANATNELDHRIHQNENKANAGISSAMAMASMPQAY 1990 1325 VTTDATTAQGTNANERGKVVVKGSNGATATETDKKKVATVGDVAKAINDAATFVKVENDD 1384 1356 ----GDALVKASDIVAHLNTLSGDIQTAKGASQANNSAGYVD-----ADGNKVIYDS 1403 1712 - NGDGKK-----FVDASGLADALNKLSWTA-TAGKEGTGEVDPANSAGQ----EVKA 1757 1650 ---SSNRTVIKAGT----VLGG----VLGG----IQVG 1681 1929 QVRNANEVKFKSGNGINVSGKTLNGTRVITFELAKGEVVKSNEFTVKNADGSETNLVKVG 1988 1682 -----VDKDGNANGDLSNVWVKTQK------DGSKKALLATYNAAGQTNYLTNN 1724 1991 IPGRSMVTGGIATHNGQGAVAVGLSKLSDNGQWVFKINGSADTQGHVGAAVGAGFHF 2047 1385 SATIDDSPTDDGANDALKAGDTLTLKAGKNLKVKRDGKNITFALANDLSVKSATVSDKLS 1208 VGNNNGK-----GIVIDSQNGQNT---ITGLSNTLANVTNDKGSVRTTEQGNIIK -DTSKTSKVVYDVNVDDTTIEVKDKKLGVKTTTLTSTG----TGAN-KFALSNQAT----1667 T-----KANDGSITVKYNVKVADGLKLDGDKIVADTTVLTVADGKVTAPN-----1513 GETLTIKGGOTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSV-----NAG----GTKI 1775 -ADGEAAVAIGRQTQAGNQSIAIGDNAQATGDQ-----SIAIGTGNVVAGKHSGAIG 1826 DPSTVKADNSYSVGNNNQFTDATQTDVFGVGNNITVTESNSVALGSNSAISAGTHAGTQA 2139 NKIVKKADGKW-----YELNADGTASNKEVTLGNVDANGKK-----VV 1564 KDNGKRTEV------KIGAKTSVIKDHNGKLFTGKELKDANNNGVTVTET 1610 NVQQL--NEVRNLLGLGNAGNDN----ADGNQVNIAD-----IKKDPNSGS-----1725 PAEAIDRINEQGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAK-----1255 1306 1869 1203 1404 1934 2237 QQ g g g ρp qq Ob q a QΥ q ολ ŏ g δ g q ò g ò qq δ à ò ò δ ŏ ð ŏ δ δy á

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                                                               GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Barenkamp, Stephen I.

APPLICANT: St. Geme III, Joseph W.

TITLE OF INFORMENTION: Heamophilus Adhesion Proteins

NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert

STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: CA

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/409,995

FILING DATE: 24 MAR.1995

CLESSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouerý Match 7.7%; Score 792.5; DB 1; Best Local Similarity 22.7%; Pred. No. 2.3e-40; Matches 474; Conservative 239; Mismatches 652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGIGSTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61053/RFT
TELECOMMUNICATION INFORMATION:
TELEFRA: (415) 781-1989
TELEFRA: (415) 398-3249
TELEFRA: (415) 781-1989
TELEFRA: 1910 277299
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1912 amino acids
TYPE: amino acid
STRANDEDNESS: double
                 Sequence 4, Application US/08409995
Patent No. 5646259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown
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US-08-409-995-4
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qq	301 DNTDEGNGLVTAKAVIDAVNKAGWRVKTTTANGQNG	DFATV ASGINVTFESGDGTTAS 3	8 8
Οy	72	3	98
Dp	359 VTKDTNGNGITVKYDAKVGDGLKI	TVKYDAKVGDGLKFDSDKKIVADTTALTVTGGKVAEIAKEDDKKKLVNAG 4	18
Qy	387AETNALTDNNI	4	13
qq	:       :   419 DLVTALGNLSWKAKAEADTDGAL	DLVTALGNLSWKAKARAEADTDGALEGISKDQEVKAGETVTFKAGKNLKVKQDGANFTYSLQ 4'	478
ογ	414 KILNNLTEVNTTILNATITVKVG	-	472
QQ	479 DALTGLTSITLGGTTNG	SVTKDGI	531
δy	473 KFTNNAËTTAAIG	YLDKKQL	515
qq	532 KAGNKAITNVASGLRAYDDANFD		587
Qy	516 KVGSVAITIDNGIDA	AKGSSANDAVTIEQLKAAKPTLNAGAGIS	267
OD	588 VTDSTAATVGDLRKLGWVVSTKNGTKEESN-	QVKQADEVLFTGAGAA	633
Qy	568 VTPTEISVDAKSGNVTAPTYNIGVKTTE	LNSDGTSDKFSVKGSGTNNSLVTAEHLA	623
qq	634TVTSKSEN-GKHTITVS		683
οy	624 SYLNEVNRTADSALQSFTVKE-E	KNGLTVATK	682
qq	684		731
δy	683 KDGTVTFGLSQDSGL	GLSODSGLTIGKSTLNNDGLTVKDTNEQIQVGANGIKFT- 7	728
qq	₽	LTFKAGKNLKVKRDGKNITF	787
Qy	729 NVNGSN	GSDGAVDTNKPYLD	191
qq	788 DLAKNLEVKTAKVSDTLTIGGNT	NITSTADGLNFA	833
QY	768 QDKLQVGNVKITNTGINAGGRAI	TNTGINAGGKAITGLSPTLPSIADQSSRNIELGNTIQDKDKSNAA 8	823
QQ	834		879
οy	824 SINDILNTGFNLKNNNNPIDEVS	SINDILNTGENLKNNNNPIDEVSTYDIVDFANGNATTATVTHDTANKTSKVVYDVNVDDT 8	883
qq	880		921
Qy	884 TIHLTGTDDNKKLGVKTTKLNK	NFNVNSSDEDALVNAK	930
q	922 TOKADGKGADVKIGAKTSVIK-	DLKDANNGATVSEDDGKDTGTGLVTAK	616
δλ	931	DIAENLNTLAKEIHTTKGTADTALQTFTVKKVDENNNADDANAITVGGKNANNQVN S	986
Ор	980 TVIDAVNKSGWRVTGEGATAETGATAV	NAGNAETVTSGTSVNFKNGNAT	1028
δy	987	KSTLNDGGLSIKNPTGSE	1037
QQ	1029 TATVSKDNGNINVKYDVNVGDGLKIG	DDKKIVADTTTLTVTGGKVSVPAGAN	1080
Qy	1038 QIQ		1053
q	: 1081 SVNNNK		1139
Qy	1054		1087
QQ	1140	KQSEKDFTYSLQDTLTGLTSITLGGTANGRNDTGTVINKDGLTITLANGAAAGTDASNGN	1199
Qγ	1088	VTGGKIYDLKTELENKI	1132
qq	1200 TISVTKDGISAGNKEITNVKSALKTYKDTONTADE	-TODKEFHAAVKNANEVEFVGKNGA	1258
٥y	1133 SSTAKTAQNSLH	EFSVADEQGNNFTVSNPYSSYDTSK	1169

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                                                                                                                     1379 VENDDSATIDDSPTDDGANDALKAXDTLTLKAGKNLKVKRDGKNITFALANDLSVKSATV 1438
                                                                                                                                                   TPKLTVGNNNGK------GIVIDSQNGQNT---ITGLSNTLANVTNDKGSVRTTEQ 1249
                                                                                                                                                                      SDKLSLGTNGNKVNITSDTKGLNFAKDSKTGDDANIHLNGIASTLTDTLLNSGAT-TNLG 1497
                                                                                                                                                                                                            GNIIKDEDKTRAASIVDVLSAGFNLQG------NGEAVDFVSTYDTVNFADGNATTAK 1301
                                                                                                                                                                                                                             VTYD--DTSKTSKVVYDVNVDDTTIEVKDKKLGVKTTTLTSTG----TGAN-KFALSNQA 1354
                                                                                                                                                                                                                                                                                           T-----GDALVKASDIVAHLNTLSGDIQTAKGASQANNSAGYVDADGNKVIYDSTD 1405
                                                                                                                                                                                                                                                                                                                                                               1602 TVTETDGKDEGNGLVTAKAVIDAVNKAGWRVKTT-GANGQNDDFATV-ASGTNVTF---- 1655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1508 -TAKKLGETLITKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSV----NAG-- 1559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GQEVKAGDKVTFKAG------DNLKIKQSXKDFTYSLKKELKDLTSVFFKDANGGTG 1801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1560 --GTKIDDKGVSFVDSSGQA-----KANTPVLSANGLDLGGKVISNVGKGTK 1604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1462 INEDNAFVKGLEKAASDN----KTKNAAVTVGDLNAVAQTPLTFAGDTGT---
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STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08685467
Patent No. 6060059
GENERAL INFORMATION:
APPLICANT: St. Geme III, Joseph W.
APPLICANT: Barenkamp, Stephen J.
TITLE OF INVENTION: HAEMOPHILUS ADHESION PROTEINS
NUMBER OF SEQUENCES: 6
                              ---TSDVITFAGENG----ITTKVNKGVVRVGIDQTKGLT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,467
FILING DATE: 22-UTL-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,995
FILING DATE: 24-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----TVTSKSEN-GKHTITVSVAETKADCGLEKDGDTIKLKVDNQNTDNVLTVGN--- 683
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MNHIYKVIFNKATGTFMAVAEYAKSHSTGGGSCATGQVGS-----VCTLSFARIAALAV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 -----LVIGATLSGSAYAQKKDTKHIAIGEQNQPRRS-----GTAKADGDRAIAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----TASGHASTAVGAMSYAQGHFSNAFGTRATAKSAYSLAVGLAATAEGQSTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215 AGWNIKGAKTAGGNVESVDLVSAYNNVEFIT--GDKNT-----LDVVLTAKENXKTTEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGSDATSSSLGAIALGAGTRAQLQGSIALGQGSVVTQSDNNSRPAYTPNTQALDPKFQAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             314 NNTKAGPLSIGSNSIKRKIINVGAGVNKTDAVNVAQLEAVVKWAKERRITFQGDDNST--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  414 KTINNLTEVNTTTINATTTVKVGSSSSTTAELLSDSLTFTQPNTGSQSTSKTV-YGVNGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     473 KFTNNAETTAAIG------TTRITRDKIGFARDG--DVDEKQAPYLDKKQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               516 KVGSVAITIDN-----GIDAGNKKISNLAKGSSANDAVTIEQLKAAKPTLNAGAGIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  588 VIDSTAATVGDLRKLGWVVSTKNGTKEESN------QVKQADEVLFTGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      568 VTPTEISVDAKSGNVTAPTYNIGVKTTE----LNSDGTSDKFSVKGSGTNNSLVTAEHLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------AETNALTDNNI-GVVKEAD------NSGLKVK-----LA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 AIGSDDLHLLDQHGNPKHPKG--TLINDLINGHAVLKEIRSSKDNDVKYRRT-----
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 727;
                                                                                                                                                                                                                                                                                                                                                                   Length 1912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----DVKIGLDNT-LTIKGG-----
                                                                                                                                                                                                                                                                                                                                                                                                               Matches 474; Conservative 239; Mismatches 652;
                                                                                                                                                                                                                                                                                                                                                                   DB 3;
                                                                                                                                                                                                                                                                                                                                                            Query Match 7.7%; Score 792.5; DB 3
Best Local Similarity 22.7%; Pred. No. 2.36-40;
                     A-61053-2/RFT/RMS
                                                              TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1912 amino acids
REGISTRATION NUMBER: 38,304
REFERENCE/POCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-685-467-4
                                                                                                                                                                                                       TYPE: amino acid STRANDEDNESS: unk
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Db 1656ADGNGTTAEVTKANDGSITVKYNVKVADGLKLDGDKI 1692  Qy 1462 INEDNAFVKGLEKAASDNKTKNAAVTVGDLNAVAQTPLTFAGDTGT	RESULT 6 105-084-099-95-2 1 Sequence 2, Application US/0840995 1 Sequence 2, Application US/0840995 1 CEMERAL INPORMATION: 2 CEMERAL INPORMATION: 3 APPLICANT: Barenkamp, Stephen I. 3 APPLICANT: St. Geme III, Joseph W. 3 TITLE OF INVENTION: Haemophilus Adhesion Proteins NUMBER OF SEQUENCES: 3 ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400 3 CITY: San Francisco 3 COUNTRY: USA 4 COUNTRY: USA 5 COUNTRY: USA 6 COMPUTER READABLE FORM: 6 COMPUTER READABLE FORM: 7 COMPUTER: ISAPPC COMPUTER: ISAPPC COMPUTER: 8 MEDIUM TYPE: Tlopy disk 7 COMPUTER: LAMP COMPUTER: LAMP COMPUTER: 8 MEDIUM TYPE: LAMP COMPUTER: 9 COMPUTER: LAMP COMPUTER: LAMP COMPUTER: 9	COPENATING SYSTEM: PC-DOS/MS-DOS CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/409,995 FILING DATE: 24-MAR-1995 CLASSIFICATION: ATORNEY/AGENT INFORMATION: NAME: Silva, Robin M. FREISTRATION NUMBER: 38,304 FREERENCE/DOCKET NUMBER: A-61053/RFT TELEPAX: (415) 711-1999 TELEPAX: (415) 398-3249 TELEFAX: (415) 398-3249 TELEFAX: (415) 398-3249 TELEFAX: 910 277299 TELEFAX: 910 277299 TELEGTH: 1098 amino acids TYPE: amino acid TOPOLOGY: unknown	Query Match 6.6%; Score 678.5; DB 1; Length 1098; Best Local Similarity 23.6%; Pred. No. 1.1e-33; Matches 304; Conservative 157; Mismatches 428; Indels 399; Gaps 5 Qy 944 HTKGTADTALQTFTVKKVDENNNADDANAI-TVGGKNANNOVNTLTL 990
Db 684NGTAVTKGGFETVKTGATDADRGKVTV-KDATANDADKKVATVKDVATA 731  Qy 683 KDGTVTFGLSQDSGLTIGKSTLNNDGLTVKDTNEOLOGAGANGIKFT 728  T32 INSAATFVKTENLTTSIDEDNPTDNGKDDALKAGDTLTFKAGKNLKVKRDGKNITF 787  Qy 729NVNGSNPGTGIANTARITRDKIGFAGSDGAVDTNKPYLD 767  Db 788 DLAKNLEVKTAKVSDTLTIGGNTPTGGTATPKVNITSTADGLNFA	QY         824 SINDILNTGFNIKNNNNPIDEVSTYDIVDFANGNATTATVTHDTANKTSKVVYDVNVDDT 883           II	1054	OY 1203 TPKLTYCNNNKGIVIDSQNCQNTITGLSNTLANVTNDKGSVRTTEQ 1249  1439 SDKLSLGTNGNKUNITSDTKGLNFAKDSKTGDANIHIGMASTLTDTLLKSGAT_TNLG 1497  OY 1250 GNITKDEDKTRAASIVDVLSAGFNLQGNGEAVDFVSTYDTVNFADGNATTAK 1301

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62 INEDNAFVKGLEKAASDN-----KTKNAAVTVGDLNAVAQTPLTFAGDTGT----- 1507
                                      : : | : | | : | | 1750
93 VADTTVLTVADGKVTAPNNGXGKKFXDASGLAGCLNKLSXT--ATAGKEGTGEVDPANSA 1750
                                                                                                                 38 -TAKKLGETLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSV-----NAG-- 1559
                                                                                                                                                        51 GQEVKAGDKVTFKAG------DNLKIKQSXKDFTYSLKKELKDLTSVEFKDANGGTG 1801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 KGENGLNIKTDKNGTVTFGINTTSGLKAGKSTLNDGGLSIKNPTGSEQIQVGADGVKFAK 1050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 KGLLNLN----EKNASDKLLVEDNTAATVGNLRKLGWVLSSKNGTRNEKSQ----QVKHA- 137
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                                                                                                                                                                                                                                                                   PLICANT: Barenkamp, Stephen I.
PLICANT: St. Geme III, Joseph W.
MLE OF INVENTION: Haemophilus Adhesion Proteins
MRE OF SOUGHCES: 6
RRESPONDENCE ADDRESS:
ARRESEEE Flahr, Hobbach, Test, Albritton & Herbert
STRRET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTY: USA

ZIP: 9411-4187

COMPUTER REABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,995

FILING DATE: 24-MR-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: $11va, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: 34,61053/RFT
FELECOMMUNICATION INFORMATION:
TELEPAN: (415) 781-1989
TELERA: (415) 398-3249
TELERA: (415) 398-3249
GORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1098 amino acids
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t No. 5646259
RAL INFORMATION:
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STRANDEDNESS: double
TOPOLOGY: unknown
409-995-2
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us-09-361-619-7.rai

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                                                               KTSDVITFAG--ENGITTKVNKGVVRVGIDQTKGLTTPKLFV-GNNNGKGIVIDS--QNG 1223
                                                                                                                                                                                                    ----GNGEAVDFVSTYDTVNFADGNATTAKVTYDDTSKTSKVYYDVNVDDTTIEVKDKKL 1331
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                                                                                              175 TVSDTLTIGGGAAAGAT------TTPKVNVTSTTDGLKFAKDAAGANG
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                                                                                                                                                                                                                                ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400 CITY: San Francisco STATE: California COUNTRY: United States ZIP: 94111-4187
                                                                         GENERAL INFORMATION:
APPLICANT: St. Geme III, Joseph W.
APPLICANT: Barenkamp, Stephen J.
TITLE OF INVENTION: HAEMOPHILUS ADHESION PROTEINS NUMBER OF SEQUENCES: 6
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llarity 23.6%; Pred. No. 1.1e-33;
Conservative 157; Mismatches 428
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TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,995
FILING DATE: 24-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/685,467
FILING DATE: 22-JUL-1996
CLASSIFICATION: 424
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                              ; Sequence 2, Application US/08685467
; Patent No. 6060059
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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Best Local Simi
Matches 304;
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US-08-685-467-2
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GV-KTTTLTSTGTGANKFALSNQATGDALVKASDIVAHLNTLSGDIQTAKGASQANNSAG 1390
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                  390 VASGTNVTFASGNGTTATVTNGTDG--ITVKYDAKVGDGLKLDGDKIAA----DTTALT
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1224 QNTI--TGLSNTLANVTNDKGSVRTTEQGNIIKDEDK--TRAASIVDVLSAGFNLQ-
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US-09-377-155-32 ; Sequence 32, Application US/09377155

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 304; Conservative 157; Mismatches 428; Indels 399;
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Pred. No. 1.1e-33;
                                                               TITLE OF INVENTION: NOVEL SURFACE ANTIGEN FILE REFERENCE: 065064/0128 CURRENT APPLICATION NUMBER: US/09/377,155 CURRENT FILING DATE: 1999-08-19 PRIOR PAPLICATION NUMBER: PCT/AU98/01031 PRIOR PILING DATE: 1998-12-14 PRIOR FILING DATE: 1997-12-12 NUMBER OF SEQ ID NOS: 33 SOFTWARE: Patentin Ver: 2.0
GENERAL INFORMATION:
APPLICANT: PEAK, IAN Richard Anselm
APPLICANT: JENNINGS, Michael Paul
                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Haemophilus influenzae
US-09-377-155-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 23.6%;
                                                                                                                                                                                                                                                                                                                   SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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                                KKFGDANFDPLTSSADNLTKQNDDAYKGLTNLDEKGTDKQTPVVADNTAATVGDLRGLGW 655
                                                                                                                                                                     710 VKSNEFTVKETNGKETSLVKVGDKYYSKEDIDLTTGQP------KLKDGN- 753
                                                                                                                                                                                                                                                                                                                    891 DGQTKWYELNADGTADMTKEVTLGNVDSDGKKVVKDNDGKWYHAKADGTADKTKGEVSND 950
                                                                                             VISADKTTGGSTEYHDQVRNANEVK---FKSGNGINVSGKTVNGRREITFEL---AKGEV
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1604 KDTDAANVQQL-----NEVRNLLGLGNAGNDN-----ADGNQVNIAD-
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Patent No. 6200578

GENERAL INFORMATION:

APPLICANT: St. Geme, Joseph

TITLE OF INVENTION: HAEMOPHILUS ADHESION PROTEINS

TUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr Hobbach Test Albritton & Herbert LLP

STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California
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APPLICATION NUMBER: US/08/913,942
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29-DEC-1997
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APPLICATION NUMBER: US 08/409,995
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/4031
FILING DATE: 22-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                    TESNSVALGSNSAISAGTHAGTQAK----
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                     A-61053-1/RFT/RMS/DAV
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.6%; Score 678.5; DB 4;
Best Local Similarity 23.6%; Pred. No. 1.1e-33;
Matches 304; Conservative 157; Mismatches 428;
                NAME: Vance, Dolly A.
REGISTRATION NUMBER: 39,054
REFERENCE/DOCKET NUMBER: A-610
TELECOMMULCATION INFORMATION:
TELERAX: (415) 398-3249
TELEX: 910.277299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENTH: 1098 amino acids
ATTORNEY/AGENT INFORMATION: NAME: Vance, Dolly A.
                                                                                                                                                                                                                                                                            SS: unknown
unknown
                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-08-913-942-2
                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: unl
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1915 AVSVG------ASGAERRIQNVAAGEVSATSTDAVNGSQLY---KATQSIANAT 1959
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                                                                                                                                                                                        --SNVWVKTQKDGSKKALLAT---YNAAGQTNYLTNNPAEAIDRINEQGIRFFHVNDGNQ 1747
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                                                                                      656 VISADKTTGGSTEYHDQVRNANEVK---FKSGNGINVSGKTVNGRREITFEL---AKGEV
                                                                                                                                                                                                                                                                                                                                                                                          EPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGRQTQAGNQSIAIGDNAQATGDQS
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APPLICANT: Barenkamp, Stephen J.
TITLE OF INVENTION: HAEMOPHILUS ADHESION PROTEINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP
STREET: Four Embarcadero Center, Suite 3400
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FAPLICATION NUMBER: US/08/913,942
FILING DATE: 29-DEC-1997
CLASSIFICATION: 514
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REGISTRATION UNMERS: 39,054
REFERENCE/DOCKET NUMBER: A-61053-1/RFT/RMS/DAV
                                                                                                                                                                                                                                                                                    710 VKSNEFTVKETNGKETSLVKVGDKYYSKEDIDLTTGQP-
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APPLICATION NUMBER:
ILING DATE: 24-NAR-1995
PRIOR APPLICATION NUMBER: PCT/US96/4031
APPLICATION NUMBER: PCT/US96/4031
FILING DATE: 22-NAR-1996
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
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STATE: California
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1641 -IKKDPNSGSSS-
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NGK-GIVIDSQ------NGONTITGLSNTLANVTNDKGSVRTTEQGNIIKDEDKTR 1260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 DSSGNAVGSSTITFRAGDN---LKIKQS----GNDFTYSLKKELKNLTSVETEKLSFGAN 148
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                                                                                                                                                                                                                                                                                                                                 Length 679;
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Best Local Similarity 23.5%; Pred. No. 1.7e-27;
Matches 232; Conservative 118; Mismatches 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSYDTSKTSDVITF-AGENGITTKVNKGVVRVGIDQT---
INFORMATION
TELEFAX: (415) 781-1989
TELEX: 910 277299
SEQUENCE CHRACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid
STRANDEDNESS: unicappology.
                                                                                                                                                                                                                    TOPOLOGY: unknown
MOLECULE TYPE: protein
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TADTALQ----TFTVKKVDENNNADDAN----AITVGQKNANNQVNTLTLKGENGLNIKTDK 1002
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                                               288 ADSVSKDKSGNIVLSAKEGEAEIGGVISAQNQQAKGGKLMITGD--KVTLKTGAVIDLSG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        434 AKEW-LLDPDDVSIETLTSGRNNTGENQGYTTGDGTKESPKGNSISKPTLTNS--TLEQT 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGVNKTDAVNV-----AQLEAVV----KWAKERRITFQGDDNSTDVKIGLDNTLTI 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     384 KGGAETNALTDNNIGVVKEADNSGLKVKLAKTLNNLTEVNTTTLNATTTVKVGSSSSTTA 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  346 KEGGETYLGGDER----GEGKNG---IQLAK-----KTTLEKGSTINVSGKEKGGR 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                390 AIVWGDIALIDGNINAQGSDIAKTG-----GFVETSGHDLSIGDDVIVD 433
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                                                                                                                                     HLLDQHGNPKHPKGTLINDLINGHAVLKEIRSSKDNDVKYRRTTASGHASTAVGAMSYAQ
                                                                                                                                                                                                     --AIINTNGFTASTLDISNENIKARNFTLE---QTKDKALAEIV
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      -OGGQAIAIGSSNKTVNGSSLDKIG ---
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1902 GTVKGFAGQTAVGAVSVGASGAERRIQNVAAGEVSATSTDAVNGSQLY---KATQSIANA 1958
                                     1 MNHIYKVIFNKATGTFMAVAEYAK -- SHSTGGGSCATGQVGSVCTLSFARIAALAVLVIG 58
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CORRESPONDENCE ADDRESS:
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STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
CITY: Arlington
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ZIP: 22302-0280

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,697

FILING DATE: 01-APR-1996
FILING DATE: 01-APR-1996
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                                                                                                                                                                                                                                                                DNGQWVFKINGSADTQGHVGAAVGAGFHF 2047
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APPLICATION NUMBER: US 08/302,832
FILING DATE: 05-0CT-1994
PRIOR APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
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TELEFAX: (703) 415-0810
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARATERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1600 amino acids
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Matches 418; Conserv
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US-08-617-697-10
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                                                                                                                                                                                                                                                              TTENAVINATSGT-----VNISTKTGDIKG---GIESTSGNVNITASG---NTLKVSN- 1235
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                                                                                                                                                                                                                                                                                                                                                                                                                    1236 ITGQDVTVTADAGALTTTAGSTISATTGNANITTKTGDINGKVESSSGSVTLVATGATLA 1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FVKGLEKAASDNKTKNAAVTVGDLNAVAQTPLTFAGDTGTTAKKLGETLTIKGGQTDTNK 1527
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                                                                                                                 1044 DENISGENKAEITAKNGS----DETIGNASGGNADAKK--VTFDKVKDSKIST-DGHNVT 1096
                                                                                                                                                                                           LNSEVKTSNGSSNAGNDNSTGLTISAKDVTVNNNVTSHKTINISAAAGNVTTKEGTTINA 1156
                                                                                                                                                                                                                                                                                                            TTAKVTYDDTSKTSKVVYDVNVDDTTIEVKDKKLGVKTTT----LTSTGTGANKFALSNQ 1353
GTTRITRDEIGFTGTNGSLDKSKPHLSKDGINAGGKKITNIQSGEIAQNSHDAVTGGKIY 1122
                                                                                                                                                       1181 -GITTKVNKGVVRVGIDQTKGLT--TPKLTVGNNNGKGIVIDSQNGQNTITGLSNTLANV 1237
                                                                                                                                                                                                                                TNDKGSVRTTEQGNIIKDEDKTRAASIVDVLSAGFNLQGNGEAVDFVSTYDTVNFADGNA 1297
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                                                                          DLKTELENKISSTAKTAQNSLHEFSVADEQGNNFTVSNPYSSYDTSKTSDVITFAGEN--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ...woress:
...woress:
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Virginia
COUNTRY: U.S.A.
ZIP: 2202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: F.Loppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/08617697
Patent No. 5977336
GENERALINEORMATION:
APPLICANT: Barenkamp, Stephen J
                                          GNLTISSDKVNIT
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4.9%; Score 503.5; I
Best Local Similarity 20.8%; Pred. No. 1.1e<sup>-</sup>
Matches 379; Conservative 263; Mismatches
            CLASSIFICATION: 424
PRIOR APPLICATION 1424
PRIOR APPLICATION NUMBER: US 08/302,832
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/02166
FILING DATE: 16-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Berkstresser, Jerry W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    405 NSGLKVKLAKTLNNLTEVNTTTLNATTTVKVGSS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 503.5;
Pred. No. 1.1
                                                                                                                                                                                                           NAME: BEKSTESSEY, JEITY W
REGISTRATION NUMBER: 22,651
REFERNCE/DOCKET NUMBER: 1038-557
TELEPHONE: (703) 415-0810
TELEPAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1599 amino acids
01-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
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STRANDEDNESS
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US-08-728-470-10
                                                                                                                               RESULT: 13
US-08-728-470-10
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                                                      GT---VTFGINTTSGLKAGKSTLNDG----GLSIKNPTGSEQIQVGADGVKFAKVNNNGV 1056
                                                                                                                               VGAGIDGTTRITRDEIGF-TGTNGSLDKSKPHLSKDG----INAGGKKITNIQS-GEIA 1109
                                                                                                                                                                                                        QNSHDAVTGGKIYDLKTELENKISSTAKTAQNSLHEFSVADEQCNNFTVSNPYSSYDTSK 1169
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                                                                                        664 RTYWNVT-TLNVTSGSKFNLSIDSTGSGSTGPSIRN-----AELNGITFNKATFN-- 712
                                                                                                                                                       ----IKGNISNKSGDLNIIDKKSDAEIQIG----
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1435 INAKDAKLDGAASGDRTVVNATNASGSGNVTAKTSSSV-----NITGDLNTIN--- 1482
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                                                                                                                                                                                                                                                                                                                                                               Surface Proteins
                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: 419h Molecular Weight Surface Protein TITLE OF INVENTION: 61 No. 5928651-Typeable Haemophilus NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza STREET: Arlington STATE: Visgalia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
4.9%; Score 501.5; DB 2;
Best Local Similarity 21.3%; Pred. No. 1.3e-22;
Matches 373; Conservative 238; Mismatches 670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           544 ANDAVTIEQL--KAAKPTLNAG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US PCT/US93/02166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/05
FILING DATE: 16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1038-633
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APPLICATION NUMBER: GB 9205704.1
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Berkstresser, Jerfy W
                                                                                                                                                                                                                                               Sequence 10, Application US/08728470 Patent No. 5928651
                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Barenkamp, Stephen J
                                                                                        ||::|::|
----GLNIISENGRNTVRLRG 1499
                                                      2009 AVAVGLSKLSDNGQWVFKING 2029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 103
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (703) 415-0810
TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 22202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1529 amino acids
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GNVTAPTYNIGVKTTELNSDGTSDKFSVKGSGTNNSLVTAEHLASYLNEVNRTADSAL 637 ::	QSFTVKEEDDDDANAITVAKD-TTKNAGAVSILKLKGKNGLJVAT	KKDGTVTEGLSQDSGLTIGKSTLNNDGLTVKDTNEQIQVGANGIKFTNV 730  -   -   -   -   -   -   -   -   -   -	NGSNPGTGIANTARITRDKIGFAGSDGAVDTNKPYLDQDKLQVGNVKIT 779   :   :	NTGINAGGKAITGLSPTLPSIADQSSRNIELGNTIQDKDKSNAASINDILNTGFNLKN 837 	NNNPIDFVSTYDIVDFANGNATTATVTHDTANKTSKVVXDVNVDDTTIHLTGTDDNKKLG 897	VKTTKLNKTSANGNTATNF-NVNSSDEDALVNAKDIAENLNTLAKEIHTTKGTADTALQT 956 	FTVKKUDENNNADDANAITVGQKNANNQVNTLTLKGENGLNIKTDKNGTVTFGINTT 1013 	SGLKAGK-STLNDGGLSIKNPTGSEQIQVGADGVKFAKVNNNGVVGA 1059 	GIDGTTRITRDEIGFTGTNGSLDKSKPHLSKDGINAGGKKITNIQSGEIAQNSHDAVTGG 1119 	SS	FAGENGITTKVNKGVVRVGIDQTKGLTTPKLTVGNNNGKGIVIDSQNGQNTITGLS 1231 	NTLANVTNDKGSVRTTEQGNIIKDEDKTRAASIVDVLSAGFNLQGNGEAVDF 1283  : :::     :	VSTYDTVNFADGNATTAKVTYDDTSKTSKVVYDVNVDDTTIEVKDKKLGVKTTLIFSTGT 1343	GANKFALSNQATGDALVKASDIVAHLNTLSGDIQTAKGASOANNSAGYVDADGNKVIYDS 1403 	TDNKYYQAKNDGTVDKTKEVAKDKLVAQAQTPDGTLAQMNVKSVINKEQVNDANKKOGIN 1463 	EDNAFVKGLEKAASD-NKTKNAAVTVGDLNAVAQT-PLTFAGDTGTTAKKLGETLTIKGG 1521 	QTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGTKIDDKGVSFVDSSGQAKANT 1581 
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580	638	682 273	731	780	838	898	957	1014	1060	1120	1176	1232 771	1284	1344	1404	1464 939	1522 991
oy da	OY Db	Qy Db	Qy Dp	Qy Db	oy Dp	oy Op	Qy Db	Qy Dp	oy Dp	Qy	Qy	Oy Db	Qy Dp	Qy	Qy Db	Qy Db	Oy Dp

1582 PVLSANGLDLGGKVISNVGKGTKDTDAANVQQLNEVRNLLGLGNAGNDNADGNQVNIADI 1641 1642 KKDPNSGSSSNRTV---IKAGTVLGGKGNNDTEKLATGGIQVGVDKDGNANGDLSNVWVK 1698 1056 --TVNNNVTSHKTINISAAAGNVTTKEGT--TINATTGSVEV-TAQNGTIKGNITS---- 1106 1699 TQKDGSKKALLATYNAAGQTNYLTNNPAEAIDRINEQGIRFFHVNDGNQEPVVQGRNGID 1758 1107 -----QNVTVTATENLVTTENAVINATSGTVNISTKTG-------DIKGGIE 1146 SSASGKHSVAIGFQAKADGEAAVAIGRQTQAGNQSIAIGDNAQA-TGDQSIAIGTGNVVA 1817 |:: : | | | | : : | | | | : 1147 STSGNVNITASGNTLKYGD-IN 1205 1818 GK---HSGAI------GDPSTVKADN-----SYSVGNNNQFTDATQTD 1851 1852 VFGV--GNNITVTES-NSVALGSNSAISAGTHAGTQAKKSDGTAGTTTTAGATGTVKGFA 1908 1909 GQTAVGAVSVGASGAERRIQNVAAGEVSATST------DAVNGSQLYKATQSIAN 1957 1958 ATNELDHRIHQNENKANAGISSAMAMASMPQAYIPGRSMVTGGIATHNGQGAVAVGLSKL 2017 | : | : | : | : | : | 11375 GAASGDRIVVNATNASGSGNVTAKTSSSV------NITGDLNTIN-----GLNII 1418 APPLICANT: Barenkamp, Stephen J TITLE OF INVENTION: High Molecular Weight Surface Proteins TITLE OF INVENTION: Of No. 6218141-Typeable Haemophilus NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSEE: Shoemaker and Mattare, Ltd. STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza STREET: Bldg. 1 SOTTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/719,641 PAPELICATION NUMBER: US PCT/US93/02166 FILING DATE: 16-MAR-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: GB 9205704.1 FILING DATE: 16-MAR-1992 ATTORNEY/AGENT INFORMATION: PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/02 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS RESULT 14
US-08-719-641-10
US-08-719-641-10
Sequence 10, Application US/08719641
Patent No. 6218141
GENERAL INFORMATION: 2018 SDNGQWVFKING 2029 |:||: |: | 1419 SENGRNTVRLRG 1430 CITY: Arlington STATE: Virginia COUNTRY: U.S.A. COUNTRY: U.S.A. ZIP: 22202-0286 CLASSIFICATION: FILING DATE: 1020 -----1759 Q g ò ò qq q δ q a g οy ò ŏ g ò ò

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1642 KKDPNSGSSSNRTV---IKAGTVLGGKGNNDTEKLATGGIQVGVDKDCNANGDLSNVWVK 1698
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                                                                                                                           1232 NTLANVTNDKGSVRTTEQGNIIKDED------KTRAASIVDVLSAGFNLQGNGEAVDF 1283
                                                                                                                                                                                                               1284 VSTYDTVNFADGNATTAKVTYDDTSKTSKVVYDVNVDDTTIEVKDKKLGVKTTTLTSTGT 1343
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                                          1176 FAGENGITTKVNKGVVRVGIDQTKGLTTPKLTVGNNNGKGIVIDSQN----GQNTITGLS 1231
    ---TSRAAGINMDSINITGGLDFSITSHNRNSNAFEIKKDLTIN 728
                                                                                 ATGSN------FSLKQTKD-----SFYNEYSKHAINSSHNLTILGGNVTLGGE 770
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Sequence 9, Application US/08728470; Patent No. 5928651
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Barenkamp, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2018 SDNGQWVFKING 2029
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  675 SDSSVMFDIHANL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1014 SGLK---AGK-STLNDGGLSIKN----PTGSEQIQVGADGVKFAKVNNNGVVGA 1059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --NRVTSDQISQLK-GILDSNGQVFLINPNGITIGKDAINTNGFTASTLDISN--ENIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---AGISVTPTEISVDAKS-- 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --GNVTAPTYNIGVKTTELNSDGTSDKFSVKGSGTNNSLVTAEHLASYLNEVNRTADSAL 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 -----SKDKSGNIVLSAKEGEAEIGGVISAQNQQAKGGKLMITGDKVTLKTGAVIDLS 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTGINAGGKAITGLSPTLPSIADQSSRNIELGNTIQDKDKSNAASINDILNTG--FNLKN 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NTGENOG--YTTG------DGTKESPKGNSISKPTLIN-STLEQILRRGSYVNITA 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNNPIDFVSTYDIVDFANGNATTATVTHDTANKTSKVVYDVNVDDTTIHLTGTDDNKKLG 897
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                                                                                                                                                                                                                                                                                                                                                               Indels 471;
                                                                                                                                                                                                                                                                                                                     Length 1529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QSFTVKEEDDDDANAITVAKD-TTKNAGAVSILKLKGKNGLTVAT----
                                                                                                                                                                                                                                                                                                                   Ouery Match 4.9%; Score 501.5; DB 4; Best Local Similarity 21.3%; Pred. No. 1.3e-22;
                                                                                                                                                                                                                                                                                                                                                             fatches 373; Conservative 238; Mismatches 670;
                                            1038-625
                                 REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 415-0810
TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1529 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           544 ANDAVTIEQL -----
NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-719-641-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          653 ITVAKDTTKNAGAVSILKL-KGKNGLTVATKKDGTVTFG---LSQDSGLTIGKSTLNNDG 708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 VDVHKNITLGSGFLNITTKEGDIAFEDKSGRNNLTITAQGTITSGNSNGFRFNNVSLNSL 351
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TITLE OF INVENTION: High Molecular Weight Surface Proteins TITLE OF INVENTION: of No. 5928651-Typeable Haemophilus NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza STREET: Bidg. 1
CITY: Arlington STATE: Virginia COUNTRY: U.SA.
ZIPE: 22202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COUNTRY: ISM PC compatible
    High Molecular Weight Surface Proteins of No. 5928651-Typeable Haemophilus 10
                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               766 LDQDKLQVGNVKITNTGINAGGKAI--TG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 16-MAR-1993
APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/02166
FILING DATE: 16-MAR-1993
PRIOR APPLICATION NUMBER: GB 9205704.1
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BEKKETESSET, JETTY W
REGISTRATION NUMBER: 22,651
REFENCE/DOCKET NUMBER: 1038-633
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0813
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/728,470 FILING DATE: CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
US-08-728-470-9
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TFGINTTSGLKAGKSTLNDG----GLSIKNPTGSEQIQVGADGVKFAKVNNNGVVGAGID 1062 VTGGKIYDLKTELENKISSTAKTAQNSLHEFSVADEQGNNFTVSNPYSSYDTSKTSDVIT 1175 NTLANVTNDKGSVRTTEQGNIIKDEDKTRAASIVDV----LSAGFNLQG-NGEAVDFVS 1285 TYD-----TVNFADGNATTAKVTYDDTSKTSKVVYDVNVDDTTIEVKDKKLGVKTTTLTS 1340 1341 TGTGANKFALSNQATGDALVKASDIVAHLNTLSGDIQTAKGASQANNSAGYVDADGNKVI 1400 1401 YDSTDNKYYQAKNDGTVDKTKEVAKDKLVAQAQTPDGTLAQMNVKSVINKEQVNDANKKQ 1460 1519 KGCQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGTKIDDKGVSFVDSSGQAK 1578 1579 ANTPVLSANGLDLGGKVISNVGKGTKDTDAANVQQLNEVRNLLGLGNAGNDNADGNQVNI 1638 WVKTQKDGSKKALLATYNAAGQTNYLTNNPAEAIDRINEQGIRFFHVNDGNQEPVVQGRN 1755 953 GIESTSGNVNITASGNTLKVSNITGDDVTVTADAGALTTTAGSTISATTGNANITTKTGD 1012 1815 VVAGK---HSGAI------GDPSTVKADN-----SYSVGNNNQFTDAT 1848 1849 QTDVFGV--GNNITVTES-NSVALGSNSAISAGTHAGTQAKKSDGTAGTTTTAGATGTVK 1905 --NGQTTLTAKDSSIAG-----NINAANVTLNTTGTLTTTGDSKINATSGTLTINAKDA 1180 1955 IANATNELDHRIHQNENKANAGISSAMAMASMPQAYIPGRSMVTGGIATHNGQGAVAVGL 2014 ---DKNGT---V 1006 1176 FAGENGITTKVNKGVVRVGIDQTKGLTTPKLTVGNNNG----KGIVIDSQNGQNTITGLS 1231 GIDSSASGKHSVAIGFQAKADGEAAVAIGRQTQAGNQSIAIGDNAQA-TGDQSIAIGTGN 1814 459 ANFSIKASIMPFKSNANYALFNEDISVSGGGSVNFKLNASS---SNIQTPGVIIKSQNFN 515 746 -ITNQITIKAGVEGGRSDSSEAENANLTI------QTKELKLAGDLNISGFNKAE-ITA 796 410 T-TLNVTSGSKFNLSIDSTGSGSTGPSIRN-----AELNGITFNKATFN--IAOGST 827 IS------TDGHNVTLNSEVKTSNGSSNAGNDNSTGLTISA -----QNVTVTATENLVTTENAVINATSGTVNISTKTG--------DIKG 1063 GTTRITRDEIGF-TGTNGSLDKSKPHLSKDG----INAGGKKITNIQS-GEIAQNSHDA 606 ---ANFAENKSPLNIA--GNVINNGNLTTAGSIINIAGNLTVSKGANLQAITNYTFNVAG 1461 GINEDNAFVKGLEKAASD-NKTKNAAVTVGDLNAVAQT-PLTFAGDTGTTAKKLGETLTI 1639 ADIKKDPNSGSSSNRTV---IKAGTVLGGKGNNDTEKLATGGIQVGVDKDGNANGDLSNV 862 KDV--TVNNNVTSHKTINISAAAGNVTTKEGT--TINATTGSVEV-TAQNGTIKGNITS-----IKGNISNKSGDLNIIDKKSDAEIQIG----SFDNNGASNISIARGGA----KFKDINNTSSLNITTNSDTTYRTI----961 -- KVDENNNADDANAITVGQKNANNQVN-TLTLKGENGLNIKT----199 702 728 916 1756 1072 1.007 q qq qq Ω g g δ g δy g q Qγ g q ò g g õ ò ò à ò ò g ð ò

Db 1181 KLDGAASGDRTVVNATNASGSGNVTAKTSSSV------NITGDLNTIN-----GL 1224

OY 2015 SKLSDNGQWVFKING 2029 ::|:||: :: | Db 1225 NIISENGRNTVRLRG 1239

Search completed: September 13, 2001, 12:37:49 Job time: 48185 sec

us-09-361-619-7.rpr

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September 13, 2001, 03:35:34; Search time 76.31 Seconds
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                 Run on:
```

	(without alignments) 2043.367 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-361-619-7 10303 1 MNHIYKVIENKATGTEMAVANGSADTQGHVGAAVGAGFHF 2047
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	219241'seqs, 76174552 residues

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database

PIR\_68:\* 1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	surface protein XF	_	O)	ble RTX	surface		hypothetical prote	probable invasin Z	hypothetical prote	ABC-type transport	hypothetical prote	드	hypothetical prote	mucin, submaxillar	hypothetical prote	probable membrane	hemagglutinin/hemo	hemolysin A precur	hemagglutinin/hemo	toxin-like outer m	crystalline surfac	outer membrane pro	outer membrane pro	extracellular matr	hemagglutinin/hemo	lactocepin (EC 3.4	filamentous hemagg	~	lactocepin (EC 3.4
SUMMARIES	ID	D82671	A86036	A82615	B85547	A41477	B71704	T31105	E85822	S76109	C48399	C83339	T31102	T34434	T03099	A83412	D64962	F81045	A35140	B81192	A64556	JN0896	T30852	D71630	T31110	H81193	206997	S21010	8	B45764
	Length DB				5188 2						2020 2							2514 2					1029 2					3591 1	1902 1	1902 2
æ	Query	11.1	7.6	7.6		6.1	٠	5.5			5.0	4.9	4.9	4	4	4	4.6	4.6	4.6	4.5	4.5	4.4	4.4	4.4	4.4	4.4	4.4	4.3	4.3	4.3
	Score	1143	995.5	778	641	627	582	570.5	521	518	513.5	509.5	206	494.5	491.5	479	7	477.5	471	466	462	457.5	456.5	456	452	452	451.5	448	4	447.5
	Result No.	H	7	М	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

104;

Gaps

Indels 626;

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Query Match 11.1%; Score 1143; DB 2; Length 2059; Best Local Similarity 24.0%; Pred. No. 1.4e-36; Matches 547; Conservative 342; Mismatches 766; Indels 626

A; Gene: XF1529

hemagglutinin/hemo	outer membrane pro	toxin-like outer m	lactocepin (EC 3.4	hypothetical prote	RTX toxin RtxA VC1	high-molecular-wei	probable hemagglut	toxin-like outer m	hemagglutinin-like	hypothetical prote	high-molecular-wei	hypothetical prote	hemagglutinin-like	hemagglutinin-like	hemolysin A - Serr
G81044	JC1340	B64635	A32634	B81989	C82199	A43855	E83641	C71953	E82750	A83080	B43855	F83068	E82589	B82519	A28182
7	7	7	~	N	~	N	~	~	7	7	~	~	~	7	7
1995	1651	2529	1962	2015	4558	1536	3535	2902	3282	1417	1477	2154	3442	3455	1608
4.3	4.3	4.3	4.3	4.3	4.2	4.2	4.2	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.0
446.5	443	443	441.5	440	437	433.5	433.5	425.5	425	421	419	419	418	418	417
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 B08261. B08261. B08262. B0826	M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L. A.Reference number: A59328 A.Contente: anontation	A;Contents: annotation
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LAA 263	IG 376 306	VG 436 :  IG 342	OK 493   	AN 545 : ST 417	EL 596 VD 475	DD 647 527	KS 702 : FT 587	-VN 731    	AI 790 691	-SI 825     KSI 746	VD 881  -  VD 803	NS 920 : SE 860	-A 950 VV 920	LT 989 LT 980	3A 1043 KV 1025	KK 1099   KV 1072	VS 1159 :  IS 1125	IV 1217 '
:   : :    :  ::	LSIGSNSIK-RKIINVGAGVNKTDAVNVAQLEAVVKWAKERRITFQGDDNSTDVKIG         ::    ::     :	LDNTLTIKGGAETNALTDNNIGVVKEADNSGLKVKLAKTLNNLTEVNTTTLNATTTVKVG	SSSSTTAELLSDSLTFTQPNTGSQSTSKTVYGVNGVKFTNNAETTAAIGTTRITRDK	IGFARDGDVDEKQAPYLDKKQLKVGSVAITIDNGIDAGNKKISNLAKGSSAN	DAVTIEQLKAARPTLNAGAGISVTPTEISVDAKSGNVTAPTYNIG-VKTTEL 	NSDGTSDKFSVKGSGTNNSLVTAEHLASYLNEVNRTADSALQSFTVKEEDD 	DDANAITVAKDTTKNAGAVSILKLKGKNG-LTVATKKDGT-VTFGLSQDSGLTIGKS 	TLNNDGLTVKDTNEQ1QVGANGIKFTN	GSNPGTGIANTARITRDK-IGFAGSDGAVDTNKPYLDQDKLQVGNVKITNTGINAGGKAI 	TGLSPTLPSIADQSSRNIELGNTI	NDILNTGFNLKNNNNPIDFVSTYDIVDFANGNATTATVTHDTANKTSKVVYDVNVD : ::	DTTIHLTGTDDNKKLGVKTTKLNKTSANGNTATNFNVNS   :  :  :  :  :  :  :  :  :  :  :  :  :	SDEDALVNAKDIAENLNTLAKEIHTTKGTA :   :    : :       TSTDAVNGSQLNAVQVQASQPVTFTGNEGAVKRSLGQSVVISGESSTAGTYSGGNLKSVV	DTALQTFTVKKVDENNNADDANAITVGQKNANNQVNTLT 	LKGENGLNIKTDKNGTVTFGINTTSGLKAGKSTLNDGGLSIKNPTGSEQIQVGA	DGVKFAKVNNNGV-VGAGID-GTTRITRDEIGFTGTNGSLDKSKPHLSKDGINAGGKK   :	ITNIQSGEIAQNSHDAVTGGKIYDLKTELENKISSTAKTAQNSLHEFSVADEQGNNFTVS  :::	NPYSSYDTSKTSDVITFAGENGITTKVNKGVVRVGIDQTKGLTTPKLTVGNNNGKGIV
207	321	377	437	494	546	597	648 528	703	732	791	826	882	921	951 921	990	1044	1100	1160
qq	Qy Dp	Qy Db	oy Op	90 dg	Qy	Qy Db	Qy Db	Oy Dp	oy Ob	Oy Db	Oy Dp	Qy Db	Qy Dp	Oy Dp	Qy	Oy Op	oy Op	δy

-----GESSTAGTYSGGN-LKSVVDEAAGRIHLQLA---DSPKFGNVVINNGGK--- 1170 1278 GEAVDFVSTYDTVNF--ADGNATTAKVTYDDTSKTSKVVYDVNVD------DTTIEVK 1327 1206 GANGSKVASGGTVDLKNTDGNLTISK-----SGDSNDVVFNLSKDFKVDGMTSGTTVVNN 1260 D---GVKVGSDVALGTTGLTTANGPAVTASGIDAGSKVISHV-----AAGAVSETS 1308 SAGYVDADGNKVIYDSTDNKYYQAKNDGTVDKTKEVAKDKLVAQAQTPDGTLAQMNVKSV 1447 : : | | : : | | : : | | 1309 TDAVNGSQLNAVQVQASQPVTFTG-NEGAVRRS--LGQSVVISGESSTAGTYSGGNLKSV 1365 1448 INKEQ-----VNDANKKQGI----NEDNAF----VKGLEXAASDNKTK 1482 1366 VDEAAGTIHLQLADSPKFGNVVINNGGKISGVTAGTEETDAVNFSQLKSISTAVDQGWTL 1425 1483 NAAVTVG------DL-NAVAQTPLTFAGDTGTTAKKLGETLTIK------G 1520 1426 TASGANGSKVASGGTVDLKNTDGNLTISKSGDSNDVVFNLSEDLKEKSITVGNTQLDKDG 1485 1521 GQTDTNKLTDNNIGVVAGTDGF----TVKLAKDLTNLNSVNAGGTKIDDKGVSFVDSSGQ 1576 1577 AKANTPVLSANGLDLGGKVISNVGKGTKDTDAANVQQLNEVRNLLGLG-NAGNDNADGNQ 1635 1636 V---NIADIKK-DPN---SGSSSNRTVI------KAGTVLGGKGNNDTEKLATGGIQVG 1681 1604 VVSGGTVDLKNTDGNLAISKSGDSNDVVFNLSKDFKVDEVTAG-----NTVVNTDGVKVG 1658 1682 VDKDGNANG----DLSNVWVKTQKDGSKKALLATYNAAGQTNYLTNNPA---EAIDRINE 1734 QGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGRQTQA-GNQS 1793 1794 IAIGDNAQATGDQSIAIGTG-----NVVAGKHSG------AIGDPSTVKADNSY 1836 1867 VALGSNSAISACTHAGTQAKKSDGTAGTTTTAGATGTVKGFAGQTAVGAVGASGAERR 1926 1927 IQNVAAGEVSATSTDAVNGSQLYKATQSIANATNELDHRIHQNENKANAGISSAMAMASM 1986 1987 PQAYIPGRSMVTGGIATHNGQGAVAVGLSKLSDNGQWVFKINGSADTQGHVGAAVGAGFH 2046 1218 IDSQNGQNTITGLSNTLANVTNDKGSVRTTEQGNIIKDEDKTRAASIVDVLSAGFNLQGN 1277 DKKLGVKTTTLTSTGTGANKFALSNQATGDALVKASDIVAHLNTLSGDIQTAKGASQANN 1387 : W 2059 2047 F 2047 1328 1261 1388 1735 1126 1171 QΩ 셤 qq g qq g qq Dp ò qq g ò pp g g δλ ò g à ŏ δ q ò ò g ò q οy ò à ò ò οy ð

09	QY   978   OKRANDOWNTTLEGEBKCINITRON NO "TYPECHNTTSCLKAGKSTLNDOGGLSTRUPT 1034	
probable adhesin 25029 [imported] - Escherichia coli (strain 0157:H7) C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001 R;Perna, N.T.: Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001 A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7. A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Recession: A86036 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-1588 cSTO> A;Cross-references: GB:AE005174; NID:g12518349; PIDN:AAG58749.1; GSPDB:GN00145; UWGP:25G A;Cross-references: GB:AE005174; Substrain EDL933 C;Genetics: A;Genetics:	15.78; Score 995.5; DB 2; Length 1588;  23.08; Pred. No. 4.8e-31;  505; Conservative 267; Mismatches 665; Indels 761; Gamhalty 23.08; Pred. No. 4.8e-31;  10.11;	641 TYREEDDDANAITYRANDTYRNAGAVSILKIKGKNOLTVYRKDGTVTFGLSQD 694 1   1   1   1   1   1   1   1   1   1

147 SGDASIAIGSDDLHLLDQHGNPKHPK-GTLINDLINGHAVLKEIRSSKDNDVKYRRTTAS 205  116SLYVNEGKLGLVUISGATYSMRLGSIATMNGSAGIDSI	424 559 466 619 484 679	501 734 541 794 571 851 601	971 ANAITYGGKNANNQVNTLTLKGENGLNIKTDKNGTVFFGINTTSGLKAGKSTLNDGGLSI 1   1   1   1   1   1   1   1   1   1
		B:GN001 Db r. R.; A cy rrer, H cy rrer, H cy rtain; Ealgr rtins, E Db rii, D.A cy Sawasak cy	
OY 1715 AGGTNYLTINNPAEAIDRINEGGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAK 1774	RESULT 3 A82615 surface protein XF1981 [imported] - Xylella fastidiosa (strain 9a5c) C; Species: Xylella fastidiosa C; Species: Xylella fastidiosa C; Species: Xylella fastidiosa C; Species: Xylella fastidiosa C; Accession: A82615 R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Nature 406, 151-157, 2000 A; Title: The genome sequence of the plant pathogen Xylella fastidiosa. A; Reference number: A82515; MID:20365717 A; Note: for a complete list of authors see reference number A59328 below	A.Status: preliminary A.Molecule type: DNA A.Residues: 1-1190 <81NA A.Residues: Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.S.; Buench, M.S.; Buench, M.S.; Buench, M.S.; Buench, A.J.S. Briones, M.R.; Berro, J.A.; Franga, J.S.; Franca, A.J.S. A.Authors: Ferratian, V.C.A.; Ferro, J.A.; Franga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junquelra, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.C.; Martins, E.A.Authors: Martins, E.M.F.; Mateukuma, A.Y.; Menck, C.F.M.; Maracca, E.C.; Malyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, M.C.; de Oliveira, M.C.; de Silva, A.M.; de Nora, M.A.; de Silva, A.M.; Sawasak, A.A.thors: de Silva, A.M.; Salva, A.M.; Sal	M.; Tsuback, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Aimelda, S.; Veltore, A.; Reference number: A59328 A;Contents: annotation C;Genetics: A;Gene: XF1981 Query Match Best Local Similarity 20.5%; Pred. No. 8.2e-23; Best Local Similarity 20.5%; Pred. No. 8.2e-23; Matches 429; Conservative 185; Mismatches 432; Indels 1044; Gaps 72; Qy 64 SAYAQKKDTKHIAIGEONQPRRSGTAKAD

Thu Sep

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C. Species: Rickettsia rickettsii C. Species: Rickettsia rickettsii C. Species: Rickettsia rickettsii C. Species: B. Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 08-Oct-1999 C. Accession: A41477 R. Anderson, B.E.; McDonald, G.A.; Jones, D.C.; Regnery, R.L. Infect. Immun. 58, 2760-2769, 1990 A; Title: A protective protein antigen of Rickettsia rickettsii has tandemly repeated, A; Reference number: A41477; MuID:90354033 A; Receute type: DNA A; Messiques: 1-2249 <AND> A; Residues: 1-2249 <AND> A; Cross-references: GB:M31227; NID:9152465; PIDN:AAA26380.1; PID:9152466 A; Cross-references: GB:M31227; NID:916465; PIDN:AAA26380.1; PID:9152466 A; Cross-references: GB:M3127; NID:916465; PIDN:AAA26380.1; PID:9152466 A; Cross-references: GB:M31277; NID:9152465; PIDN:AAA26380.1; PID:9152466 A; Cross-references: GB:M31277; NID:915465; PIDN:AAA26380.1; PID:9152466 108; 3312 VSDLAGNLGSASKGVTVDTTAPVISFNTVAGDDVINNVEHIQAQIISGTATGAVAGDRLV 3371 --FAGQ-----TAVGAVSVGASGAERRIQNVAAGEV--SATSTDAVNGS------QLY 1949 1824 IGDPSTVKADNSYSV---GNNNQFTDATQTDVFGVGN-NITVTESNSVALGSNSAISAGT 1879 ---HAGTQAKKSDG-TAGTT-----TTAG---------ATGTVKG---- 1906 1950 KATOSTANATNELDHRIHQNENKANAGISSAMAMASMPQAYIPGRSMVTGGIAT--HNGQ 2007 3430 TAAVSLSVSTISGDNLI----NAAEAG--SALTLSG-----TGTNFATGTVVTVLLNGK 3477 202 255 GSDA-----TSSSLGAIALGAGTRAQLQGSI-----ALGQGSVVTQSDNNSRPAYT 300 301 PNTQALDPKFQATNNTKAGPLSIG-----SNSIKRKIINVGAGVNKTDAVNVAQL 350 DAINAAEKGAALTLSGSTSGVEAGQTVTVTFGGKTYTTTVAANGSWSTTVPAADLAALRD 3204 97 IAIGENA-----NAQGGQAIAIGSSNKTVNGSSLDKIGTDATGQE---SIAIGGDVKA 146 147 SGDASIAIGSDDLHLLDQHGNPKHPKG-----TLINDLI-NGHAVLKEIRSSKDNDVKY 199 200 RRTTASGH----ASTAVGAMSYAQGHFSNAFGTRATAKSAYSLAVGLAATAEGQSTIAI 254 Gaps 44 IATUNNAAFSNNVGNNNWNEITAAGVAN------GTPAGGPONNWAFTYGGDYTV 92 GEAAVAIGRQTQAGNQSIAIGDNAQATGDQSI-----AIGTGNVVAGKHSGA---Query Match
6.1%; Score 627; DB 2; Length 2249;
Best Local Similarity 22.2%; Pred. No. 1.3e-16;
Matches 477; Conservative 233; Mismatches 754; Indels 684; 2008 GAVAVGLSKLSDNGQW 2023 3478 GYSAT----IQSNGSW 3489 1777 3205 3258 1907 Dρ g ò qq δλ QQ ò g ò ò g δ g δ Ω òγ 셤 ò q ò

λ	411	KLAKTLNNLTEVNTTTLNATTTVKVGSSSSTTAELLSDSLTFTQPNTGS 459	
q	358	NVGNT	
λζ :	460	QSTSKTVYGVNG-VKFTNNAETTAAIGTTRITRDKIGFARDGDVDEKQAPYLDKKQLKVG	
Q.	406	ATVNVG	
≿ £	519	SVAITIDNG-IDAGNKKISNLAKGSSANDAVTIEQLKAAKPTLN 561	
g .	<b>d</b> 1	2	
<u>≻</u> 4	562	AGAGISVIPTEISVDARSGNVTAPTYNIGVRYTEINSDGTSDRFSGT 612	
ā	504	26	
≿ £	613	NNSLVTAEHLASYLNEVNRTADSALQSFTVKEEDDDDANAITVAKDTTKNAGAVSILKLK 672     :   : : :     :     :	
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ჯ გ	673	GKNGLIVATKROGTVTFGLSQDSGLTIGKSTLNNDGLTVKD 713 NANAVLTGAIDNTTGGDNVGVLNINGALSOVTGJIGNTNSLATISVGAVIKA 678	
>	714		
. A	679	VVVTGAIDSTGNANNGIVTFTGNSTVTG	
λ	771		
q	724		
Ā	828	ILNTGFNLKNNNNPIDFVSTYDIVDFANGNATTATVTHDTANKTSKVVYDVNVDDTIHL 887	
ą	764	I HI	
ζ	888	TGTDDNKKLGVKTTKLNKTSANGNTATNFNVNSSDEDALVNAKD 931	
ą	815	TATLGGAVIKATTIKLINAASVLTLINANAVLTGAVDNTTGGDNVGVLNLNGALSQVTGD 874	
λ	932	IAENLNTLAK EIHTTKGTADTALQTFTVKK	
q	875	IG-NTNSLATISVGAGTATLGGAVIKATTTKLTNAASVLTLTNANAVLTGAIDN 927	
λ	975	LNIKTDKNGTVTFGINTTSC	
ą	928	TTGGD	
χ 4	1030	IKNPTGSEQIQVGADGVKFAKVNNNGVVGAGIDGTTRITRDEIGFTGTNGSLDKSKP     :	
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≿ ≴	1087	HLSKDGINAGGKKITNIQSGEIAQNSHDAVTGGKIYDLKTELENKISSTAKTAQNSLHEF	
<b>?</b> .		LAT VNVGAGLLQVQGGVVKANT I NLTDNASAVIFT NPVVVI	
<u></u>		SVADEQGNNFTVSNPYSSYDTSKTSDVITFAGENGITTKVNKGVVRVGIDQ :::     ::	
ð		GAIDNTGNANNGIVTFTGNSTVTGNVGNTNALATVNVG	
χ̈́	1198	TKG	
ą	1112		
<i>≿</i>	1234	LANVTNDKGSVRTTEQGNIIKDEDKTRAASIVDVLSAGFNLQGNGEAVDF 128	
ą	1170	NALATVNVGAGITLQAGGSL-	
χ̈́	1284	VSTYDIVNFADGNAITAKVTYDDISKISKVVDVNVDD 1321	
ą	1223	IANGNNAILNVNTKLLTASHLTIGTVAEINIGAGNLFTIDASVGDVTILNAON 1275	

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1594 VKIGEIQGTGTNT-----LTLPAHFNLTG-------SINKTGGQALKLNFMNGGS 1636
                                                                                                                     1437 D-------PDNDDEGIVI----LNSVTAGKKLTIAG--GKTFGGAHKL-QTILFKG 1478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------LELG------ATTANVVLFNDAVQLTQTGNIGGFLDFNAKNGMV 1539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1804 -GDQSIA---IGTGNVVAGKHSGAIGDPSTVKADNSYSVGNNNQFTDATQTDVFGVGNNI 1859
1322 TTIEVKDKKLGVKTTTLTSTGTGANKFALSNQATGDALVKASDIVAHLNTLSGDIQT--- 1378
                                             1276 INFRARDSVLVLSNL----TGVGVNNILL------AADLVAP----GADEGTVVF 1316
                                                                                          ---AKGASQANNSAGYV----DADGNK----VIYDS---TDNKYYQAKNDGTVDKTKEVA 1424
                                                                                                                                                                                         1425 K-------DKLVAQAQTPDGTL--AQMNVKSVINKEQVNDANKKQGINE 1464
                                                                                                                                                                                                                                    1377 SSTAFNAGAIQINDATYTIDANNGNLNIPAGNIQFAHADAQLVLQNSSGNDRTITLGANI 1436
                                                                                                                                                                                                                                                                                      1465 DNAFVKGLEKAASDNKTKNAAVTVGDLNAV-AQTPLTFAGDTGTT---AKKLGETLTIKG 1520
                                                                                                                                                                                                                                                                                                                                                                                     1521 -GQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGTKIDDKGVSFVDSSGQAKA 1579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1633 -- GNQVNIADIKKDPNSGSSSNRTVIKAGTVLGGKGNNDTEKLA---TGGIQVGVDKDGN 1687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1747 QEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGRQTQAGNQSIAIGDNAQAT--- 1803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1672 GGTTSFANTFINTGAVTLAK-------GSITSFAKNVTATSF-VANSA 1711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1637 VSGVV-------GTAANSVGDITTAGATSFASSVNAKGTALL 1671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1860 TVTESNSVALGSNSAISAGTHAGTQAKKSDGTAGTTTTAGA----TGTVKGFAGQTAVG 1914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1712 TINFSNSLAFNSN--ITGG------GTTLTLGANOVTYTGT-GSFTDTLTLN 1754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1915 AVSVGA--SGAERRIQNVAAGEVSATSTDAVNGSQLYKATQSIANATN 1960
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RESULT 6
B71704
coll surface antigen (sca3) RP451 - Rickettsia prowazekii
c; Species: Rickettsia prowazekii
C; Species: Rickettsia prowazekii
C; Species: Rickettsia prowazekii
C; Date: 21-Nov-1998 #sequence\_revision 21-Nov-1998 #text\_change 03-Nov-2000
C; Accession: B71704
R; Andersson, S.G. E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark Nature 396, 133-140, 1998
A; Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A; Reference number: A71630; MUD:99039499
A; Reference number: A71704
A; Status: prellminary; nucleic acid sequence not shown; translation not shown A; Modecule type: DNA
A; Residues: 1-2140 CAND>
A; Residues: 1-2140 CA

A; Gene: sca3; RP451

Query Match 5.6%; Score 582; DB 2; Length 2340; Best Local Similarity 21.2%; Pred. No. 7.2e-15; Matches 499; Conservative 313; Mismatches 879; Indels 658;

Gaps 119;

<u>ک</u> ۾	252	SHSTGGGSCATGQVGSVCTLSFARIAALAVLVIGATLSGSAY-AQKKDTKHIAIGEQNQP 83 ::
λα qo	4 8	RRSCTAKADGDRAIAIGENANAQGQAIAIGSSNKTVNGSSLDKIGTDATGQESIAIGGD 143 
yy Ob		VKASGDASIAIGSDDLHLLDQHGNPKHPKG-TLINDLINGHAVLKBIRSSKDN 195 :   :   :
ž d	196	D-VKYRRTTASGHASTAVGAMSYAQGHFSNAFGTRATAKSAYSLAVGLAATAEGQSTIAI 254     : :   : :   :                   :   :   :
o de	255	GSDATSSSLGAIALGAGTRAQLQGSI-ALGQGSVVTQSDNNSRPAYTPNTQALDPKFQAT 313
3 2 4	314	TVKTEATK
a ko	345	VNVAQLEAVVKWAKERRITFQGDDNSTDVK IGLDNTLTIKGGAETNALTDNNIGVVKEAD 404
QQ	573	TKLLSINSTGQITFNRTLDLGAGGNIAFGKHGTLVVNGVTGSITTSENNOGILTI 627
QY	405	NSGLKVKLAKTLNNLTEVNTTLNATTTVKVGSSSSTTAELLSDSLTFTQPN 456
οy	457	
QQ	829	
رن م	514	OLKVGSVAITIDNGIDAGNKKISNLAKGSSANDAVTIEQLKAAKPTLNAGAGISVTPTEI 573
٥y	574	SVDAKSGNVTAPTYNIGVKTTELNSDGTSDKFSVKGSGTNNSLVTAEHLASYLNEVNRTA 633
οp	166	:   :
Oy	634	DSALOSFTVREEDDDDANAITVAKDTTKNAGAVSILKLKGK 674
g &	80T 675	ONFIVAHSAANVYITGELIGAENTROJGILEMIGGELGGELGGELGGELGGELGGGELGGELGGELGGELGG
qq	856	GAMIDGSVE
οy	722	ANGIKFTNVNGSNPGTGIANTARITRDKIGFAGSDGAVDTNKPYLDQDKLQVGNVKITNT 78
qq	606	ANDIFVDNIHETNGGI-LQLGGNLTTHNIDFGANGGTLEFNGN
δ.	782	GINAGGKAITGLSPTLPSIADQSSRNIELGNTIQDKDKSNAASINDILNTGFN 834
ò	835	LKNNNNPIDFVSTYD-IVDFANGNATTATVTHDTANKTSKVVYD
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δλ	988	HLTGTDDNK-KLGVKTTKLNKTSANGN-TATNFNVNSSDEDALVNAKD 931
QQ	1057	NLTISGNNGIKLGSKGNELSSLNIKGKVTVTNDLDIQNIHQLNINNGALFDDQSLTSAK -
Q. d	932	JAENLNTLAKEIHTTKGTADTALQTFTVKKVDENNNADDANAITVGGKNAN 982   Jaenly
ò	983	NOVNTLTLKGENGLN

Oy Db Oy

0y 0y 0y 0b

O.Y D.D

2098 1847 1848 -------TQTDVFQVGNNITVTESNSVALGSNSAISAGTHAGT------ 1883 1648 GSSS---NRTVIKAGTVLGGKGNNDTEKLATGGIQVGVDKDG----NANG-----DLSNV 1695 WVK------TQKD-GSKKALLA---TYNAAGQTNYLTNNPAEAIDRINEQGIR 1738 FFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGRQTQAGNQSIAIGD 1798 1559 GGTKIDDKGVSFVDSSGQAKANTPVLSANGL----DLGGKVISNVG-----KGTKDTDAA 1609 1879 -----NGCRDNCDVGNISNNSSNEAGGSSSDKN-YGITDVVPIFDPSFILDYTKNNYVAS 1932 1402 DSTDNKY--YQAKNDGTVDKTKEVAKDKLVAQAQTPDGTLAQMNVKS-----VI 1448 1509 AKKLGETLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNS-----VNA 1558 1247 TE-----QGN--IIKDEDKTRAASIVDVLSAGFNLQGNG----EAVDFVSTYDTVNFADG 1295 NA---TTAKVTYDDTSKTSKVVYDVNVDDTTI--EVKDKKLGVKTTTLTSTGTGANKFAL 1350 1351 SNQATGDALV-----KASDIVAHLNTLSGD-IQTAKGASQAN-NSAGYVDAD-GNKVIY 1401 1621 KNLDIPDALIDLDVLPRSLSLENYFTDIKADNLNFADDTATANFKDAVVIDAHIDNGGIL 1680 1681 KFNDNAWLTQEIKNANII----EIASDKFM------LLQKNIKAATLIADNANLVLL 1727 NKEQVNDANKKQGINEDNAFVKGLEKAASDNKTKNAAVTVGDLNAVAQTPLTFAGDTGTT 1508 VGNNNGKGIVIDSQNGQNTIT------1246 1391 IINAGSVNFSNTLKSGNIVISDGATMOVNNNYTATDISGKNANNGTLKLNNHTPINITST 1450 LSIKNPTGSEQIQVGADGVKFAKVNNNGVVGAGIDGT-TRITRDEIGFTGTNGSLDKSKP 1086 NENDDIEIDGSVTSTGNVNGTLNFNGSCKVTG-----LINNIVMLOAGAGDVSLSA 1330 1610 NVQQLNEVRNLLGLGN-----AGNDNADGNQVNIADIKK--DPN-----S 2042 LKRLNTNNQAIIAAGDE--DNIVTGIWGMSFYGKIKQNSKNS-ASGYQSNTGGGIIGFDY NAQATGDQSIAIGTGNVVAG----KHSGAIGDPSTVKADNSYSVG-----NNNQFTDA--HLSKDGINAGGKKITNIQSGEIAQNSHDAVTGGKIYDLKTELENKI----SSTAKTAQNS LHEFSVADEQG---NNFT-VSNPYSSYDTSKT-------1696 1993 1739 1296 1449 1728 1208 1225 1280 1143 1165 1028 1087 á Op 셤 ŏ qq ŏ ογ g δý g δ g δý qq Ω qq δ S G ò QQ Q Dp Db Qy Db Ω g Qy Db Qy Db

qq	2155 VYGRNKIKNYEKRITTITDQIAIGKFINTFYSYELLGGYNYLISHRTTITPMFGMRY 2211		
ò	1884 OAKKSDGTAGTTTTAGGATGTVKGFAGOTAVGAVSVGASGAFRRTONVAAGEVSATSTD 1941	Qy	444
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ò	NAGTSSAMAMASMDOAVIDGRSM	Οy	497
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3	NATCIDOGO	Qy	604
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hypo	othetical protein 2 - Haemophilus ducreyi	Qy	661
C; Da	Decres: natural ducrey. 1te: 22-oct-1999 #sequence_revision 22-oct-1999 #text_change 22-oct-1999	q	681
R; Wa	CCSSION: 131103 11d C.K.; Lumbley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, E.J. 2008-1100 6013-603-1009	Qy	693
A;Ti	occentra 100, 0013, 0021, 1530 ittle: Haemophilus ducreyi secretes a filamentous hemagglutinin-like protein. Farance numbar. 970004. MITTH.00130126	QQ	741
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A; MO	olecule type: DNA Jecule 1909-1919 Jecule 1919-1919 Jecule 1919 Jane 1-4019 Jane 1-4019	QQ	786
A;Cr C;Ge	A.Cross references: EMBL:AF057696; NID:g3929021; PID:g3929023; PIDN:AAC79761.1 C;Genetics:	Οy	812
A;Ge	ene: LspA2	qq	816
ā		QY	845
Ma Ma	Similarity 19.2%; Pred No. 5.3e-14; 4: Conservative 353; Mismatches 914: Indels	qq	876
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2	THE THE PROPERTY OF THE PROPER	δ	1002
S é	OLONANDO CONTRACTOR INTERPRETATION OF THE CONTRACTOR OF THE CONTRA	Dp	1041
3 8	EN VIVINTENET DE LEGISDENIE ONE NIETNONYE NINGINGENOUGEDVOLLIGGENNN MEGONGEN. VITORDARIO ORGENIETNOSTA TORDATHE DO CONTARIO ORGENIETNOSTA TORDATHE DO CONTARIO ORGENIETNOSTA TORDATHE DO CONTARIO ORGENIETNOSTA TORDATHE DE CONTARIO ORGENIETNOSTA TORDATHE DO CONTARIO ORGENIETNOSTA TORDATHE DE CONTARIO ORGENIETNOSTA ORGENIETNOSTA DE CONTARIO ORGENIETNOSTA ORGENIETNOSTA DE CONTARIO ORGENIETNOSTA ORGENIETNOSTA DE CONTARIO ORGE	Qy	1060
5 A		qq	1093
ò	VIKET PERKETNING YPPTPT SCHAROLD CAMEN ACCENTION	Qy	1102
3 8	FUASTREWURDHINDORY TERMINATURAN TRANSPORTED TRANSPORTED TO THE TOTAL TRANSPORTED TO THE TRANSPORTED TO THE TOTAL TRANSPORTED TO THE TOTAL TRANSPORTED TO THE TRANSPORTED	qa	1144
3 8	TABLED VERTILING LING LING VERTILION LOS CONTROLES AND LANGUAGE LING. LING LING LING LING LING LING LING LING	Qy	1156
3 2	CHARLEMOND I TATION DATE SONO CALLEMOND I RANDING COLATION OF THE SONO CALLE	qq	1185
3 3	VARIATEQUES REGISTRE A CATOLOGY OF FAMOULT I TO THE CATOLOGY OF THE CATOLOGY O	Qy	1210
Z q	JOI FNIÇALDERICATIONINATAGELEGENSINKRIINVGACVNKIDAVN 340	qq	1245
ě	U	δδ	1249
S da	I LTDDGNSRLNKVYADVVVVV GKDIELANNGQIHA - DQQLILINATGHVKLNDGSSVIS	qa	1299
Qy	DNNIGVVKEADNSGLKVKLAKTLNNLTEVNTTTLNATTTVKVGSSSSTTA	Οy	1306
7 g	:  : :  :  :  :  :  :  :  :  :  :  :  :	qq	1354

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RQQLNLTAVADNITNDSNISNKIAVLHSLGNISLNSKDQVYNL---GEIYAGNNISVKAH 1040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FTVSNPYSSYDTSKTSDVITFAGE---NGITTKVNKGVVRVGIDQTKGLTTP----KLTVG 1209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QLKNDVKLMGDITTK-----TKEGQASYKLYQASNGGHFGNDGSSGYSEGDLNIKGK 1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIDGTTRITRDEIG--FTGTNGSLDKSKPHLSKDGINAGGK-------KIT--- 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----NIQSGEIAQNSHDAVTGGKIYDLKTELENKISSTAKTAQNSLHEFSVADEQGNN 1155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGNIIKDEDKTRAASIVDVLSAGFNLQGNGEAVDFVSTYDTVNFADG---NATTAKVTYD 1305
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                                                                                                                549
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ELLSDSLTFTQPNTGSQSTSKTVYGVNGVKF-----TNNAETTAAIGTTRITRDKIGF 496
                                  582
                                                                                                                                                                                                                                        603
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                                                                                                                                                                                                                                                                                    -SKLSANKLDLN-----VTDNVTLNSKS-----TLSAGELTFKKVKNVTLNNDSE--
                                                                                                                                                                                                                                                                                                                                                            KFSVKGSGTNNSLVTAEHLASYLNEVN---RTADSALQSFTVKEEDDDDANAITVAKDTT
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                                                                                                                                                                                                                                     IEQLKAAKPTLNAGAGISVTPTEISVDAKSGNVTAPTYNIG-----VKTTELNSDGTSD
                                                                                                                                                                            NTSNNITLK - - - - NKSKFTAGNMTLNVTNNVTLNNDSELAANNLTLNVTKNVTLNDA - -
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UWGP:

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probable invasin 23135 [imported] - Escherichia coll (strain 0157:H7)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C;Accession: E85822
C;Accession: E87822
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IHQNENKANAGISSAMAMASMPQAYIPGRSMVTGGIATHNG---QGAVAVGLSKLSDNGQ 2022
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                                                                        KTEVNGQEVLVPQVYLAKQTIEEVEKQRGVGTGQIRAGIIDVKVDDVRNTGTIAGYAVGL 1616
VAHL--NTLSGDIQTAKGASQ-----ANNSAGYVDADGNKVIYDSTDN----KYYQAK 1412
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                                                                                                                                                                                                         NDGTVDKTKEVAKDKLVAQAQTPDGTLAQMNVKSVINKEQVNDANKKQGINEDNAFVKGL
                                                                                                                                                                                                                                                                  LDTEDDKLKGIKR-----IGDNYFEHQLITRLIEKVADNHLTLKHGLH-DIALVKKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----IKGGQTDTNKLTDNNIGVVAG-TDGF
                                                                                                                                                                                                                                                                                                                                                                                                        EKAASDNKTKNAAVTVGDLNAVAQTPLTFAGDTGTTAKKLGETLT----
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A; Accession: E85822
A; Accession: preliminary
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-2660 <STO>
A; Cross-references: GB: AE005174; NID: 912516151; PIDN: AAG57041.1; GSPDB: GN00145; N
A; Experimental source: strain 0;57:H7, substrain EDL933
C; Genetics:
A; Gene: Z3135
                                                                                                                                                                                                                                                                     103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            425 TILNATITVKVGSSSSTTAELLSDSLTFTQPNTGSQ--STSKTVYGVNGVKFTNNAETTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  483 AIGTTRITRDKIGFARDGDVDEKQAPYLDKKQLKV---GSVAITIDNGIDAGNKKISNLA
                                                                                                                                                                                                                                                                                                                                                                                                          ------EGVQDITLSDWKDNGDGSYTQILTTGAMSGTL--TLMPQLNGVDAAKAPAV
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                                                                                                                                                                                                                                                                                                                                                                             83 PRRSGTAKADGDRALAIG---ENANAQGGQALAIGSSNKTVNGSSLDKI-GTDATGQESI
                                                                                                                                                                                                                                                                                                          AKSHSTGGGSCATGQVGSVCTLSFARIAALAVLVIGATLSGSAYAQKKDTKHIAIGEQNQ
                                                                                                                                                                                                                                                                                                                                         546 ADSHST-----TRH-----TRH-----
             enterohemorrhagic Escherichia coli O157:H7
MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                   Length 2660;
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                                                                                                                                                                                                                                                          Best Local Similarity 20.8%; Pred. No. 1.9e-12;
Matches 484; Conservative 277; Mismatches 880;
                                                                                                                                                                                                                                   5.1%; Score 521; DB 2; 20.8%; Pred. No. 1.9e-12;
Nature 409, 529-533, 2001
A; Title: Genome sequence of
A; Reference number: A85480;
A; Accession: E85822
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Qy	735	PG-TGIANTARITRDKLGFAGSDGAVDTNKPYLDQDKLQVGNVKITNTGINAGGKA 789       : :     :     :     :   PADTQLSQSKSNTNDSGVAEVTFKGTVLGVHTAEATLPNGNNDTKIVNIAPDASNAQ 1345	
Qy	790	ITGLSPTLPSIADQSSRNIELGNTIQDKDKSNAASINDILNTGFNLKNNNNPIDFVSTYD 849 :	
Qy	850 1396	IVDFANGNATTATVTHDTANKTSKVVYDVNVDDTTIHLTGTDDNKKLGVKTTKLNKTSAN 909  :	
Oy Dp	910	GNTATNFNVNSSDEDALVNAKDIAENLNTLAKEIHTTKGTADTALQTFTVKKVDENNNAD 969 	
Qy Db	970	DANAITVGQKNA-NNQVNTLTLKGENGLNIKTDKNGTVTFGINTTSGLKAGKSTLNDG 1026  :	
Qy Db	1027 1508	GLSIKNPTGSEQIQVGADGVKFAKVNNNGVVGAGIDGTTRITRDEIGFTGTNGSLDKSKP 1086  ::	
Qy Dp	1087	HLSKDGINAGGKKITNIQSGEIAONSHDAVTGGKIYDLKTELENKISSTAKT 1138	
Qy Db	1139	AQNSLHEFSVADEQGN-NFTVSNPYSSYDTSKTSDVITFAGENGITTKVNKGVVR 1192  ::  :	
Oy Dp	1193 1659	VGIDQFKGLTTPKLIVGNNNGKGIVIDSQNGQNTITGLSNTLANVTNDKGS 1243 :	
Qy Dp	1244	VRTTEQGNIIKDEDKTRAASIVDVLSAGFNLQGNGEAVDFVSTYDTVNFADGNATTAKVT 1303	
Qy Db	1304	YDDTSKTSKVVYDVNVDDTTIEVKDKKLGVKTTTLTSTGTGANKFALSNQATGDA 1358 	
Qy Dp	1359	LVKASDIVAHLNTLSGDIQTAKGASQANNSAGYVDADGNKVIYDSTDNKYYQAKNDGTVD 1418  ::	
Oy B	1419	KTKEVAKTOKLVAQAQTPDGTLAQMNVKSVINKEQVND 1455	
Qy Dp	1456	ANKKOGINEDNAFVKGLEKAASDNKTKNAAVTVGDLNAVAQTPLTFAGDTGTTAKKLGET 1515	
Qy Db	1516	LIIKG-GQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGG 1560 	
Qy Db	1561	TKIDDKGVSFVDSSGQARANTPVLSANGLDLGGKVISNVGKGTKD 1605  :::      ::       :    IKVNFRGTSVTLSSTSVETDDRGFAEILVTSTEVGLKTVSASLADKPTEVISRLLNAKAD 2061	
0y	1606	TDAANVQQLNEVRNLLGLG1636	
Op	2062	INSATITSLEIPEGQVMVAQDVAVKAHVNDQFGNPILNESVTFSAEPPEHMTISQNIVST 2121	
ر ا	1637	NIADIKKDPNSGSSSNRTVIKAGTVLGGKGNNDTEKLATGGIQVGVDKDGN 1687     :	
S &	1688		

qq	2179	
٥y	1740	FHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGRQTQAGNQSI 1794
Op	2209	
0y	S	IGDNAQATGDQSIAIGTGNVVAGKHSGAIGDPSTVKADNSYSVGNNNQFTDATQTDVFG
g	2242	NGVTIQTQTIVKVTGNSSTAHVASFIADPSTIAATNSDLSTLKATVEDG 2290
δÿ	1855	VGNNITVTESNSVALGSNSAISAGTHAGTQAKKSDGTAGTTTTAGATGTVKGFA 1908
οgα	2291	SGNLIEGLTVYFALKSGSATLTSLTAVTDQNGIATTSVRGAITGSVTVSA 2340
δ	1909	GQTAVGAVSVGASGAERRIQNVAAGEVSATSTDAVNGSQLYKATQSIANATNELDHR 1965
qa	2341	VTTAGGMQTVDITLVAGPADASQSVLKNNRSSLKGDFTDSAELHLVLHD 2389
δλ	1966	Ţ
qq	2390	ISGNPIKVSEGLEFVQSGTNAPYVQVSAIDYSKNFSGEYKATVTGGGEGIATLIPVLNGV 2449
Oy de	2004	HNGQGAVAVGLSKLSDN-GQWVFKINGSADTQGHVGA 2039
3		
RESU S761 hypo C:Sp	JLT 9 109 othetica	RESULT 9 876109 hypothetical protein - Synechocystis sp. (strain PCC 6803) C.Species: Synechocystis sp.
A; Va C; Da	riety:	PCC 6803 - Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C; AC R; Ka O, K	Accessio (aneko, ' K.; Oku	nn: S76109 T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, Imura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yanada, M.: Yas
DNA A;Ti	Res. 3 itle: S	1996 nalysis of the genome of the unicellular cyanobacterium Synechocy
S. A;Re	eferenc	e number: S74322; MUID:97061201
A; Ac A; St	ccessio tatus: ]	Accession: S76109 Status: preliminary
A; Re A; Cr A; No	ssidues ross-re ote: th	A; Residues: 1-3029 <kan> A; Residues: EMBL:D63999; GB:AB001339; NID:g1001396; PIDN:BAA10087.1; PID:d101 A; Ortes: the nucleotide sequence was submitted to the EMBL Data Library, June 1996</kan>
Ö	lery Ma	5.0%; Score 518;
Wa	Matches 57	Similarity Zi.8%; 21; Conservative 256
δλ		VIGATLSGSAYA
q	627	VSGATISNVSGSGSVYTVTVTGIANNNGTVNLDFASGQNIRDTANNALSNTTPTTDEQYT 686
δ	82	RSGTAKADGDRAIAIGENAN-AQGGQAIAIGSSNKTVNGSSLDKIGTDAT 133
QQ	289	LDNTAPAASITLDANITADDIINIAESGQAIPITGTVGGEFNVGDTVTLTVNDKTFTGAV 746
Οy	134	GQESIAIGGDVKASGDASIAIGSDDLHLLDQHGNPKHPKGTLINDLINGHAVLKEI 189
qq	747	GAGGLESINVPGSDLIVDADLTIAASIATTDAAGNL 782
δλ		21
Ор		GSATDNQTYTVDTTAPIPIITVNDVTADNIINAAESGQAIPITGTVGGEFNVGDTVTLTV 842
Oy		
qq	843	NGKPFTGTVDANGDFSIDVLGGDLVNGSDLT1AASVATTDAAGNPGSASDNOTYTVDTTA 902

Oy Db	259	TSSSLGAIALGATTRAQLQG-SIALGQGSVVTQS-DNNSRPAYTPNT ::	303 962
QY	304	•	362
Ob	963	PVADIANFEATEEVVATVSDLAGNPATPATRITVDTVAPAV	1004
Qy Dp	363	TFQGDDNSTDVKIGLDNTLTIKGGAETNALTDNNIGVVKEADNSGLKVKLAKTLNN	418 1045
οy	419	LTEVNTTLNATTTVKVGSSSSTTAELLSDSLTFTOPNTGSQSTSKTV	466
qq	1046		1097
Qy Dp	467	YGVNGVKFTNNAETTAAIGTTRITRDKIGFARDGDVDEKQAPYLDKKQLKVGSVAI :	522 1139
Qγ	523		571
qq	1140	TIDGNTYTATVTGNAWTFNIPVADIANFEATEEVVATVSDLAGNPATPATRNITVDTTAP	1199
ΟŸ	572		608
QQ	1200	TVTINAIAVDDIINAVEAGSPVAVSGTTTGVEDGQVVTVTIDGNTYTATVTGNAW	1259
QV Dp	609	GSGTNNSLVTAEHLASYLNEVNRTADSALQSFTVKEEDDDDANAITVAKD :	658 1315
δý	629		718
qq	1316		1363
کم ہو	719	OVGANGIKFTNVNGSNPGTGIANTARITRDKIGFAGSDGAVDTNKPYLDQDKLOVGNVKI	778 1408
3 8	779	TNTGINA GGKAITGLSPTLPSIADOSSRNIEL-GNT	831
g 20	1409		1462
δλ	832	GFNLKNNN	882
qq	1463	FEATEE	1509
Qy Db	883	TTIHLTGTDDNKKLGVKTTKLNKTSANGNTATNENVNSSD : : ::	922 1565
δλ	923		982
qq	1566	::  :	1614
ογ	983	NQVNTLTLKGENGLNIKTDKNGTVTFGINTTSGLKAGKSTLNDGGLSIKNPTGS	1042
g	1615	- NDDTLVFNGTAEADSTVVVSLDGIEIGTVTANGAGEWTLDYTGTLL	1660
ò	1043	ADGVKFAKVNNNGVVGAGIDGTTRITRDEIGFTGTNGSLDKSKPHLSKDGINAGGKKI	1100
3	1001	TOPOL!	
oy Oy	1101	TNIQSGEIAQNSHDAVTGGKIIDLKTELENKIDSTAKIAQUNSLHERSII   :       :	1768
ò	1148	VADEQGNNFTVSNPYSSYDTSKTSDVITFAGENGITTKVNKG-VV	1191
. a	1769		1828
οy	1192	RVGIDQTKGLTTPKLTVGNNNGKG1-VIDSQNGQNTITGLSNTLANVTNDKGSVRTTEQG	1250

1865 --NSVALGSNSAISAGTHAGTQAKKSDGTAGTTTTAG--ATGTVKGFAGQTAVGAVSVGA 1920 2404 PVAVSG-----TTTGVEDGQVVTVTIDGNTYTATVTGNAMTENIPVADIANFEATEEV 2456 1838 VGN-------NNQFTD---ATQTDVFG----VGNNITVTES----- 1864 2691 IINAVEAGSPVAVS-GTTTGVE---DGQVVTVTIDGNTYTATVTGNAWTFNIPVADIA- 2744 1545 KLAKDLTNLNSVNAGGT---KIDDKGVSFVDSSGQ--------AKA 1579 2224 VVSLDGIEIGTVTANGAGEWTLDYTGTLLADGDYELSVTATNPTGNSATATQTIVVDTTA 2283 1580 NTPVLSA-----NGLDLGGKV-ISNVGKGTKDTDAANVQQLNEVRNLLGLGNAGNDNA 1631 2284 PIVIINAIAVDDIINAVEAGSPVAVSGITIGVEDGQVVIVIIDGNIYIAIVTGNAWIFNI 2343 DGNQV------IKAGT 1660 -----ANGDLSNVW 1696 1697 VKTQKDGSKKALLATYNAAGQTNYLTNN---PAEAIDRINEQ---GIRFFHVND----- 1744 CNQE---PVVQGRNGID----SSASGKHSVAIGFQAKADGEAAVAIGRQTQAGN---- 1791 2167 NIIKDEDKTRAASIVDVLSAGFNLQGNGEAVDFVSTYDTVNFADGNA----TTAKVTYDDT 1307 1365 IVAHLNTLSGD--IQTAKGASQANNSAGYVDADGNKVIYDSTDNKYYQAKNDGTV---- 1417 : : | | | | 1988 PTVTINAIAVDDIINAVEAGSPVAVSGTTTGVEDGQVVTVTIDGNITYTATVTGNAWTFNI 2047 1492 NAVAQTPLTFAGDTGTTAKKLGETLTIKGGQTDTNK-----LTDNNIGVVAGT--DGFTV 1544 EIGTVTANGAGEWILDYTGTLLADGDYELSVTATNPTGNSAT-----ATQTIVVDTTA 1987 ---SKTSKVVYDVNVDDTTIEVKDKKLGVKTTTLTSTGTGANKFALSNQATGDALVKASD 1364 2457 VATVSD-----LAGNPATPATRNITVDTVAPAVTIDSISDDTGAQANDFITNDDTLVFN |:| : | | | | | |:|: 2571 QTIVVDTTAPTVTINAIAVDDIINAVEAGSPVAVSGTTTGVEDGQVVTVTIDGNTYTATV 2511 GTAEADSTVVVSLDGIEIGTVTANGAGEWTLDYTGTLLADGDYELSVTATNPTGNSATAT QSIAIGDNAQATGDQSIAI-----GTGNVVAGKHSGA-IGDPSTVKAD-NSYS--------DKTKEV-----AKDKLVAQAQTPDGTLAQMNVKSVINKEQVN-2048 PVADIANFEATEEVVATVSDLAGNPATPATRNITVDTTAPTVTINAIAVDDIINAVEAGS 1921 SGAERRIQNVAAGEVSATSTDAVNGSQLYKATQSI-----ANATNELD 1963 1661 VLGGKGNNDTEKLATGGIQVG----VDKDGN-----1745 2745 1792 1632 1251 1882 1308 1935 1418 1455 qq qq Ob g δ qq g δ qq δý Dp δ g ٥y Ω δ d οχ ОÞ οχ QQ Qγ δ ò QQ Ω q οχ qq Qγ δ ò

RESULT 10
C48399
ABC-type transport protein ydbA.2 - Escherichia coli
C.Species: Escherichia coli
C.Species: Escherichia coli
C.Spate: 19-Nov-1993 #sequence\_revision 16-oct-1998 #text\_change 08-oct-1999

no.

784 NAGGKAITGLSPTLPSI 636 NGNNNS'TLARDLKVV 832 GFNLKNNNPIDFVSTY 695 GINVYGSDNNVTLDGKL 892 DNKKLGVKTTKLNKTSA 751GLELLGEKNALA 949 TADTAL 940 TADTAL 940 TADTAL 940 TADTAL 940 TA	863   GFAFVŢGENTGTINSĠSISĹLONĠKDPAPSPIYLLATNĠGSATNA 907   1055   GVVGAGIDGTTRITRDEIGFTGTWGSLDINSKRPHLSKDGINA-GGKKITNIQSGEIA 1109	1229 GLSNTLANVTNDKGSVRTTEQGNIIKDEDKTRAASIVDVLSAGFNLQGNGEAVDFVSTYD 1288  1051 GASNTVINQGTINLEKNGNYDDSLAANTLVGMAVYEHGTAIND 1093  1289 TVNFADGNATTAKVTYDDTSKTSKVVYDVNVDDTT	1415 GTVDKTKEVAKDKLVAQAQTPDGTLAQMNVKSVINKE	1387   DVSAKSLVVSANNAGDQNAFFWNQDNGVINFDHDSASAVKVTHSNFIAQ   1435   1531   NN-IGVVAGTDGFTVKLAKDLTNLNSVNAGGTKIDDKGVSFQDSGQAKANTPVLSAN   1587
in Escherichia cc Db Oy Oy () V.; Riley, M.; Cc Qy Db	PID: g1787668; QY	97; 997; 99 90 90 90		a & a & a & a
C; Accession: C48399; D64891; H64891 R; Moszer, I.; Glaeer, P.; Danchin, A. Biochimie 73, 1361-1374, 1991 A; Title: Multiple IS insertion sequences near the replication terminus in B; A; Reference number: A48399; MUID:92190338 A; Accession: C48399 A; Molecule type: DNA A; Residues: 464-2020 < MOS> A; Cross-references: GB:DB5081; NID:93041754 A; Cross-references: GB:DB5081; NID:93041754 A; Experimental source: strain K-12 A; Note: sequence extracted from NCB1 backbone (NCBIN:88089, NCBIP:88090) A; Note: sequence extracted from NCB1 backbone (NCBIN:88089, NCBIP:88090) B; Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Science 277, 1453-1462, 1997 A; Rose, D.J; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A; Title: The complete genome sequence of Escherichia coli K-12. A; Reference number: A64720; MUID:97426617 A; Accession: D64891 A; Status: nucleic acid sequence not shown; translation not shown	Molecule type: DNA  Prossidues: 1-839, 'IDLPLYFOTSVIT' <bla1>  Prossidues: 1-839, 'IDLPLYFOTSVIT' <bla1>  Prossidues: 1-839, 'IDLPLYFOTSVIT' <bla1>  Prossidues: 1-839, 'IDLPLYFOTSVIT' <bla1>  Prossidues: GB.AE000237; GB.U00096; NID:91787665; PIDN:AAC74483.1;  Procession: H64891  Proces</bla1></bla1></bla1></bla1>	Duery Match  5.0%; Score 513.5; DB 2; Length 2020;  Best Local Similarity 21.1%; Pred. No. 2.6e-12;  Matches 426; Conservative 266; Mismatches 786; Indels 539; Ga and Devenous and Development and Developmen	DD 278 KGTMTVTDPESMGIQIDGDKAIVN-NEGESTITNGGTGTQI-NGDDATANNNGKTTVDGK 335  QY 455 PNTGSQSTSKTVYGVNGVKFTNNAETTAAIGTTRIT-RDKIGFARDGDV 502  :  ::  :	

Db 1589 AGIILDLNEGTLANGAQGLIATPGTLLLRQLGWUNSGGEISSDRAFTLTTSALTNGGGR 1648  Qy 310FQATNNTRAGPLSIGSNSIKRIINVGAGVNKTDAVNVAQL 350  Db 1649 LRSGGVLTLRIAQALDNSLEGVLS-GTGGLDIRALALDNRSGSIGSKGAVDIDVSRLEND 1707  QY 351EAVVKWAKERRITFQGD	604  2050  653  653  2107  2107  2103  746  72233  7243  7343  73436  73436  73436  73436  73436  73436  73436  73436  73436
0.0   0.0	RESULT 11  RESULT 11  REGARDATOR 11  RECALCAS DETACLED PROTECT LIMPORTED   - PSEUDOMODIAS SETUDIOSS (STRAIN PAOL)  Phypothecical protect PRAZAGZ (imported) - PSEUDOMODIAS SETUDIOSS (STRAIN PAOL)  C. Species 15-Sep-2000 # Sequence_revision 15-Sep-2000 # text_change 31-Dec-2000  C. Accession: C3333 X

Qy	1065 TRITRDEIGFTGT  :  2656 LRLTVQRL	TRITRDEIGFTGTNGSLDKSKPHLS-KDGINAGGKKITNIQSGEI-AQNSHDAVTGGKIY	1122 2707
Ολ Db	1123	VSNPYSSY               :         :	1165 2767
Oy Db	1166	NGGVRVGIDQTKGLTTPK	1205 2826
Qy Dp	1206		1253 2884
oy op	1254	KDEDKTRAASIVDVLSAGFNLOGNGEAVDFVSTYDTVNFADGNATTAKVTYDD :	1306 2940
Qy Db	1307	TSKTSKVVYDVNVDDTTIEVKDKKLGVKTTTLTSTGTGANKFA ::	1349 3000
Qy Dp	1350	VKASDIVAHLNTLSGDIQTAKGASQANNSAGYVDADGNKVI   ::	1400 3060
S G	1401	GTVDKTKEVAKDKLVAQAQTPDGTLAQMNVKSV 	1447 3120
0 <u>y</u>	1448		1497 3175
Qy Dp	1498	PLTFAGDTGTTAKKLGETLTIKGGQTDTNKLTDN :	1531 3235
Oy Op	1532	DNGQGGLVSAQRALSFERDDTLNnagg-ringssllk	1566 3292
Oy Dp	1567 3293	GVSFVDSSGQAKANTPVLSANGLDLGGKVISNVGKGTKDTDAANVQQLNEVRNLLGLG	1624 3334
Qy Dp	1625 3335	NAGNDNADGNQVN IADIKKDPNSGSSSNRTVIKAGTVLGGKGNNDTEKLATG :	1676 3394
Oy Op	3395	GIQVGVDKDGNANGDLSNVWVKTQKDGSKKALLATYNAAGQTNYLTNNPAEAIDRINEQG :::	1736 3437
Qy Db	1737 IR 3438	IRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGRQTQA :	1789 3491
0y Db	1790 GN 1: 3492 GH	NQGGGLYASGLLSLDGQRFLNQGAAAGQGGKVGAGRIDFSLA	1819 3551
Oy	1820		1845
a à	3552		3611 1901
2 g	3612		3671

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filamentous hemagglutinin 1 - Haemophilus ducreyi
C;Species: Haemophilus ducreyi
C;Species: Haemophilus ducreyi
C;Species: Haemophilus ducreyi
C;Species: Haemophilus ducreyi
C;Accession: T31102
R;Ward, C.K.; Lumbley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, E.J.
Bacteriol. 180, 6013-56022, 1998
A;Title: Haemophilus ducreyi secretes a filamentous hemagglutinin-like protein.
A;Reference number: 220984; MuID:99030326
A;Accession: T31102
A;Accession: T31102
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-4152 <WAR>
A;Residues: 1-4152 <WAR>
A;Residues: 1-4152 <WAR>
A;Gross-references: EMBL:AF057695; NID:93929017; PID:93929018; PIDN:AAC79757.1
A;Gene: 1spAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126;
1902 GTVKGFAGQTAVGAVSVGASGAERRIQNVAAGEVSATSTDAVNGS---QLYKATQSIANA 1958
                                                                                                                          ---GGANVILGAGNLLVNRGRIT 3767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 AVLVIGATLSGSAYAQKKDTKHIAIGEQNQPRRSGTAKADGDRAIAIGENANAQGGQAIA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 IGSSNKTVNGSSLDKI-----GTDATGQESI--AIGGDVKASGDASIAIGSDDLHLLDQ 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --SPLKVFKGKSLSVVLLSLMPATPLLAQQNYAEALNGKVYVDSQHS-----STRIYEQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    285 GSVVTQSDNNSRPAYTPNTQALDPKFQATNNTKAGPLSIGSNSIKRKIINV-GAGVNKTD 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           344 AVN----VAQLEAVVKWAKERRITFQGDDNSTDVKIGLDNTLTIKGGAETNALTDNNIGV 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227 TINTDREVVSTSDIIPHRENGLLSVRNG-----KVTID-----KGGVATNGLSHFEV-V 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334 ADSAGS-----MYGSNIKFVVTDKGAGVKHKGIIFSEN-DINIKMDGGNASLKELYAKK 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          499 DGDVDEKQAPYLDKKQLKVGSVAITIDNGIDAGNKKISNLAKGSSANDAVTIEQLKAAKP 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 HGNPKHPKGTLINDLINGHAVLKEIRSSKDNDVKYRRTTASGHASTAVGAMSYAQGHFSN 224
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                            1959 TNELDHRIHQNENKANAGISSAMAMASMPQAYIPGRSMVTGGIATHNGQGAVAVGLSKLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 NKRYKLIFSKVKNCLVPVAENIKSASGNSGSSSNSKIAEDQEEEPDSLACSLS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 AFGTRATAKSAYSLAVGLAATAEGQSTIAIGSDATSSSLGAIALGAGTRAQLQGSIALGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----VTGDHES-----NIQ-----GALEVAGKKADLIIVNPNGITLNGVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      400 VKEADNSGLKVKLAKTLN--NLTEVNTT----TLNATTTVKVGSSSSTTAELLSDSLTFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 NHIYKVIFNKATGTFMAVAEYAKSHSTGGGSCATGQVGS----
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                                                                                                                                                                                                              3768 AAGDLV----ASAASLNNYGTLGGGG 3789
                                                                                                                     3726 TSLGDFAL----NAASLDLGNAASLA----
                                                                                                                                                                            2019 DNGQWVFKINGSADTQGHVGAAVGAG
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qq	387 DIDILAKDIELTEKGGLQANNKILLNSTGKINLRNASEVSADNVNVKSENLALENA 442	
οy	(2)	
QQ	VVANKITLNV	
ζö		
QQ	7 TENNOSKLSAKUMEENVIHNIIENNISKLSAKUMATAITAINOISKELSAKUMEN TANOSKLSAKUMEENVIHNIINIINIINIINIINIINIINIINIINIINIINIINI	
Oy Dp	655 VAKDTTKNAGNVSILKLKGKNGTTVATKKDGTYTFGLSQDSGLII-GKSTLNNU /V/   1	
٥y	708 GLTVKDTNEQIQVGANGIKFTNVNGSNPGTGIANTARITRDKI 750	
Db	604 DIVSKDKAIVTFSNNSDFTSNGSKLVDAQNNLTVNVNNFNITQGSEIILHGNVTLNAK 661	
ΟŊ		
qu	VSIENLNISSK	
οy		
οg	SLASNKSLDIYGNNFTNNGTIESVKSLNITN	
Oγ	VYDVNVDDTTIHLT 88	
q	ANIINKNLLAG	
Qy	GTDDNKKLG I I	
qq	0	
Qy	TALQTETVKKVDENNNADDANAITVGQKNANNQVNTL 98	
ДQ	VKTNSIGGGLHDANSIRVGE 934	
οy	10	
qa	NQLKVALRGKIYAGSNLTFKAKEGEKEQKSTAQAKIINRGTINVKNKL 992	
δy	FTRIT	
Dp	993 EYGSUVDVENNMRSMQVNLYEKIFNGDNPITLTLKNGVTFAKDFSNRRRRASNDG 1047	
Qy	1069 RDEIGFIGTNGSLDKSKPHLSKDGINAGGKKITNIOSGEIAQNSHDAVTGGKIYDL- 1124	
q	1048EGTNKKTFDNVAHLIEEAFSGYSNGNDHRASDDGHVKSPYYLL 1090	
οy	1125KTELENKISSTAKTAQNSLHEFSVADEQGNNFTVSNPYSSY 1165	
qq		
Οÿ	1166 -DTSKTSDVITFAGENGI-TTKVNKGVVRVGIDOTKGLTTPKLTVGNNNGKGIVIDS 1220	
qq	1147 GENNHSINLNIYPADEGVEKAKIFAGVLRNGTNGVEDKVYQELNDKAKKEYEDKFAK 1203	
δý	12210NGONTITGLSNTLANVINDK-GSVRTTEQGNIIKDE1256	
Q	1204 KFQGRFKSRFQNGEFDWAGDWAKEGNESYGSKETEEKYNGIKKEHTVNIGKHEIKVP 1260	
Qy	1257DVLSAGFNLQGNGEAVDFVSTY 1287	
Dp	1261 TVSFENLNNINHQQDKSDGIDKSIISELLAQPIYVAKADVPDVDPRVAQNDKAVDEDGLY 1320	
QY	1288 DTVNFADGNATTAKVTYDDTSKTSKVVYDVNVDDTTIEVKDKKLG 1332	
, da	1321 RTRLSYINQNNYLGAKYFFNQLDTEDDKLKGIKRIGDNYFEHQLITRLIEKVADNHLT 1378	
Οy	1333 VKTTLTSTGTGANKFALSNQATGDALVKASDIVAHLNT- 1371	

QQ	1379	LKHGLHDIALVKKLIDSASIQAKDLNLKVGEALTKEQKDNLKEDIVWYVKTE	1430
δy	1372	LSGDIQTAKGASQANNSAGYVDADGNKVIYDSTDNKYYQAKNDG	1415
Op	1431	VNAQEVLVPQVYLAKQTIEEVEKGRGVGTGQIRAGIIDVKVDDVRNTG	1478
Qy		TVDKTKEVAKDKLVAQAQTPDGTLAQMNVKSVINKEQVNDANKKQ	1460
Dp	1479	TIAGYAVGLEAKNKLKNTGDILSQKLSKLVGNNGLES10V11VDE1GATAV	
οy	1461	GINEDNAEVKGLEKAASDNKTKNAAVTVGDLNAVAQTPLTFAGD	20
QQ	1534	IKSEGHIYLETDKDKNVDLTASELKGNTGOIKAKDLNLNDIYETSYKYKYEKLFGKNGGE	1593
δλ	1505	TGTTAKKLGETLTIKGGQTDTNKLTDNNIGVVACTDGFTVKLAKD	1549
qq	1594	IGDRVTQTSQAKSVGTDASFDHLHLSLEGDVNQTGSNLKANRTTGVVKGDFNTKAGKD	1691
Qγ	1550	LTNLNSVNAGGTKIDDKGV-SFVDSSGQAKANTPVLSANGLDLG	1592
qq	1652	LEHRQIDIVISGTVYSASASGGGQSAGISLTDQGVETYTNKTATAGANADV	1702
QY	1593		1643
g	1703	:     :: : : : :         : : : : : : :	1758
οy	1644	AGTVLGGK	1703
Сp	1759	GORABEBAKKABVKBNEASETAAKETE-EAENDNVAEKDKTKPKFKKLTD-	1807
δy	1704		1758
Op	1808		1865
ò	1759		1806
쉼	1866	:	, 1921
٥y	1807		1866
Op	1922		1961
δλ	1867		1926
QC	1968	::  : ::   :   :   :   :   :   :   :	. 2022
ΟŸ	1927		1983
qq	2023	:   : : : :   : :   : :   :   :   :	\$ 2079
Οy	1984		
qq	2080	STREERGYNYSVSAGVGVSTAGGARPNGSVGLGVSAENENSKIV 2123	

RESULT 13
T34414
hypotherical protein K06A9.1a - Caenorhabditis elegans
c; Species: Caenorhabditis elegans
C; Species: T34434
C; Species: T3453
C; Species: T353

Map position: X Introns: 38/1; 75/3; 103/3; 132/2; 158/2; 222/1; 1088/1; 1367/1; 2039/1; 2049/1; 2075/	qq	: : : : : : :     : :  :     : :  :     : :       : :       : :       : :       : :       : :       : :       :   :       :       :
uery Match 4.8%; Score 494.5; DB 2; Length 2232; est Local Similarity 18.0%; Pred. No. 1.6e-11; atches 385; Conservative 326; Mismatches 958; Indels 467; Gaps 72;	Qy Db	KTDKNGTVTFGINTTSGLKAGKSTLNDGGLSIKNPTGSEQIQVGADGVKFAKV
17 MAVAEYAKSHSTGGGSCATGQVGSVCTLSFARIAALAVLVIGATLSGSAYAQKKD 71 : :	QQ QQ	NNNGVVGAGIDGTIRITRDEIGFIGINGSLDKSKPHLSKDGINAGGKKITNIQSGEIA : :   :   :   :   :   :   :   :   :   :
72 TKHIAIGEQNQPRRSGTAKADGDRAIAIGENANAQGGQAIAIGSSNKTV 120	y g	1110 QNSHDAVTGGKIYDL-KTELENKISSTAKTAQNSLHEFSVADEQGNNFTVSNPYSSYDTS 1168
121 NGSSLDKIGTDATGQESIAIGGDVKASGDASIAIGSDDLHLLDQHGNPKHPKGTLI 176 :  :	QY Dp	KTSDVITFAGENGITTKVNKGVVRVGIDQTKGLTTPKLIVGNNNGKGI :
177 NDLINGHAVLKEIRSSKDNDVKYRRTTASGHASTAVGAMSYAQGHFSNAFGTRATAKSAY 236	Qy Dp	1217 VIDSQNGQNTITGLSNTLANVTNDKGSVRTTBQGNIIKDEDKTRAA 1262 
TQSD 292     TIVP 487	qα	1263 SIVDVLSAGFNLQGNGEAVDFVSTYDTVNFADGNATTAKVTYDDTSKT 1310
293 NNSRPAYTPNTQALDPKFQATNNTKAGPLSIGSNSIKRKIINVGAGVNKTDAVNVAQLEA 352 1	oy O	1311 SKVVYDDNVDDFTIEVKDKKLGVKTTTLTSTGTGANKFALSNQATG 1356  1
VVKWAKERRITEQGDDNSTDVKIGLDNTLTIKGGAETNALTDNNIGVVKEADNSGLKVKL	Qy Db	1357 DALVKASDIVAHLNTLSGDIQTAKGASQANNSAGYVDADGNKVIYDSTDNKYYQA 1411 :     : :     : :     : :     :     :
AKTLNNLTEVNTTTLNATTTVKVGSSSTTAELLSDSLFFTQPNTGSQSTSKTVYGVNGV 	Qy Ob	1412 KNDGTVDKTKEVAKDKLVAQAQTPDGTLAQMNVKSVINKEQVNDANKKQGINEDNAFVKG 1471 :  -  -  -  -  -  -  -  -  -  -  -  -  -
KFTNNAETTAAIGTTRITRDKIGFARDGDVDEKQAPYLDKKQLKVGSVAITIDN :   ::   ::     ::     ::	Qy Dp	1472 LEKAASĎNKTKNAAVTVGDLNAVAQTPLTFAGDTGTTAKKLGETLTIKGGQTDTNKLTDN 1531
ISVTPTEISVDAKSGNVTAPT :   :   :   :   SPSSTOSSGAOSTLTTPS	Qy Db	1532 NIGVVAGTDGFTVKLAKDLTNLNSVNAGGTKIDDKQVSFVDSSGQAKANTPVLSANGLDL 1591 11
YNIGYKTTELNSDGTSDKFSYKGSGTNNSLVTAEHLASYLNEVNRTADSALOSFTVKEED  :  -  -  -  -  -  -  -  -  -  -  -  -  -	Qy Dp	1592 GGKVISNVGKGTKDTDAANVQQLNEVRNLLGLGNAGNDNDDGNQVNIADIKKDPNSGSSS 1651
TLNN : EAST	Qy Db	1652 NRTVIKAGTVLGGKGNNDTEKLATGGIQVGVDKDGNANGDLSNVWVKTQKDGSKKALLAT 1711
KPYL 	Qy Dp	1712 YNAAGGTNY-LTNNPAEAIDRINEQGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIG 1770 ::
PSIADQSSRNIELGNTIQDKDKSNAASIN  :: : :  :: : :	Qy Dp	1771 FQAKADGEAAVAIGRQTQAGNQSIAIGDNAQATGDQSIAIGTGNVVAGKHSGAIGD 1826 
DILNTGENLKNNNNPIDEVSTYDIVDEANGNATTATVTHDTANKTSKVYDVNVDDTTIH  DILNTGENLKNNNNPIDEVSTYDIVDEANGNATTATVTHDTANKTSKVYDVNVDDTTIH	Qy Db	1827 -PSTVKADNSYSVGNNNQFTDATQTDVFGVGNNITYVTESNSVALGSNSAIGATHAG 1882 
THTT 	Qy Db	1883 TQAKKSDGTAGTTTTAGATGTVKGFAGQTAVGAVSVGASGAERRIQNVAAGEVSATST 1940 
KGTADTALQTETVKKVDENNNADDANALTVGQKNANNQVNTLTLKGENGLNI	δδ	1941 DAVNGSQLYKATQSIANATNELDHR-IHQNENKANAGISSAMAMASMPQAY-IPGRSMVT 1998 

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-----LDKSKPHLSKDGIN---AGGKKITNIQSGEIAQNSHDAVTGGKIYDLKTELE 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2285 SPGATGASIGQPETSRISVAGSSGAPAVSSGASQAAGTSGAGPGTTASSVGVTETA---R 2341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2383 SVAGSSGAPAVSSGASQAAGTSGAG------PGTTASSVGVTETARPSVAGSGTTGTV 2434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGAPAVSSGASQAAĞTSGAGPGTTASSVGVTETARPSVAGSGTTGTVS-GASGSTGSSSG 2284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2050 IGQPETSRISVAGSSGAPAVSSGAŠQAAGTSGAGPGTTASSVGVTETARPSV-AGSGTTG 2108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKIGFAGSDGAVDTNKPYLDQDKLQVGNVKITNTGINAGGKAITGLSPTLPSIADQSSRN 807
1709 SGSTGSSSGSPGATGASICQPETSRISVAGSSGAPAVSSGASQAAGTSGAGPGTTASSVG 1768
                                                                                                                                                          GAS-----QAAGTSGAGPGTTASS------VGVTETARPSVAGSGTTGTVSGASG 1872
                                                                                                                                                                                                                                                 1873 STGSSSGSPGATGASIGOPETSRISVAGSSGAPAVSS---GASQAAGTSGAGPGTTASSV 1929
                                                                                                                                                                                                                                                                                                                                                      1930 GVTETARPSVAGSGTTGTVSGASGSTGSSSGSPGATGASIGOPETSRISVAGSSGAPAVS 1989
                                                                        2653 TTASSVGVTETARPSVAGSGTTGTVSGASGSTGSSSGS-----PGATGASIGQPETSRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          864 THDTANKTSKVVYDVNVDDTTIHLTGTDDNKKLGVKTTKLNKTSANGNTATNFNVNSSDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2435 SGASGSTGS-----SSGSPGATGASIGQP---ETSRISVAGSSGAPAVSSGASQAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            924 DALVNAKDIAENLNTLAKEIHTTKGTADTALQTFTVKKVDENNNADDANAITVGQKNANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2484 TSGAGPGTTASSVGVTETARPSVAGSGTTGTVSGASGSTGSSSGSPGATGASIGQP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ETSRISVAGSSGA-----PAVSSGASQAAGTSGAGPGTTASSVGVTETARPSVAGSGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----TGSEQIQVGADGVKFAKVNNNGVVGAGIDGTTRITRDEIGFTGTNGS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NKISSTAKTAQNSLHEFSVADEQGNNFTVSNPYSSYDTSKTS-----DVITFAGENGIT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GSTGSSGSPGATGASIGQP----ETSRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTVSGASGSTGSSSGSPGATGASIGQPETSRISVAGSSGAPAVSSGASQAAGTSGAGPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KSTLNNDGLTVKDTNEQIQVGANGI-----KFTNVNGSNPGT-----GIANTARITR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2109 TVSGASGSTGSSSGSPGATGASIGQPETSRISVAGSSG---APAVSSGASQAAGTSGAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -TELNSDGTSD--KFSVKGSGTNNSLVTAE-HLASYLNEVNRTADSALQSFTVKEEDDDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANAITVAKDTTKNAG-----AVSILKLKGKNGLTVATKKDGTVTFGLSQDSGLTIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     808 IELGNTIQDKDKSNAASINDILNTGFNLKNNNNPIDFVSTYDIVDFAN----GNATTATV
                                                                                                                                                                                                                                                                                                                                                                                                                            RRITFQGDDNSTDVKIGLDNT--LTIKGGAETNALTDNNIGVVKEADNSGLKVKLAKTLN
                                                                                                                                                                                                                                                                                                                                                                                                  YGVNGVKFTNNA---ETTAAIGTTRITRDKI-GFARDGDVD------EKQAPYLD
                                                                                                                                NTQALDPKFQATNNTKAGPLSIGSNSIKRKIINVGAGVNKTDAVNVA--QLEAVVKWAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKQLKVGSVAITIDNGIDAGNKKISNLAKGSSANDAVTIEQL---KAAKPTLNAGAGISV
                                                                                                                                                                                                                                                                                                           NLTEVNITIL -- - NATTIVKVGSSSSTIAELLSDSLT --- FTQPNT ----- GSQSTSKTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----PTEISVDAKSGNVTAPTYNIGVKT-----
                                                 -SIALGOGSVVTQSDNNSRPAYTP
                                                        AI-----ALGAGTRAQLQG-
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A; Residues: 1-13288 CECK>
A; Residues: 1-13288 CECK>
A; Cross-references: EMBL.AF005273; NID:92581863; PIDN:AAC62527.1; PID:92581864
A; Cross-references: EMBL.AF005273; NID:92581863; PIDN:AAC62527.1; PID:92581864
A; Eckhardt, A.E.; Timpte, C.S.; Abernethy, J.L.; Zhao, Y.; Hill, R.L.
A; Title: Porcine submaxillary mucin contains a cystine-rich, carboxyl-terminal domain in A; Recession: A40009; MUID:91236743
A; Recession: A40009
A; Molecule type: mRNA
                                                                                                                                                                                                                                            C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Mar-1999 #scuence_revision 24-Mar-1999 #text_change 02-Jun-2000
C;Date: 24-Mar-1999 #scuence_revision 24-Mar-1999 #text_change 02-Jun-2000
C;Accession: T03099; A40009; A28528; B29789
R;Eckhardt, A.E.; Timpte, C.S.; DeLuca, A.W.; Hill, R.L.
J; Biol. Chem. 272, 33204-33210, 1997
J; Biol. Chem. 272, 33204-33210, 1997
A;Title: The complete cDNA sequence and structural polymorphism of the polypeptide chain A;Reference number: Z14839; MUID:98070526
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A; Residues: 12139-12167, 'T',12169-12641 <TIM>
A; Cross-references: GB:M21174; GB:J03512; NID:g164321; PIDN:AAA30990.1; PID:g552360
A; Cross-references: GB:M21174; GB:J03512; NID:g164321; PIDN:AAA30990.1; PID:g552360
A; Experimental source: submaxillary gland
B; Eckhardt, A.E.; Timpte, C.S.; Abernethy, J.L.; Toumadje, A.; Johnson Jr., W.C.; Hill,
J. Blol. Chem. 262, 1139-11344, 1987
A; Title: Structural properties of porcine submaxillary gland apomucin.
A; Reference number: A92606; WUID:g7280230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 12139-12167, T', 12169-13288 <EG3>
A; Cross references: GB: MG1883; MID: 9454837; PIDN: AAA30998.1; PID: 9164374
A; Timpte, C.S.; Eckhardt, A.E.; Abernethy, J.L.; Hill, R.L.
J. Biol. Chem. 263, 1081-1088, 1988
A; Title: Porcine submaxillary gland apomucin contains tandemly repeated, identical
A; Reference number: A28528; MUID: 88087170
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                     -----TSGTNPSSPRSLSQITITPSPSQSTESTQTSLPSSSPSPSTHSVS 2005
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                                                                   GGIATHNGQGAVAVG--LSKLSDNGQWV-FKINGSA 2031
                                                                                                              SSEGITMSSGATTSGDKMSFLSSTGTTVSFSSRGSS 2041
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A; Molecule type: protein
A; Residues: 1572-1607 < EC2>
C; Suporfamily: pig submaxillary mucin
C; Keywords: tandem repeat
                                                                                                                                                                                                                              mucin, submaxillary - p1g
N;Alternate names: apomucin
                                   1955 TVTIGS---
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STGSSGGSPGATGABIGOPETERES 3193  **TYQKDGSKRALLATYNAAGCTNYLTNNPAEA 1728		VR-NLIGLGNAGN-DNADGNQVNIADIKKDPNSGSSSNRTVIKAGTVLGGKGNNDTEKLA	qu
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                                 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bi
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itle: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic parceesses number: A82950; MUID:20437337
ccession: A83412
tatus: preliminary
colecule type: DNA
sesidus: 1-2468 <570>
ross-references: GB.AE004613; GB:AE004091; NID:g9947856; PIDN:AAG05263.1; GSPDB:GN an, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lory, S.; Olson, M.V. 1re 406, 959-964, 2000 66 57 IGATLSGSAYAQKKDTKHIAIGEQNQPRRSGTAKADGDRAIAIG---ENANAQGGQAIAI 113 278 GSIALGQGSVVT----QSDNNSRP--AYTPNTQALDPK------FQATNNTKAGP- 320 --LSIGSNSIKRKIINVGAGVN-----KTDAVNVAQLEAVVKWAKERRITFQGDDNS 370 114 GSS-----NKTVNGSSLDKIGTDATGQESIAIGGDVKASGDASIAIGSDDLHLL-DQH 165 157 GSSVPPDTTPPKAASGLKIAPDGSSISGQAEAGASVGIDTNGD-----GKPDLTVIADAN 211 166 GN---PKHPKGTLINDLINGHAVLKEIRSSKDN-----DVKYRRTTASGHASTAVGAMSY 217 218 AQGHFSNAFGTRATAKSAYSLAVGLAATAEGQSTIAIGSDATSSSLGAIALGAGTRAQLQ 277 304 INPPLINGETVIVIVIDPAGNNSTPVIVEAPDITAPAPATDVQVAPDGSSSVIGNAEPGAI 363 364 VGVDTDGDGQPDTTVVVGPGGSFEVPLNPPLINGETVTVIVTDPAGNSSTPVTAEAPDFP 423 371 TDVKIGLDNTLTIKGGAE---TNALTDNN---IGVVKEADNSGLKVKLAKTLNNLTEVNT 424 425 TTLNATTTVKVGSSSSTTAELLSDSLTFTQPNTGSQSTSKTVYGVNGVKFTNNAETTAAL 484 485 GTTRITRDKIGFARDGDVDEKQAPYLDKKQLKVGSVAITIDNGIDAG---NKKISNLAKG 541 529 TLTDGNGNPIG-QTTADAN-----GNWSFTPSTPLPDGTVVNVARDAAGN 573 601 662 NAGAVSILKLKGKNGLTVATKKDGTVTFGLSQDSGLTIGKSTLNNDG------708 ----LTVKDTNEQIQVGANGIKFTNVNGSNP-----GTGIANTAR----IT-----RDK 749 602 SDKFSVKGSGTNNSLVTAEHLASYLNEVNRTADSALQSFTVKEEDDDDANAITVAKDTTK 661 629 GNWTFTPSTPLPNGTV-----VNATA----TDPSGNASSPA-SVTV 664 Gaps 18 AVAEYAKSHS-----TG----GGSCATGQVGS-----VCTLSFARIAALAVLV 56 542 SSANDAVTIEQLKAAKPTLNAGAGISVTPTEISVDAKSGNVTAPTYNIGVKTTELNSDGT uery Match 4.6%; Score 479; DB 2; Length 2468; est Local Similarity 21.4%; Pred. No. 7.3e-11; atches 467; Conservative 248; Mismatches 933; Indels 532; enetics: ene: PA1874 265

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1863 FTPGTPLANGTVINAVAEDAAGNASGPASTTVDSVAPSAPLLSISADGALLTGTAEPNSQ 1922 1808 ASTIVDIVAPAIPVINPSNGSVITGIAE----VGAKVILIDGNGNPIGETIADGSGNWT 1862 1882 GTQAKK-SDGTAGTTTTAGATGTVKGFAGQT------AVGAVSVGASGAERR 1926 NAAGQTNYLTNNPAEAIDRINEQGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQ 1772 STVKADN-----SYSVGNNNQFTDATQTDVFGVGNNITVTESNSVALGSNSAISAGTHA 1881 1773 AKADGEAAVAIGRQTQAGN---QSIAIGD-NAQATGDQSIAIGT-GNVVAGKHSGAIGDP 1759 ILTDGN-----GNPIGQTLADGSGNWSFTPGTPLANGTVVNAVAQDPAGNTSGP 1927 IQNVAAGEVSATSTDAVNGS 1946 :: | |:: | |:11 1923 VRIVVNGDTANPITVTVDGA 1942 1713 1828 qq ογ g δ g οy pp ά

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.sib.ch).
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=783;
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ID 190K_RICRI STANDARD; PRT; 2249 AA.
AC P15921;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE 190 KDA ANTIGEN PRECURSOR (CELL SURFACE ANTIGEN).
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Antigen; Repeat; Signal; S-layer; Glycoprotein.
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MEDLINE-9426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
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CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CODING FOR THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT BETWEEN AMINO ACIDS 839 AND 840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALLEY M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., May B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92190338; PubMed=1665988;
Moszer I., Glaser P., Danchin A.;
"Multiple IS insertion sequences near the replication terminus in
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
NCBL_TaxID=562;
                                                                                                                                                                    YDBA_ECOLI STANDARD; PRT; 2003 AA. P3665; P76856; P766859; P76859; P76856; P768708; P768859; P768859; P76889; P768899; P768999; P7689999; P768999; P768999; P768999; P768999; P768999; P768999; P76899
   -----VVTATN 1791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mau B., Shao Y.; "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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35 I -> V (IN REF. 2).
205949 MW; B83Al2C8B53220EE CRC64;
1755 TTFDGAAKSGGNILIKSGSTLDLSGVSTLAL---
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EMBL; AE000237; AAC74487.1; ALT_SEQ.
EMBL; D90778; BAA15009.1; ALT_SEQ.
EMBL; D90778; BAA18880.1; ALT_SEQ.
EMBL; D90779; BAA18881.1; ALT_SEQ.
EMBL; X62680; -; NOT_ANNOTATED_CDS.
ECOGene; EG11307; ydbA.
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Biochimie 73:1361-1374(1991).
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                                                                                                                                                                                                                                                            218 VITGDNATVNNNGKTTVDGKDSTGTEINGNNGKVIQDGDLDVSGGGHGIDITGDSATVDN
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                                                                                                                                                                                                                                                                                                                ----VKEADNSGLKVKLAKTLNNLTEVNTTTLNATTTVKVGSSSSTTAELLSDSLTFTQ
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                                                 554;
  DB 1; Length 2003;
4.9%; Score 506; DB 1
21.0%; Pred. No. 3e-11;
                                                 Conservative 264; Mismatches
                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1817 ALRYDVHNLDS-----SRSIAFG-NINKTADTDVKQQYLEFRSEGAKTFEPSEGLKVTP 1869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1898 -AGA--TGTVKGFAGQTAVGAVSVGA-SGAERRIQNVA-----AGE----VSATSTDAV 1943
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                                                                                                 NAGVMTNNVDVSGGILNNAGEMTAQITMNAG---ADSSLVNNTGTINKIVQNAGVFNNSG 1253
                                                                                                                                                                              -- OVNDANK 1458
              1077
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   ASDIVAHLNTLSGDIQTAKG---ASQANNSAGYVDADGNKVIYDSTDNKYYQ----AKNDG
                                                           TGVININVGTGQAFYNDGTGTI-VNYGTICTFGVCQSGNEYNNTDDFTSLIYTGGDTITR
                                                                                      -----IEVKDKKLG--VKTTTLTSTGTGANKFALSNQATG-----
                                                                                                                                                                                                                                                                                                1371 VSAKSLVVSANNAGDQNAFFWNQDNGVINFDHDSASAVK-----
                                                                                                                                                                                 1416 TVDKTKEVAKDKLVAQAQTPDGTL---AQMNVKSVINKE-----
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ID HLYA_PROMI STANDARD;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its wise by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPWA REQUIRES HPMB FUNCTION.
SUBCELLLALAR LOCATION: OUTER MEMBRANE. SUBCELLLALS ITE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPMA MAY BE RESPONSIBLE FOR PORE FORMATION. SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA).
                                                                                                                                                                                                                                                                                                         MEDLINE-9017087; PubMed-2407716; MEDLINE-917087; PubMed-2407716; MEDLINE-917087; PubMed-2407716; MEDLINE-917087; PubMed-2407716; Melch T.S., Welch R.A.; He Proteus mirabilis calcium-independent "Nucleotide sequencing of the Proteus sequence similarity with the Seriatia marcescens hemolysin genes (shlA and shlB)."; Jaccescens hemolysins Rectariot. 172:1206-1216(1990).

J. Bacteriol. 172:1206-1216(1990).

CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---TSANG---
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                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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1577 AA; 165869 MW; 175975EOC924B2D9 CRC64;
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21.8%; Pred. No. 4e-10;
Last sequence update)
Last annotation update)
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Hemolysis; Toxin; Outer membrane; Signal.
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   01-AUG-1990 (Rel. 15,
01-NOV-1990 (Rel. 16,
HEMOLYSIN PRECURSOR.
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                                                                                                                       Proteus mirabilis.
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                                                                                                                                                                  958 TVKKVD----ENNNADDANAITV-GQKNANNQVNTLTLKGENGLNI-KTDKNGTVTFGIN 1011
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466
                                                                                                    410 TLDAAKINAGNNLAINANKDIHINGLVEKESRSENGN---KRNHTSRLESGSWSNSHQTE
                                                                                                                                                                                                                                                                                           527 MWGGIGGGONKNNNNQQQVSHAT----QLTADGQLLLAADNNVNITGSQVKGNQGAFVK
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                                                                   -----NTATNFNVNSSDE---DALVNAKDIAENLNTLAKEIHTTK---GTADTALQTF
                                                                                                                                                                                                               467 TLKASELTAGKDLGLDAQGSITAQGAKLHANENVLVNAKDNINLNVQKTNNDKTVTDNHV
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1333 NSNKDLTLSGANVTADSVTGNVGGSLNIASQKES---DRHVTVGVNVGYNHTNDPKSSQV 1389
                                                                                                                                                                                                                                                                                                                               1751 VQGRNGIDSSASG-----KHSVAIGFQAKADGEAAVAIGRQTQAGNQSIA----IGDN 1799
                                                                                                            NK-----TAKAGGSLLEKTIKDTIDSGIKSSTD-----AISDKYNSLSSTIADKTGISDE 1439
                                                                                                                                                                       1800 AQATGDQSIA-IGTG--NVVAGKHSGAIGDPSTVKADNSYSVGNNNQFTDATQTDVFGVG 1856
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(SURFACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SCA5) (ROMP B)
(CONTAINS: 120 KDA SURFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTIGEN)
(120 KDA OUTER MEMBRANE PROTEIN OMPB); 32 KDA BETA PEPTIDE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92167802; PubMed=1724278; Gilmore R.D. Jr., Cieplak W. Jr., Policastro P.F., Hackstadt T.; Gilmore R.D. Jr., Cieplak W. Jr., Policastro P.F., Hackstadt T.; "The 120 kilodalton outer membrane protein (rOmp B) of Rickettsia rickettsii is encoded by an unusually long open reading frame: evidence for protein processing from a large precursor."; Mol. Microbiol. 5:2361-2370(1991).
                                                                                                                                                                                                                                                                                          1857 NNITVTESNSVALGSNSAISAGTHAGTQAKKSDGTAGTTTTAGATGTVKGFAGQTAVGAV
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                                                                                                                                                                                                                               1440 TKAKIDQGFGKVGNGIKNIVTG-----AEGHTANADIKVTHVDNDAVTKTT----
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32 KDA BETA PEPTIDE.
POLY-THR.
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=783;
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(Rel. 39, Last sequence update)
(Rel. 39, Last annotation update
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1654; 629; G 629; G STLNNDGL     :NVGV	TODKI  TODKI  TODKI  TOTAL  TO	FFTVK FFTVK LKAGK GQ	STNGS	ENGIT         TNNIT LANVT   :   AVDEV	LISTC LGGEN BADGNE BADGNE NDANE	-LTFAGDTGT     :    FNTVALENGT TVKLAKDLTN 
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; Le ; In SQDSG   : DQTAA TRD-K :	SSRNI SSRNI ATKNP DFANC 	TETGTDO RETGTDO RETGTO RET	RITRDE	SASAD QNTIT QNTIT	DKKLG :  IGTIG OANNS :  RTTNP IVKSVI	TP TVGG( TVA(
DB 1; 8-10; 561; VTFGLS GFD	SIADQ     OAA TYDIV   LGDNA	EIHTT EIHTT DGQLT NKNGTV	IDGTTI        	NGTLE: SQNG: NGKVN LSAG- IGAGG	TIEVK        TINGK  S  S 	NAVAÇ    :   NIVSG   NNIGV  :  :   DGTGI
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ice 469.5; DB 1; dd. No. 4.8e-10; Mismatches 551; ELTVATKKDGTVTFGLS; -AATTVDGAGFD GGGGGGANTARIT	AITGL TITGO TITGO NNNNP H	INANTI ILAENI ILI ILI ILI ILI ILI ILI ILI ILI ILI I	DGVKFAKVNNNGVVGAGIDGTTRI:	KTSDV   :     NTAGV G   IFKLA       KTRAA	FDDGNATTAKVTYDDTSKTSKVYDVNVDDTTIEVKDKKLGVKTT	GSFVE GQTDT
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arit; conse: CDTTK! SFAGS	CLQVG   vvH   CNTG-    COGGR	LVKAI TATNE	NPTGS        NATG- GINAG	QGNNE         IDQTN         VVQLS	ADGNA:	VKG: NVGEG
tch al Similarity 22.1%; Pred. No. 4.88-10; 386; Conservative 174; Mismatches 561; Indels 629; Ga ANAITVAKDTTKNAGAVSILKLKGKNGLTVATKKGTVTFGLSQDSGLTIGKSTLNNDGL                                 ASTATIVASFAGSAMGAAIQONTITNGAATTVDGAGEDQTAAPANVGV TVKDTNEQIQVGA-NGIKFTNNVGSNPGTGIANTARITRD-KIGFAGSDGAVDTN TALNAVITANANNIINFNTPAGSENGL-LLNTANNILAVTVSEDTTLGFITN	KPYLDQDKLQVGNVKITNTGINAGGK-AITGLSPTLPSIADQSSRNIELGNTIODKDKSN		DGGLSIKNPTGSEQIQVGADGVKFAKVNNNGVVGAGIDGTTRITRDEIGFTGTNGSLDKS	EFSVADEGGNNET VSNPYSSYDTSKTSDVITF	TVN TVD ALS 11 VLS DNK	NEDNAFVKGLEKAASDNKTKNAAVTVGDLNAVAQTPLTFAGDTGT
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                                                                                                                                                                                                                                                                    Infect. Immun. 60:159-165(1992).
-!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
-!- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.
-!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
S-LAYER WITH HEXAGONAL SYMMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAYSLAVGLAATAEGQSTIAIGS----DATSSSLGAIALGAGTRAQLQG-SIALGQGSVV 288
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                                                                                           MEDLINE-92114896; Pubmed-1370573;
Ching W.M., Carl M., Dasch G.A.;
"Mapping of monoclonal antibody binding sites on CNBr fragments of
the S-layer protein antigens of Rickettsia typhi and Rickettsia
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MEDLINE-92104668; PubMed-1729180;

MEDLINE-92104668; PubMed-1729180;

Hackstadt T., Messer R., Cieplak W., Peacock M.G.;

"Evidence for proteolytic cleavage of the 120-kilodalton outer membrane protein of rickettsiae: identification of an avirulent mutant deficient in processing:";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane; Cell wall.
1353 120 KDA SURFACE-EXPOSED PROTEIN.
11645 32 KDA BETA PEPTIDE.
1429 MEMBRANE ANCHOR (POTENTIAL).
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V -> I (IN REF. 2).
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W; OCB5641C7EB185EE CRC64;
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Similarity 21.7%; Pred. No. 1.3e-09;
72; Conservative 206; Mismatches 634;
                                                                                                                                                              Mol. Immunol. 29:95-105(1992)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IKFTNVNGSNPGTGIANTARI - - TRDKIGFAGS -
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Carl M., Dobson M.E., Ching W.M., Dasch G.A.; Characterization of the gene encoding the protective paracrystalline-surface-layer protein of Rickettsia provazekii: presence of a truncated identical homolog in Rickettsia typhi."; proc. Natl. Acad. Sci. U.S.A. 87:8237-8241(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                      AVGAVSYGASGAERRIQNVAAGEVSATSTDAVNGSQLYKATQSIANATNELDHRIHQNEN 1971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDVATFIGA-----IATDTGAAVATVNLNDTQ--KTQDLLGNRLGAL--RYLSNSE 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A--TGDQSIAIGTGNVVAGKHSGALGDPSTVKADNSYSVGNNNQFT-----DATQTDVF 1853
                                                                                                                                                                                                                                                                                                                                                                      1911
                                                                                                                                                                                                                                                                                                                                                                                             1192 ANFSGTOTYTLIQG---CARFNGTLGAP-----NFDVTGNNIFVKYELIRDANQDYVL 1241
                            S-----GQAKANTPVLSANGLDLGGKVISNVGKGTKDTDAANVQQLNEVRNLLGLGN 1625
                                                                                                                    1086 TGNDSGVGLQGNIHSQNID---FGTYNLTILNSDVILGG------GTTAINGEIDLL 1133
                                                                                                                                                                 1741
                                                                                                                                                                                                                                1742 VNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGRQTQAGNQSIAIGDNAQ 1801
                                                                                                                                                                                                                                                          OMPB_RICPR STANDARD; PRT; 1643 AA.
053020; Q9ZCM0;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
0UTER MEMBRANE PROTEIN B PRECURSOR (168 KDA SURFACE-LAYER PROTEIN)
(SURFACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SCA5) (ROMP B)
(CONTAINS: 120 KDA SURFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTIGEN)
(120 KDA OUTER MEMBRANE PROTEIN OMPB); 32 KDA BETA PEFTIDE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KANAGISSAMAMASMPQA-----YIPGRSMVTGGIATHNGQGA-VAVGLSKL
                                                                                                                                                                GN----ANGDLSNVWVKTQKDGSKKALLATYNAAGQTNYLTNNPAEAIDRINEQGIRFFH
                                                                                                                                                                                                                                                                                                                                                                      GVGNNITVTESNSVALGSNSAL - - SAGTHAGTQAKKSDGTAGTTTTAGATGTVKGFAGQT
                                                                                               AGNDNADGNQVNIADIKKDPNSGSSSNRTVIKAGTVLGGKGNNDTEKLATGGIQVGVDKD
----IAGTD-FDGKI-----TLGSING-----NANVKFVDR
                                                    Rickettsia prowazekii.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
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MOTOD C.G., Yu X.J., Walker D.H.;
Moton C.G., Yu X.J., Galker and Strokettsia prowazekil.";
"Sequence analysis of ompB of Rickettsia prowazekil.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
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                                                                                                                                                                                           TNNLIFANG--TSTW-----GNNTSLSTTLN---
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MEDLINE-91045972; PubMed-2122457;
                                                                                                                                                                                                                                                                          1158 VSNGNVGQIV-----
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its week by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-92104668; PubMed-1729180;
Hackstadt T., Messer R., Cleplak W. Jr., Peacock M.G.;
Hackstadt T., Messer R., Cleplak W. Jr., Peacock M.G.;
"Evidence for proteolytic cleavage of the 120-kilodalton outer
membrane protein of rickettslae: identification of an avirulent mutant
deficient in processing.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Infect. Immun. 60:159-165(1992).

-infect. Immun. 60:159-165(1992).

-i. FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR

STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL

STRUCTION: THE 32 KDA DEPARTOR NUMINOGEN DURING INFECTION.

-i. FUNCTION: THE 32 KDA BEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.

-i. SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-

LAYER WITH HEXAGONAL SYMMETRY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                    Ching W.M., Carl M., Dasch G.A.; "Mapping of monoclonal antibody binding sites on CNBr fragments the S-layer protein antigens of Rickettsia typhi and Rickettsia
                                                                                                       of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 KDA SURFACE-EXPOSED PROTEIN.
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                  Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund Eriksson A.-S., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the origin
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1 -> D (IN STRAIN BREINL).

A -> S (IN STRAIN BREINL).

AA -> VC (IN REF. 1).

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Q -> L (IN REF. 1).

Q -> L (IN REF. 1).

D -> G (IN REF. 2).

T -> S (IN REF. 2).
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ilarity 21.1%; Pred. No. 1.5e-09;
Conservative 254; Mismatches 647
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EMBL; AF161079; AAD42234.1; -.
EMBL; AJ235273; CAA15140.1; -.
                                                                                                                                                                                                                                                                                 MEDLINE-92114896; PubMed-1370573;
MEDLINE-99039499; PubMed-9823893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTIFICATION OF CLEAVAGE SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                Mol. Immunol. 29:95-105(1992).
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LGGGSVVTQSDNNSRPAYTPNTQALDPKFQATN-NTKAGPLSIGSNSIKRKIINVGA 337	NATTTYVKGSSSTTAELLSDSLTFTQPNTGSQSTSKTVYGV 469		THEQIOUGAN	SNAASINDILNTGFNLKNNNNDIDEVSTYDIVDFANGNATTATVTHDTANKT 871     :	IKSTVGNGTVDNFNAPIVVVSGIDSMINNG-QIIG GKSTLNDGGLSIKNPTGSEQIOVGADGVKFAKVNNNGVV-GA
LGGGSVVTQSDNNSRPAYTPNTQALDPKF 	GGAANAVIGTDNGAGRAAGFIVS'	TTENANGALVSASTDPNI TTENANGALVSASTDPNI NIGVKTTELNGIHIAELRLGNGGSIF	VGGAIHF	SNAASINDILNT GENLKNNNN     : :	SLGTSLFLPSGTPLDVLTIKSTV DKNGTVTFGINTTSGLKAGKSTLI     :   :   :     DKKNITALSLGSDNSITVNANTLI GIDGTTRITRDEIGFTGTNGSLDI GLENGS     :     GLE
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1146 WGDNTSISTTLNVSSGNIGQVVIAED-----AQVNATTTGTTTIKIQDNANANFSGTQA 1199
                                                                                                                                                                  1455 DANKKQGI----NEDNAFVKGLEKAASDNKTKNAAVTVGDLNAVAQTPLTFAGDTGTTAK 1510
                                                                                                                                                                                                                                                                                                                                     1511 KLGETLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGTKIDDKGVSF 1570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 1626 AGNDNADGNQVNIADIKKDPNSGSSSNRTVIKAGTVLGGKGNNDTEKLATGGIQVGVKD 1685
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                                      -GONTITGLSNTLANVTNDKGSVRTTEQGNIIKDEDKTRAASIVDVLSAGFNLQGNGEAV 1281
                                                                                                                                                                                                                                                             1415 GTVDKTKEVAKDKL----VAQAQTPD-----GTLAQMN----VKSVINKEQVN 1454
                                                                                                                                                                                                                                                                                        1315 NDTOKTODLLSNRLGTLRYLSNAETSDVAGSATGAVSSGDEAEVSYGVWAKPFYN---IA 1371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AFR-1990 (Rel. 14, Created)
01-AFR-1990 (Rel. 14, Last sequence update)
15-701-1998 (Rel. 36, Last annotation update)
PIT-TYPE PROTEINASE PRECURSOR (EG. 3.4.21.96) (LACTOCEPIN) (CELL WALL-ASSOCIATED SERINE PROTEINASE) (LP151).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid pLP763.

Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae; Lactococcus.
                                                                  -----NVILGGGTTAINGEIDLLTNNL-IFANGTST
                                                                                             -- DFVSTYDTVNFADGNATTAKVTYDDTSKTSKVVYDVNVDDTTIEVKDKK----LGVKT
                                                                                                                                                                                                        1376 IQTAKGASQ-----ANNSAGYVDADGNKVIY--DSTD-----NKYYQAKND
                                                                                                                                                                                                                                                                                                                                                                                          TTLTSTG-------TGAN---KFALSNQATGD-ALVKASDIVAHLNTLSGD--
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                                                                  FGTYNLTILNS-----
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1216 IVIDSQN------GQNTITGLSNTLANVTNDKGSVRTTEQGNIIKDEDKTRAASIV 1265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -TVTFGINTTSGLKA---GKSTLNDGGLSIKNPTGSEQIQVGADGVKFAKVNNNGVVGAG 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             965 NNNAD-----DANAITVGQKNANNQVNTLTLKGENG-----LNIKTDKNG---- 1004
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                                                                                                                                                                                                                                                                                                                                                                                                                         RTT----HELTYQMDSNTDTNAVYTSA-TDPNSGVLYDKKIDGAAIKAGSNITVPAGKIA 789
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693 VKAAIDALEKNPSTVVAENGYPAVELKDFTSTDK-------TFKLTFTN 734
                                                                                                                                                    ---SLTFTQPNTGSQSTS 463
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SLGSDSGNQTLEDPELAAVQNANESGTAAVISAGNSGTSG---SATEGVNK-DYYGLQDN
                                                        EMVGTPGTSRGATTVASAENTDV---ITQAVTITDGTGLQLGPETIQLSSNDFTGSFDQK
                                                                                                                                                                                                             KTVYG-VNGVKFTNNAETTAALGTTRITRDKIGFARDGDVDEKQAPYLDKKQLKVGSVAI
                              EAVVKWAKERRITFQGDDNSTDVKIGLDNTLTIKGGA-----ETNALTDNNIG-----
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                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
POTENTIAL.
PILTYPE PROTEINASE.
PILTYPE PROTEINASE.
EXTRACELLULAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CHARGE RELAX SYSTEM (BY SIMILARITY).
CHARGE RELAX SYSTEM (BY SIMILARITY).
CHARGE RELAX SYSTEM (BY SIMILARITY).
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
PROTEINS.
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            ALTHOUGH IT HAS BEEN SHOWN TO HYDROLYSE HEMOGLOBIN AND OXIDIZED
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pfam; pr00746; Gram_pos_anchor; 1.
prints; pr00723; SUBTLILSIN.
pr0SITE; Ps00136; SUBTLILSE_ASP; 1.
pr0SITE; Ps00138; SUBTLIASE_ASP; 1.
pr0SITE; Ps00138; SUBTLIASE_ERR; 1.
pr0SITE; Ps00343; GRAM_POS_ANCHORING; 1.
prosite; Ps00343; GRAM_POS_ANCHORING; 1.
prosite; Ps00343; Gram_Pos_ANCHORING; 1.
prosite; Ps00343; Gram_Pos_ANCHORING; 1.
                                           SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. CELL WALL. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
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4.4%, Score 451.5; DB 1;
Best Local Similarity 20.9%; Pred. No. 2.5e-09;
Matches 463; Conservative 238; Mismatches 825;
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HSSP; P00782; 2SBT.
MEROPS; S08.019; -.
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Relman D.A., Domenighini M., Tuomanen E., Rappuoli R., Falkow (Filamentous hemagglutinin of Bordetella pertussis: nucleotide aequience and crinial role in adherence."

MEDLINE-89202384; PubMed-2539596;

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         DVLSAGFNLQGNGEAVDFVSTYDTVNFADGNATTAKVTYDDTSKTSKVYYDVNVDDTTIE 1325
                                                                                                      DIQTAKGASQANNSAGYVDADGNKVIYDSTDN-KYYQAKNDGT-----VDKTKEVAKDK 1427
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=90355839; PubMed=2388559;
Relman D.A., Domenighini M., Tuomanen E., Rappuoli R., Falkow "Genetic characterization of Bordetella pertussis filamentous haemagglutinin: a protein processed from an unusually large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bordetella pertussis.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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SEQUENCE OF 1-3261 FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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sequence and crucial role in adherence.";
Proc. Natl. Acad. Sci. U.S.A. 86:2637-2641(1989).
-!- FUNCTION: EVIDENCE FOR A ROLE IN HOST-CELL BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 4.3%; Score 448; DB 1; Le
Best Local Similarity 20.5%; Pred. No. 7e-09;
Matches 486; Conservative 291; Mismatches 948;
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:     :::  : VRVVQARS-LADISLGAEGGATLGAVEAAGSIDVRGGSTVAANSLHANRD 875	LKLKGKNGLTVATKKDGTVTFGLSQDSGLTIGKSTLNNDGLTVKDTNEQIQVGANGIKFT 728 :::	NVNGSNPGTGIANTARITRDKIGFAGSDGAVDTNKPYLDQDKLQVGNVKTTNTGINAG 786	GKAIT-CLSPTLPSIADQSSRNIELGNTIQDKDKSNAASINDILNTGFNLKNNNNPI 842 	DEVSTYDIVDFANGNATTATVTHDTANKTSKVVYDVNVDDTTIHLTGTDDNKKLGVKTTK 902     :     :   :   :   :   :   :   :   :	LNKTSANGNTATNENVNSSDEDALVNAKDIAENLNTLAKEIHTTKGTADTALQTETVKKV 962	ARKALKUDF FTPGS V V KANGAN I V GRO GENIKTDK NGTVTFGINTTSGL KAG 	NDALT ENGINE TO TECHNOLOGY IN THE TECHNOLOGY I	SVKVAKKLELNGTLKAVNDNNETMSGKQIDVVDGN HLSKDGINAGGKKITNIQSGEIAQNSHDAVTGGKIYDL		KTELENKISSTAKTAQNSLHE-FSVADEQGNTTV-SNPYSSYDTSKTSDV 1173	ITFAGENG-ITTKVNKGVVRVGIDQTKGLTTPKLITVGNNNGKGIVIDSQNGQNTI 1227 GTEOSOADAGTAGALVVKAAFAIVHDGYWATKGEMQIAGKGGSPTVTAGAKATTSA 1364	TGLSNTLANVINDKGSVRTTEQGNIIKDEDKTRAASIVDVLSAGFNLQ 1275	GNGEAVDFVSTYDTVNFADGNATTAKVTYDDTSKTSKVVVDVNVDDT 1322	TIEVKDKKLGVKTTTLTSTGTGANKFALSNQATGDALVKASDIVAHLNTLSGDIQTAK 1380	GASQANNSAGYVDADGNKVIYDSTDNKYYQAKNDGTVDKTKEVAK 1425	DKLVAQAQTPDGTLAQMNVKSVINKEQVNDANKKQGINEDNAFVKGLEKAASD 1478  DKLVAQAQTPDGTLAQMNVKSVINKEQVNDANKKQGINEDNAFVKGLEKAASD 1478	NKTKNAAVT-VGDLNAVAQTPLTFAGDTGTTAKKLGETLTI 1518	KGGQTDTNKLTDNNIGVVAGTD	NLNSVNAGGTKIDDKGVSFVDSSGQAKANTPVLSANGLDLGGKVISNVGKGTKDTDAA 1609
:     ::  : VRVDQARS-LADISLGAEGGATLGAVEAP				DFVSTYDIV		A DENNNADDANAITVGQKNAN   :	DPHQGVLAQGDIMDAKG KSTLNDGGLSIKNPTGSEQIQVG :  ::  :	ESKISOSVLAAKGDKGKPAV TRITRDEIGFTGTNGSLDKSKPH				TGLSNTLANVTNDKGSVRTTDKGSVRTT	GNGEAVDFVSTYDT			DKLVAQAQTPD+-GTL             H HDFTVQAQRIDNSGTMAAG			
0b 827	Oy 669 Db 876		Qy 787 Db 973	Qy 843		Db 1060 Qy 963	Db 1099 Oy 1020	Db 1147 Qy 1065	Db 1202	Qy 1125 Db 1249							Oy 1479		Oy 1552

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(2) SEQUENCE OF 189-196. MEDILING-92226694; PubMed-1564442; NabLINE-92226694; PubMed-1564442; Naes H., Nissen-Meyer J.; Perminal amino acid sequence determination of the "purification and N-terminal amino acid sequence paracase; subsp. cell.wall.bound proteinase from Lactobacillus paracase; subsp.
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                                                                                                                                                                                                                      -----GSKKALLATYNAAGQTNYLTNNPAEAIDRI 1732
1760 NKRAALIEAGGNARLTAAVALLNKLGRIRA-----GEDMHLDAPRIENTAKLSGEVQRK 1813
                               1610 NVQQL--NEVRNLLGLG-----NAGNDNADGNQVNIADIKKDPNSGS--SSNRTVIKAG 1659
                                                 1814 GVQDVGGGEHGRWSGIGYVNYWLRAGNGKKAG---TIA----APWYGGDLTAEQSLIEVG 1866
                                                                                                               1925 TALDNRAGLSPATWNFQSTYELLDYLLDQNRYEYIWGLYPTYTEWSVNTLKNLDLGYQAK 1984
                                                                                                                                                                                                                                                    1985 PAPTAPPMPRAPELDLRGHTLESAEGRKIFGEYKKLQGEYEKAKMAVQAVEAYGEATRRV 2044
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01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1998 (Rel. 36, Last annotation update)
PII-TYPE PROFEINASE PRECURSOR (EC 3.4.21.96) (LACTOCEPIN) (CELL WALL-ASSOCIATED SERINE PROTEINASE) (LP151).
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Bacteria: Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
Lactobacillus.
NCBL_TaxID=1597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning, sequencing and expression of the gene encoding the cell-enveloper-associated proteinase from Lactobacillus paracasel subsp. paracasel NCDO 151.", J. Gen. Microbiol. 138:1353-1364(1992).
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2045 HDQLGQRYGKALGGMDAETKEVDGIIQEFAADLRTVYAKQADQATIDAETDKVAQRYKSQ
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                                                                                              1660 TVL----GGKGNNDTEKLATGGIQVGVDKDGNANGDLSN-----
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STRAIN-NCDO 151;
MEDLINE-92381481; PubMed-1512565;
HOLCK A., Nacs H.;
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                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----IAIGGDVKA-----SGDA----SIAIGSDDLHLLDQHGNPK- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENANAQGGQAIAIGSSNKTVNGSSLDKI--------GTDATGQES- 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TDTTAATTNQAIATOLAAKGIDYNKLNKVQQQDTYVDVIVQMSAAPASENGTLRTDYSST 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTLAKVYYPTDAKANSMANVQAVWSNYKYKGEGTVVSVIDTGIDPTHKDMRLSDDKDVKL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --HFSNAFGTRATAKS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 TKYDVEKFTDTAKHGRYFTSKVPYGFNYADNNDTITDDTVDEOHGMHVAGIIGANGTGDD 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SILLAGTVALGALAVLPVGEIQAKAAISQQTKVSSLA----NTVKAATAKQ-----AA 57
FUNCTION: PROTEASE WHICH BREAKS DOWN MILK PROTEINS DURING THE GROWTH OF THE BACTERIA ON MILK.

CATALYTIC ACTIVITY: ENDOPEPTIDASE ACTIVITY WITH VERY BROAD SPECIFICITY, ALTHOUGH SOME SUBSITE PREFERENCE HAVE BEEN NOTED, E.G. LARGE HYDROPHOBIC RESIDUES IN THE PI AND PA POSITIONS, AND PRO IN THE P2 POSITION. BEST KNOWN FOR ITS ACTION ON CASEINS, ALTHOUGH IT HAS BEEN SHOWN TO HYDROLYSE HEMOGLOBIN AND OXIDIZED
                                                                                                                                 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. CELL WALL. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE SUBTILASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEIQQETNKVIAAQASVKAAVEQVTQQTAGESYGYVVNGFSTKVRVVDIPKLKQIAGVKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative 237; Mismatches 831; Indels 689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL). MEMBRANE ANCHOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                             Pfan: PF00046; Gram_pos_anchor; 1.
Pfan: PF00082: Peptidase_S8: 3.
PRINES: PR00723: SUBTILIASIN.
PROSITE: PS00136; SUBTILIASE_ASP; 1.
PROSITE: PS00137: SUBTILASE_HIS; 1.
PROSITE: PS00138; SUBTILASE_ESP; 1.
PROSITE: PS00343; GRAM_POS_ANCHORING; FALSE_NEG.
Hydrolase; Serine protease; Cell wall; Zymogen; Signal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PII-TYPE PROTEINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 447.5; DB 1
Pred. No. 3.5e-09;
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                                                                                                                     INSULIN B-CHAIN
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MEROPS; S08.019; -.
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1136 QGGGTYTFSGTYPAAVDGTYTDAQGKKHDLNTTYDAATNSFTASMAVTNADYAAQVDLYA 1195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -GGKIYDLKTELENKISSTAKTAQNSLHEFSVA-DEQGNNFTVSNPYSSYDTSKTSDVIT 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -- TQPNTGSQSTSKT 465
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                                                                                                                                                                                                                                                                                                                                 EMVGTPGTSRGATTVASAENTDV-ISQAVTITDGKDLQLGPETIQLSSNDFTGSFDQKKF 463
                                                                                                                                                                                                                                                                                                                                                                                                    ---IGVVKEAD-NSGLKVKLAKTL------NNLTE 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             694
294
                                                                                                                                                                                         SLGSDSGNQTLEDPEIAAVQNANESGTAAVISAGNSGTSG---SATQGVNK-DYYGLQDN 404
AYSLAVGLAATAEGQSTIAIGSDATSSSLGAIALGAGTRAQLQGSIALGQGSVVTQSDNN
                                                                                                                                 SRPAYTPNTQALDPKFQATNNTK----AGPLSIGSNSIKRKIINVGAGVNKTDAVNVAQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  464 YVVKDASGDLSKGAAADYTADAKGKIAIVKRGELNFADKQKYAQAAGAAGLIIVNNDGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              824 PYMGFFGDWNDGKI-----VD----SLNGIIYSPAGGNYG-----TVPLLINKNI
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                                                           PTKSVVGVAPEAQLLAMKVFTNSDTSATTGSATLVSA----IEDSAKIGADVL----NM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPLTSIRLTTFPTFGLSSKTGQKLVDWVTAHPDDSLGVKIALTLLPNQKYTEDKMSDFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VYG-VNGVKFTNNAETTAAIGTTRITRDKIGFARDGDVDEKQAPYLDKKQLKVGSVAITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYGPVSNLSF--KPDITAPGGNIWSTQNNNGYTNMSGT-SMASPFIAGSQALLKQALNNK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                573 ISVDAKSGNVTAPTYNIGVKTTELNSDGTSDKFSVKGSGTNNSLVTAEHLASYLNEVNRT
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                                                                                                                                                                                                                                                               EAVVKWAKERRITFQGDDNSTDVKIGLDNTLT----IKGGAETNALTDNN--
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--QAQAGTQT---ADQLQA----SLAKVLDAVLAKLAEG-----IKAATPAEVGNAK- 1743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----TOKAQTALDQTDASVDSLTGANRDLQT-----AINQLAAKLPADKKTSLL-- 1665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NPAEAIDRINEQGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAI 1783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1606 TDAANVQQLNEVRNLLGLGNAGNDNADGNQVNIADIKKDPNSGSSSNRTVIKAGTVLGGK 1665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1744 --DAATGKTWYADIADTLTSGQASADASDKLAHLQALQSLKTKVAAAVEAAKTAGKGDDT 1801
                                                                                                                                                                                                                                                                           TLSGDIQTAKGASQANNSAGYVDADGNKVIYDSTDNKYYQAKNDGTVDKTKEVAKDKLVA 1430
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----YYEPKKTLAAPTVTPS-----TTEPAKTVT--LTAN-----AAATGETVQYSA 1534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-BECURSON (168 KDA SURFACE-LAYER PROTEIN)
(SURFACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SCAS) (ROMP B)
(CONTAINS: 120 KDA SURFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTIGEN)
(120 KDA OUTER MEMBRANE PROTEIN OMPB); 32 KDA BETA PEPTIDE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1892 AGTTTTAGATGTVKGFAGQTAVGAVSVGASGAERRIONVAAGEV------SATSTD 1941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1802 TGTSDKGGGQGTPAPAPGDT-----GKDKGDEGSQPSSGGNIPTKPATTTSTSTD 1851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GNNDTEKLATGGIQ---VGVDKDGNANGDLSNVWVKTQKDGSKKALLATYNAAGQTNYLTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRQTQAGNQSIAIGDNAQATGDQSIAIGTGNVVAGKHSGAIGDPSTVKADNSYSVGNNNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----NOLOSVKAALGTDLGNQTDPSTGKTFTAALDDLVA---
                                                                                                                                                                                                        TTIEVKDKKLGVK-----TTTLTSTGTGANKFAL-----SNQATGDALVKASDIVAHLN
                                                                                                                                                                                                                                        TTLOVDGKQISIKNDLTFSFTLDLGTLGOKPFGVVVGDTTONKTFQEALTFILDAVA--P
                                                                                                                                                                                                                                                                                                              TLSLDSST-----DAPVYTNDPNFQITGTATDNAQYLS------LAI
                                                                                                                                                                                                                                                                                                                                                QAQTPDGTLAQMNVKSVINKEQVNDANKK--QGINEDNAFVKGLEKAASDNKTKNAAVTV
                                                                                                                                                                                                                                                                                                                                                                      GDLNAVAQTPLTFAGDTGTTAKKLGETLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D------GGKTYQDVPAAGVT-VTANGTFKFKSTDLYGNESPAVDYVVTNI----KA
                                                                                                                                   VDVLSAGFNLQGNGEAVDFVSTYDT-VNFA--DGNATTAKVTYDDTSKTSKVYYDVNVDD
                                                                                                                                                          DKAHTQLLKHFDTKVRLTAPTFTDLKFNNGSDQTSEATIKVTGTVSSDTKTVNVGDTVA-
                                                                 GIVIDSON-------GONTITGLSNTLANVTNDKGSVRTTEQGNIIKDEDKTRAASI
                                                                                       -----YTALDAQHHFSVDVPVNYGDVTIK-----VTATDEDGNT-TTEQKTITSSYDP-----
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=35790;
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----VRVGIDQTKGLT-
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   1176 FAGENGI ---- TIKVNKGV-
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006653;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---GLSQDSGLTIGKSTLNN--DGLTVKDTNEQIQVGANGIKFTNVNGSNPGTGIANTAR 744
                                                                                                                                                                                                  (BY SIMILARITY).
SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
LAYER WITH HEXAGONAL SYMMETRY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 623; Gaps
                                                                                                                                                                   SIMILARITY).
FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
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                                                       of Rickettsia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1656;
                                                     "Sequencing of the gene encoding the protein rOmp B of Rickett Japonica.";
Saponica.";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: THE 120 KDA SURRACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 KDA SURFACE-EXPOSED PROTEIN.
32 KDA BETA PEPTIDE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 750;
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Pred. No. 4.1e-09;
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ilarity 21.4%; Pre
Conservative 237;
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Antigen; S-layer; Cell wall.
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528 53
1656 AA;
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SIVAITQNS--NFGTTDFGNLAAQVTVPDT---MTLTGN---FTG-DANNPG----NTAG 433
                                                                                                                                                                                      532 GGAALQSITLANDATK-----TLTLGGA------NIISANGGT-INFO 567
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                                          ITRDKIGFAGSDGAVDTNKPYLDQDKLQVGNVKITN--TGINAGGKAITGLSPTLPSIAD 802
                                                                                                   803 QSSRNIELGNT----IQDKDKSNAASINDILNTGFNLKNNNNPIDFVSTYDIVDFANGN 857
                                                                                                                               475 -HTAELRLGNAGSVFKLADGTVIN-GKVNQTVLVGGVLAAGAITLDGSATI-TGDIGNGG 531
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                                                                                                                                                          ATTATVTHDTANKTSKVVYDVNVDDTTIHLTGTDDNKKLGVKTTKLNKTSANGNTATNFN
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1279 NVTTEVNATNTAAYNNLLLAKNSADSANFVGTIV-----TDTSAAITNA-QLDVAKDIQA 1332
                                                                                                                                                                                                                                           1742 VNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGRQTQAGNQ---SIAIGD 1798
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                                                                                                                                                   1333 QLGNRLGALRYLGT-PEMVGSEAGAIPAAVAAGD------EAVDNV-AYGIWAKPFY 1381
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01-APR-1990 (Rel. 14, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PI-TYPE PROTEINASE PRECURSOR (EC 3.4.21.-) (WALL-ASSOCIATED SERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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-!- FUNCTION: PROTEASE WHICH BREAKS DOWN MILK PROTEINS DURING THE GROWTH OF THE BACTERIA ON MILK.
-!- CATALYTIC ACTIVITY: ENDOPEPTIDASE ACTIVITY MITH VERY BROAD SPECIFICITY, ALTHOUGH SOME SUBSITE PREFERENCE HAVE BEEN NOTED, E.G. LARGE HYDROPHOBIC RESIDUES IN THE P1 AND P4 POSITIONS, AN PRO IN THE P2 POSITION. BEST KNOWN FOR ITS ACTION ON CASEINS,
                                                                               --GNANGDLSNVWVKTQKDGSKKALLATYNAAGQTNYLTNNPAEAIDRINEQGI--RFFH
                                                                                                                                                                                                                                                                                     1855 VGNNITVTESNSVALGSNSAISAGTH--------AG-TQAKKSDGTAGTT
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. CELL WALL.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
SUBTILASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                       1799 NAQATGDQSIAIGTGNVVAGKHSGAIGDPSTVKADNSYSVGNN----NQFTDATQTDVFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1481 ANGNM----SKQIAAGNYDNMTFGGNLTVGYDYNAMQGVLVTPMAGLSYLKSSDENYKET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ą
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97;
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EXTRACELLULAR (POTENTIAL).

MEMBRANE ANCHOR (POTENTIAL).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CONSERVED IN GRAM-POSITIVE COCCI SURFACE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRPAYTPNTQALDPKFQATNNTK----AGPLSIGSNSIKRKIINVGAGVNKTDAVNVAQL 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 GENANAQGGQAIAIGSSNKTVNGSSLDKI----------GTDATGQES- 137
                                                                                                                                                                                                                                                                                                                                                                                                                                40 SVCTLSFARIAALAVLVIGATLSGSAYAQKKDTKHIAIGEQNQPRRSGTAKADGDRAIAI 99
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InterPro; IPR001899; -.
Pfam; PF00746; Gram_pos_anchor; 1.
Pfam; PF00012; Peptidase_89; 3.
PROSITE; PS00136; SUBTILIASE_ASP; 1.
PROSITE; PS00137; SUBTILIASE_ASP; 1.
PROSITE; PS00138; SUBTILIASE_RSP; 1.
PROSITE; PS00138; SUBTILIASE_RSP; 1.
PROSITE; PS00138; GRAM_POS_ANCHORING; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
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20.7%; Pred. No. 5.7e-09;
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Matches 459;
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1427 1374 : | : | : | : | : | ESST------DAPVYINDPNFQITGTATDNAQYLSLSINGSSVASQYVDININSGRPG 1458 LVAQAQTPDGTLAQMNVKSVINKEQVNDANKKQGINEDNAFVKGLEKAASDNKTKNAAVT 1487 1118 GGKIYDLKTELENKISSTAKTAQNSLHEFSVA-DEQGNNFTVSNPYSSYDTSKTSDVITF 1176 1005 -TVTFGINTTSGLKA---GKSTLNDGGLSIKNPTGSEQIQVGADGVKFAKVNNNGVVGAG 1060 ----rltdnasnatdqdasvqkpgstsfdlivnggipdkisstttg----reantq 1136 GGDKRQVFDVPFKLDSKAPTVRHV-----ALSAKTENGKTQYYLTAEAKDDLSGLDAT 1036 965 NNNAD------DANAITVGQKNANNQVNTLTLKGENG------LNIKTDKNG---- 1004 TADDGSYTYRISGVPE 983 DFANGN-----ATTATVTHDTANKTSKVVYDVNVDDTTIHLTGTDDNKKLGVKTTKLN 904 SRNIELGNTIQDKDKSNA------ASINDILNTGFNLKNNNNPIDFVSTYDIV 851 VKDKKLGVK----TTTLTSTGTGANKFAL----SNQATGDALVKASDIVAHLNTLSG 1197 KAHTOLLKHFDTKVRLTAPTETDLKFNNGSDQTSEATIKVTGTVSADTKTVNVGDTVA--DVL.SAGFNLQGNGEAVDFVSTYDTVNFADGNATTAKVTYDDTSKTSKVVYDVNVDDTTIE DIQTAKGASQANNSAGYVDADGNKVIYDSTDN-KYYQAKNDGT-----VDKTKEVAKDK 1137 GGGTYTFSGTYPAAVDGTYTNAQGKKHDLNTTYDAATNSFTASMPVTNADYAAQVDLYAD AGENGI----TTKVNKGV-----VRVGIDQTKGLT-----TPKLTVGNNNGKG 1216 IVIDSQN------GQNTITGLSNTLANVTNDKGSVRTTEQGNIIKDEDKTRAASIV 1255 -ALDAQHHFSVDVPVNYGDNTIK-----VTATDEDGNT-TTEQKTITSSYDP-----DMLK------NSVTFDQGVTFGANEF---NATSAKF-YDPKTGIATITGKVKHPTTTLQ 1061 IDGTTRITRDEIGFTGTNGSLDKSKPHLSKDGINAGG--KKITNIQSGEIAQNSHDAVT-LPYMGFFGDWNDGKI-----TVD----SLNGITXSPAGGNFG-----TVPLLTNKN ---STTHELTYQMDSNTDTNAVYTSA-TDPNSGVLYDKKIDGAAIKAGSNITVPAGKTAQ RDKIGFAG--SDGAVDTNKPYLDQDKLQVGNVKITNTGINAGGKAITGLSPTLPSIADQS TGTQYYGGMVTDADGNQTVDDQALAFSSDKNALYNDISMKYYLLRNISN-----VQVDIL KTSANGNTATNFNVNSSDEDALVNAKDIAENLNTLAKEIHTTKGTADTALQTFTVKKVDE VTFGLSQDSGLTÌGKSTLNNDGLTVKDTNEQIQVGANGIKFTNVNGSNPGTGIANTARIT TADSALQSFTVKEEDDDDANAITVAKDTTKNAGAVSILKLKGK-----NGLTVATKKDGT 572 EISVDAKSGNVTAPTYNIGVKTTELNSDGTSDKFSVKGSGTNNSLVTAEHLASYLNEVNR TVYG-VNGVKFTNNAETTAAIGTTRITRDKIGFARDGDVDEKQAPYLDKKQLKVGSVAIT 524 IDNGIDAGNKKISNLAKGSSANDAVTIEQLKAAKP-----TLNAGAGISVTPT 1428 1300 1326 1349 1407 1088 1177 1266 905 984 919 968 747 852 632 687 791 805 864 735 a g Ob qq ŏ qq ŏ q οy ò 엄 g οy qq ò рp ò qq δ g δ à à g ò Q ò g g δ g ōy

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DIDAANVQQL-NEVRNLLGLGNAGNDNADGNQVNIADIKKDPNSGSSSNRTVIKAGTVLG 1663
                                                                                                                                                                             1580 ADDPAOLQAAKQELINL----TALA 1618
                                                                                                                                                                                                                          1722 TNNPAEAIDRINEQGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAV 1781
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                                                                                              KDLTNLNSVNAGGTKIDD---KGVSFVDSSGQAKANTPVLSANGLDLGGKVISNVGKGTK 1604
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15-JUL-1998 (Rel. 36, Last annotation update)
PIII-TYPE PROTEINASE PRECURSOR (EC 3.4.21.96) (LACTOCEPIN) (CELL WALL-
                                                                                                                                                                                                                                                                                                                                                                                                                              GTAGTTTTAGATGTVKGFAGQTAVGAVSVGASGAERRIQNVAAGEV-----SATSTD 1941
                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vos P., Simons G., Siezen R.J., de Vos W.M.;
"Primary structure and organization of the gene for a procaryotic, cell envelope-located serine proteinse.";
J. Biol. Chem. 264:13579-13585[1989].
-I- FUNCTION: PROTEASE WHICH BREAKS DOWN MILK PROTEINS DURING THE GROWTH OF THE BACTERIA ON MILK.
-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. CELL WALL.
-I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE SUBTILASE FAMILY.
                                                                   --GETVQYS
                                                                                                                        AD-----GGKTYQDVPAAGVT-VTANGTFKFKSTDLYGNESPAVDYVVTNI----K
                                                                                                                                                                                                         GKGNNDTEKLATGGIO--VGVDKDGNANGDLSNVWVKTOKDGSKKALLATYNAAGOTNYL
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                                                                   V----TP----STTEPAKTVTLTANSAAT---
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MEDLINE=89340435; PubMed=2760036;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----TTLNATTTVKYGSSSSTTAELLSDSLTF-----TQPNTGSQSTS 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTLAKVYYPTDAKANSMANVQAVWSNYKYKGEGTVVSVIDSGIDPTHKDMRLSDDKDVKL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLGSNSGNQTLEDPELAAVQNANESGTAAVISAGNSGTSG---SATEGVNK-DYYGLQDN 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMVGSPGTSRGATTVASAENTDV ---ITQAVTITDGTGLQLGPETIQLSSHDFTGSFDQK 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----KGGAETNALTD-----NNIGVVKEADNS-GLKVKLAKTLN--NLTEVNT-- 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KFYIVKDASGNLSKGALADYTADAKGKIAIVKRGEFSFDDKQKYAQAAGAGLIIVNTDG 521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SILLAGTVALGALAVLPVGEIQAKAAISQQTKGSSLA-----NTVTAATAKQ-----AA 57
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                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
MEMBRANE ANCHOR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                Hydrolase; Serine protease; Cell wall; Zymogen; Signal; Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87CECBAA9345F9D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 GENANAQGGQAIAIGSSNKTVNGSSLDKI------
                                                                                                                                                                                                                                                                                                                                                 PIII-TYPE PROTEINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.2%; Score 430.5; DB 1;
llarity 20.5%; Pred. No. 1.4e-08;
Conservative 241; Mismatches 838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EAVVKWAKERRITFQGDDNSTDVKIGLDNTLTI------
                                                                                                                                                          PRINTS; PRO0723; SUBTILISIN.
PROSITE; PS00136; SUBTILASE_ASP; 1.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEINS
                                                                                                                    Pfam; PF00746; Gram_pos_anchor; 1. Pfam; PF00082; Peptidase_S8; 3.
J04962; AAA03533.1; ALT_SEQ
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              PIR; A32634; A32634.
HSSP; P00782; 2SBT.
MEROPS; SOB.019; ...
InterPro; IPR000209; ...
InterPro; IPR001899;
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                                                                                                                                                                                                                                                                                                                                                                                                    1786 QTQAGNQSIAIGDNAQATGDQSIAIGTGNVVAGKHSGAIGDPSTVKADNSYSVGNNNQFT 1845
                                                                                                                                                                                                                                                                                                                                                                                                                                       QAQAGTOT --- DDQLQAT ---- LAKILDEVLAKLAEG ----- IKAATPAEVGNAK --- 1743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DATQTDVFGVGNNITVTESNSVALGSN------SAISAGTHAGTQAKKSDGTAG 1893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1744 DAAIGKTWYADIADTLISGQASADASDKLAHLQALQSLKTKVAAAVEAAKTVGKGDGTIG 1803
                                                                                                                                                                                                                                                                                                                                                                   -----1700
                                                                                                                     NLNSVNAGGTKIDD----KGVSFVDSSGQAKANTPVLSANGLDLGGKVISNVGKGTKDTDA 1608
                                                                                                                                           1609 ANVQQL-NEVRNLLGLGNAGNDNADGNQVNIADIKKDPNSGSSSNRTVIKAGTVLGGKGN 1667
                                                                                                                                                                                                                                                            1668 NDTEKLATGGIQ--VGVDKDGNANGDLSNVWVKTQKDGSKKALLATYNAAGGTNYLTNNP 1725
                                                  NAVAQTPLJFAGDJGTJAKKLGETLTIKGGQTDJNKLTDNNIGVVAGTDGFTVKLAKDLJ 1551
1436 -LSINGSSYASQYEDININSGKPGHMAIDQPVKLLEGKNVLTVAVTDSEDN---TTTKNI 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Poole K., Schiebel E., Braun V.; *Molecular characterization of the hemolysin determinant of Serratia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA REQUIRES SHLB FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. BECLETIOL. 170:3177-3188(1988).
-!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                                                                                                                                                                                                           1584 AQLQAAKQELTNL----TALAAA--
                                                                                                                                                                                                                                                                                                1621 --TOKAQTALDQTNASVDSLTGANRDLQT-----AINQLAAKLPADKKTSLL----
                                                                                                                                                                                                                                                                                                                                   1726 AEAIDRINEQGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGR
                                                                                 TVYYEPKKTLAAPTVTPS-----TTEPAQTVT--LTAN-----AAATGETVQYSAD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1894 ITTTAGAIGTVKGFAGQTAVGAVSVG---ASGAERRIQNVAAGEVSATST 1940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: OUTER MEMBRANE. SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
HEMOLYSIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1608 AA
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SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=SN8;
MEDLINE=88257037; PubMed=3290200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=615;
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X E	Hemo]	brane; Signal.		
SO	CHAIN 31 16 SEQUENCE 1608 AA;	HEMOLYSIN. MW; D669B476FE7DAD51 CRC64;		· · · · · · · · · · · · · · · · · · ·
Q M M	Query Match Best Local Similarity 21.3%; Matches 415; Conservative 24	Score 417; DB 1; Length 1608; Pred. No. 3.5e-08. 2. Mismatches 716; Indels 578;	Gaps 103:	
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g Z	3 8	AEGGSI TAIGSDAISSSEGATALGAG   :   :   :   H   AGAYABEIVAANGANGPGVSTAATGAQVVDIVAPNGN	2/1 62	qa
Qy	272	TRAQLQGSIALGQGSVVTQSDNNSRPAYTPNTQALDPKFQATNNTKAGPLSIGSNSIK	329	δο 
QQ	:	:  :        EAGLSQLAGQLGANPNLGG	104	<u> </u>
٥y	330	RKIINVGAGVNKTDAVNVAQLEAVVKWAKERRITFQGDDNSTDVKIGLDN	379	∂ a
g	105	REASVILNEVIGRNPSLLHGQQEIFGMAADYVLANPNGISCQSCGFINTSHSSLVVG	161	
Qy Db	380	KLAKTLNNLTEVNTTTLNATTTVKVGSSS	439	
Qy	440	GVKFTNNAETTAAIGTTRITRDKIG	495	δ
QQ	191	: :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :   :     :   :     :	233	d d
Qγ	496	FARDGDVDEKQAPYLDKKQLKVGSVAITIDNGIDAGNKKISNLAKGSSANDAVTIEQLKA	555	ò à
QQ	234 -ARDGTVQASQQMPTALDSYYLGS	MQAGRINIINTAQGSGVKLA	276	
yo d	556	AKPTLNAGAGISVTPTEISVDAKSGNVTAPTYNIGVKTTELNSDGTSDKFSVGEILLI : : : : : : : : : : : : : : : : : :	607	
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7 A	392	ADRALSVKAARDVHLAGLVEKD	451	<b>a</b> a
οy	/ 691 LSQDSGLTIGK	-LTVK	712	ò i
qq	452	:       :	511	
δi	713 -	KPYLDQD : :	692	 
qq	512		553	· 8
oy .	770	LSPTLPSIADQSSRNIELGNTIQDKDKSNAAS	824	7 B
g G		SKARGQK	588	ô 
δý	825	•		; H
QQ	589	GGEVTATHGGLRIDNALSTTVDKIDARTGTAFNITSSSHKADNSYQSSTASELKSDY	645	
o o	884	TIHLTGTDDNKKLGVKTTKLNKTSANGNTATNFNVNSSDEDALVNAKDIAENLNTLAKEI	943	- da
ò	944		265	δ
op.				<b>2</b> 0
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Qy Db	998	IKTDKNGTVTFGINTTSGLKAGKSTLNDGGLSIKNPTGSEQIQVGADGVKFAKVNNNGVV 10 :	057
δλ	1058	IGFTGTNGSLDKSKPHLSKDGINAGGKKITN        :	117
qq	789	QAQSSKA	21
. Qy	1118	GGKIYDLKTELENKISSTAK-TAQNSLHEFSVADEQGNNFTVSNPYSSYDTSKTSDVITF 11:	1176
δ	11177	NGITTKVNKGV-VRVGIDQTKGLTTPKLTVGNNNGKGIVIDSQNGQNTITGLSNTLA	235
QQ	871		18
Qy	1236	RTTE	291
qq	919	NGLDIGAQGGSSEKRSSSSQAVVSSVQAGSIDINAKGEVRDQGTQYQASKGAVN 97	73
ΟŸ	1292	KVVYDVNVDDTTIEVKDKKLGVKTTLTST :	344
QQ	974	LTADSHRSEAAANRODEQSRDTRGSAGVRVYTTTGSDLTVDAKGEG 10	019
δŏ	1345	ANKFALSNQATGDALVKASDIVAHLNTLSGDIQTAKGASQANNSAGYVDADGNK-VIYDS 14	403
qa	1020	GTQRSNSSASQAVTGSIDAANGINVNVKKDAIYQG 10	1054
Οy	1404	LVAQAQTPDGTLAQMNVKSVINKEQVNDANKKQ	1460
qq	1055		1096
Οy	1461	TVGDLNAVAQTPLTFAGDTGTTAKKLGETLTIK 1	519
QO	1097	SGQQGVEL-KAGRDLTLQ 1	145
δλ	1520	GGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLFNLNSVNAGGTKIDDKGVSFVDSSG 15	575
QQ	1146	1	204
Οy	1576	EVRN 1	619
q <sub>O</sub>	1205	SGGSAALEAKNGG 1	261
οy	1620	RTVIKAGTVLGGK	1665
qq	1262	:	318
Qy	1666	NVWVKTOKDGS	1704
qq	1319	ITAGDVTLNSGKDTRLAGARVDADSVQGKVGGDLHVESRKDVENGV 1	375
Qy	1705	TUNPAEAI	762
. q	1376		425
Oy	1763	GDOSIAIGT 1	812.
qq	1426		477
Qy	1813	FTDATQTDVFGVGNNITVTESNSVALG 1	870
QQ	1478	GHLKVNADVVNNNAVGEQSAIAGKNGVALQVG	524
ΟŸ	1871	TAGTTTTAGATGTVKGFAGQTAVG 1	914
ΩD	1525	GQTQLIGGEIRSQQGKVELGGSQVSQQDVNGQRYQGGGRVDAAATVGGLLGGAAKQSVAG 15	584
οy	1915	AVSVGASGAERRIQNVAAGEVSATSTDAVNG 1945	
qq	1585	NVPFASGHASTOOADAKAG 1603	

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                                                                                                                                                                                                                                                                                                                                                                                                                                        Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Rasai H., Rashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miz T., Mizobuchi K., Mori H., Morimura K., Mori H., Mori T., Moromura K., Nashimoto H., Nishino Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takeuchi Y., Sivasundaram S., Tagami H., Takeda J., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.; A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28-0-40.1 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 595-1325 FROM N.A.
SEQUENCE OF 595-1325 FROM N.A.
MEDLINE-94100243; PubMed-8274505;
Cartwright P.J. Timms M.W., Lithgow T., Hoej P.B., Hoogenraad N.J.;
"An Escherichia coli gene showing a potential ancestral relationship to the genes for the mitochondrial import site proteins ISP42 and MOM38.";
Biochim. Biophys. Acta 1153:345-347(1993).
                                                                                                                                                                                                                                                  STRAIN-K12 / MG1655,
MEDLINE-97426617; PubMed-9278503;
MEDLINE-97426617; PubMett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANCHOR (POTENTIAL).
-!- SIMILARITY: TO E.COLI YFAL.
-!- SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS
                               YDEK_ECOLI STANDARD; PRT; 1325 AA.
P32051; P76140; P77168;
01-0CT-1993 (Rel. 27, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL 136.5 KDA LIPOPROTEIN IN HIPB-UXAB INTERGENIC REGION
                                                                                                                                         Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blochim. Biophys. Acta 1153:345-347(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i - CAUTION: REF. 3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-ACYL DIGLYCERIDE (POTENTIAL)
N -> K (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; Membrane; Lipoprotein; Signal. SIGNAL 1 18
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EcoGene; EG11780; ydeK.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=K12;
MEDLINE=97251357; PubMed=9097039;
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                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                  PRECURSOR (ORFT).
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        RESULT 14
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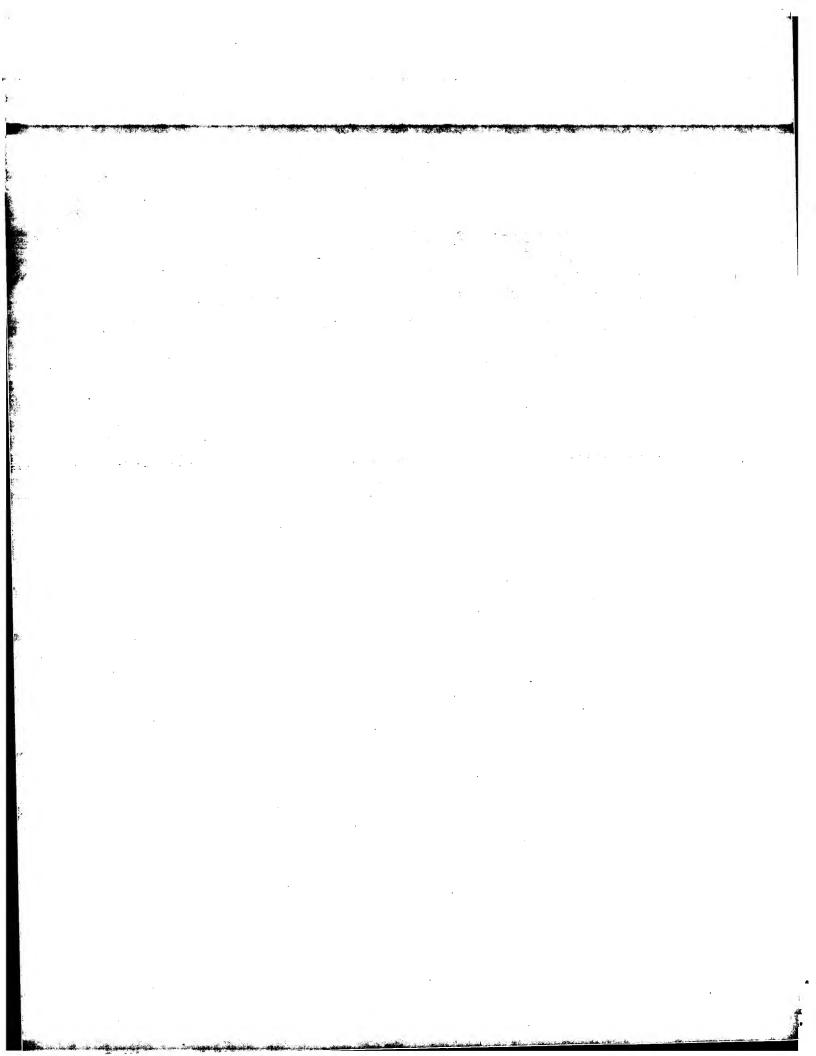
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1061 IDGTTRITRDEIGFTGTN----GSLDKSKPHLSKD--GINAG--GKKITNIQSGEIAQNS 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1168 SKTSDVITFAGENGITTKVNKGVVRVGIDQTKGLTTPKLTVGNNNGKGIVIDSQNGQNTI 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1018 A-GKSTLNDGGLSIKNPTGSEQIQVGADGV-----KFAKVNNN-----GVVGAG--- 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1113 HDAVTGGK-----IYDLKTELENKISSTAKTAQNSLHEFSVADEQGNNFTVSNPYSSYDT 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DENNNAD-----DANAITVGQKNANNQVNTLTLKGENGLNIKTDKNGTVTFGINTTSGLK 1017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    356 DGELNVSSEGKVDSGIITAGMKET------GTGNITVK-DKNSVIT-NLGTNLGYD 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 YGTGSLNITDKGYVTSSIVAILGYQAGSNGQVVVEKGGEWLIKNNDSSIEF----QIGNQ 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        854 ANGNAT-----TATVTHDTANKTSKVVYDVNVDDTTIHLTGTDDNKKLGVKTTKLNKT 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 GTGEATIREGGLVTAENTIIGGNATGIGTLNVQDQDSVI------TVRRLYN 295
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                                                                                                                                                                                                                                                                                                                                                                                        VAYDAYLVGWYGTGVLNILAG----GNASLTTITTSVIGANEDSEGTVNVLGGTWRLYDS 133
                                                                                                                                                                                                                        658 DTTKNAGAVSILKLKGKNGLTVATKKDGTVTFG-LSQDSGLTIGKS-TLNNDGLTVKDTN 715
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                                                                                                                Length 1325
1317 1317 M -> S (IN REF. 3).
1325 AA; 136514 MW; 26A3A066FA19AD7D CRC64;
                                                                                                             Query Match
3.6%; Score 375; DB 1; LA
Best Local Similarity 23.7%; Pred. No. 9e-07;
Matches 346; Conservative 175; Mismatches 578;
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              CONFLICT
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1743 NDGNQEPVYQGRN---GIDSSASGKHSVAIGFQAKADGEAAVAIGRQTQAGNQSIAIGDN 1799
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                                               LTDNNIGVVAGTDGFTVKLAKD-----LINLNSVNA-GGTKIDDKGVSFVDSSGQAKANT 1581
                                                                               958 IAQNGTVVAEGDYGFRLTTAPGNGLYVNYGLKALNIHGGQKLT-----LAEHGGAYGAT 1011
                                                                                                                 1582 PVLSANGLDLGGKVISNVGKGTKDTDAANVQQLNEVRNLLGLGNAGNDNADGNQVNIADI 1641
                                                                                                                                                                                   1642 KKDPNSGSSSNRTV-IKAGTVLGGKGNNDTEKLATGGIQVG------VDKDGNAN 1689
                                                                                                                                                                                                                                                        GDLS-----NVWVKŢQKDGSKKALLATYNAAGQTNYLTN-NPAEAIDRINEQGI-RFFHV 1742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;
"Cloning and sequencing of a 29 kb region of the Bacillus subtilis
genome containing the hut and wapA loci.";
Microbiology 141:337-343(1995).
-!- FUNCTION: STILL UNKNOWN. NOT INVOLVED IN CELL MEMBRANE METABOLISM,
MOTILITY, SECRETION OR DIFFERENTIATION.
-!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. MAY BE RELEASED
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DOMAIN: HAS TWO LIGAND-BINDING DOMAINS; THE N-TERMINUS, HAS THREE
101 AA REPEATS WHICH ARE RESPONSIBLE FOR CELL WALL BINDING; THE
898 PKPWNDPMANNPLTTLNLLEHDDSHVGVQLVKAQTVIGSGGSLTLRDLQGDEVEADKTLH 957
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Bacillus subtilis 168: evidence for processing of the product of
gene encoding a 258 kDa precursor two-domain ligand-binding
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Last annotation update)
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MEDLINE=95219088; PubMed=7704263;
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01-OCT-1994 (Rel. 30, Last seq
01-NOV-1995 (Rel. 32, Last anno
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Q07833;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps 117;
C-TERMINUS CONSISTS OF TWO BLOCKS OF RESIDUES WITH A CONSERVED MOTIF REPREPTED 31 TIMES.
SIMILARITY: THE REPEATED MOTIF IN THE C-TERMINUS HAS SOME SIMILARITY TO THE REPEAT IN E.COLI RHS GROUP OF PROTEINS (RHSA-D).
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                                                                                                                                                                                                                                                                                                    AA APPROXIMATE TANDEM REPEATS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 RPAYTPNTQALDPKFQATNNTK-AGPLSIGSNSIKRKIINVGAGVNKT----DAVNVAQL 350
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WALL-ASSOCIATED PROTEIN.
3 X 101 AA APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2334;
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                                                                                                                                   EMBL, L05634; AAA22883.1; EMBL, D31856; BAA065651; EMBL, D29985; BAA06560.1; EMBL, 299124; CAB15959.1; PIR, S32920; S32920. S32920. S30btilist; BG10797; wap. Pfam; PF02018; CBD_6; 1. Call wall; Repeat; Signal. CAINAL 29 2334 WALTH 2000AIN 504 866 3 REPEAT 636 736 11-
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Best:Local Similarity
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	KEADNSGLKVKLAKTLNNLTEVNTTTLNATTTVKVGSSSSTTAELLSDSLIFTUFNTGSQ   :	STS-KTVYGVNGVK-FTNNAETTAALGTTRIT		YLDKKQLKVGSVAITIDNG		AEIKAGKYALHLKDGSGAELPINP	NSDG	RTADSALQSFTVKEEDDDDANAITV 	-	LDPSPVYNNANGNYKGKKN	GANGIKETNVNGSNPGTGIANTARITRDKIGFAGSDGAV	DINKPYLDQDKLQVGNVKITNTGINAGGKAITGLSPTLPSIADQSSRNIELGNTIQDK	DKSNAASINDIL	DOTNAYFNKKGGKLQKVVD	TVTHDTANKTSKVVYDV                   TYDENGHVTSITGPKNKKVTYSYENDLL			947 KGTADTALOTETVKKVDENNAADDAAATIVOGKANNAVATLILANGENAANAAN 112. 11. 11. 11. 11. 11. 11. 11. 11. 11	TVTFGINTTSGLKAGKSTLNDGGLSIKNPT 	9 AGIDGTTRITRDEIGETGTNGSLDKSKPHLS	m	1112 SHDAVTGGKIYDLKTELENKISSTAKTAQNSLHEFSVADEQGNNFT-VSNPYSSYDT   :   :	
Db 409	Oy 401 Db 456	Oy 461			DD 628 Qy 551		Qy 597 Db 732	Oy 631	. 6	Db 838	Qy 721 Db 898	Oy 760		Db 1004	Qy 862		7	Qy 947 Db 1172	1 1	Qy 105	DP 128	Oy 1111. Db 134	

Search completed: September 13, 2001, 12:52:48 Job time: 798 sec



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A SIMPSON A.J.G., Reinach F.C., Araya J.E., Bala G.S., Baptista C.S.,
A Alvarenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,
A Alvarenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,
A Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
Bueno M.R.P., Cannarco A.A., Camaryo L.E.A., Carraro D.M., Carrer H.,
Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
A Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
A Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
A Fraga J.S., Franca E.E., Langeet F., Lambais M.R., Leite L.C.C.,
A Lemos B.G.M., Lemos M.V.F., Lopes C.R., Machado J.A.,
A Krieger J.E., Kuramae E.E., Lalgret F., Lambais M.R., Leite L.C.C.,
A Lemos B.G.M., Madeira A.M.B.N., Madeira H.M.F., Martun G.L.,
A Marques M.V., Martins B.A.L., Martins B.M.F., Mariou C.L.,
A Marques M.V., Martins B.A.L., Martins B.M.F., Martins B.M.F.,
A Marques M.V., Nobrega F.G., Miyaki C.Y., Monteiro-Vitorello C.B.,
A Manda M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
A de Oliveira M.C., de Sa R.G., Pereiara H.A. Jr., Pesquero J.B.,
A Quaggio R.B., Roberto P.G., Rodriques V., de Rosa A.J.M.,
A Silva A.C.R., de Silva A.M., da Silva F.R., Silva M.A. Jr.,
A da Silva A.C.R., da Silva A.M., da Silva F.R., Silva M.A.,
A da Silva A.P., Terenil M.P., Terlifi D., Tsal S.M., Tsuhako M.H.,
A Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
                                                                 scrofa
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MEDLINE=20365717; PubMed=10910347;
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                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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lla fastidios 10 CRC64;	Length 2; Indels	-VNGSSLDKIGTDATGQESIAIG :       :     SIRMGSVITMMTVA-GTNAIAIG	AVLKEIRSSK	ATAEGOSTIAIGSDATSS    :    :  GTGASSIAIGLNASAV	TQALDPKFQA  :  TKTTSTDASP	KERRITFOGDI	NLTEVNTTTLNATTT ::         DLKNTDKNLTIT	- X	-IDNGIDAGNKKISNLAKGS :    :   : VTASGIDAGSKVISHVAAGA	NVTAPTYNIG-VK :      :   GESSTAGTYSGGNLK	YLNEVNRTADSALQSF   :     :  -TEETDAVNFSQLKSI	-VTFGLSQD       :  DVVFNLSKDFK		QVGNVKITNT   : : TSGESST?	GVTAGTEETDAVNFS	TANKTSKVV)	SKSGDSNDVVI	FNFN
J.C.; en Xyle 85DD24E	1143; DB 2; No. 9.6e-40; matches 766	. >-	GDVKASGDASIAIGSDDLHLLDQHGNPKHPKGTLINDLINGHAVLKEIRSSKDNDVKYRR	TASGHASTAVGAMSYAQGHFSNAFGTRATAKSAYSLAVGLAATAFGQSTIAIGSDATS THASGHASTAVGAMSYAQGHFSNAFGTRATAKSAYSLAVGLAATAFGQSTIAIGSDATS TVASGAATAATGAKAAAAYYYVALGSGATAA	SLGAIALGAGTRAQL-GGSIALGGGSVVTQSDNNSRPAYTPNTQALDPKFQATNNTKAGP SLGAIALGAGTRAQL-GSSIALGGGSVVTQSDNNSRPAYTPNTQALDPKFQATNNTKAGP 	SIGSNSIK-RKIINVGAGVNKTDAVNVAQLEAVVKWAKERRITFQGDDNSTDV 	LDNTLTIKGGAETNALTDNNIGVVKEADNSGLKVKLAKTLNNLTEVNTTTLNATTTVKVG  SER	. ق	GPA	TLNAGAGISVTPTEISVDAKSGN :	LAS	TKKDGT   KSGDSN	TNBQIQVGANGIKFTNVN	VANNDONNY GENPETGIANTARITRDK-IGFAGSDGAVDTNKPYLDQDKLQVGNVKIINTGINAGGKA GSNPGTGIANTARITRDK-IGFAGSDGAVDTNKPYLDQDKLQVGNVKIINTGINAGGKA GSOLNANQVQASQPVTFTGNRGAVKRSLGQSVVISGESSTAGMYSGG	INNGGKIS	NDIENTGENEKNINNPIDENGSTYDTOFANGNATTATVTHDTANKTSKVVY	STAVDQGWTLTASGSNGSKVASGGTVDLKNTDGNLTISKSGDSNDVVFNLSKDFKVD	-VKTTKLNKTSANGNTATNFN- :        : :
s J., Setubal plant pathoge	Score Pred. 12; Mis	-KADGDRAIAIGENANAQGGQAIAIGSSNKT :	QHGNPKHPKG    KA	NAFGTRATAF    :     VALGSGATA	GOGSVVTQSI	SVNKTDAVNVA :	SVVKEADNSG	SSOSTSKTVY	LKVGSVAIT-    -  STTGLAITD	SVTPTEISVD:   :  TFTGNEGAVK	GSGTNNSLVT  - -  -	LKLKGKNG-1 :    ;    VDLKNTDGNI	GIKFTN  :  :  : GLTTTDGPAN	FAGSDGAVDT	:	STYDIVDFAN	ASGGTVDLKN	:
Meidani se of the (2000). (84338.1;	11.1%; / 24.0%; cvative 3	AIAIGENANA : :  : NLTLGGSLYV		AMSYAQGHFS   :     :   skasangvor	AQL-QGSIAI :  ::  VTVPDGAVAI	-RKIINVGAC  :::    TRQLSGLAAC	TNALTDNNIC	SLIFTQPNT	KQAPYLDKKQ	KPTLNAGAGI : : ! : 2VQASQPV	DKFS-    PKFGN	TTKNAGAVSI : NGSKVASGGT	TNEQIQVGAN : :   -GSDVALGTT	IANTARITRDK-IGEAGSDGAV   ::     ::	DOSSRNIEL-	CNNNNPIDEV	ASGSNGSKV	DDNKKLG- :   :
1., Zatz 10me seq 106:151- 2003982;	Similar 7; Con	TAKADGDRÜ    :   TAAEQQGASRÜ	GDVKASGDASIA ::	TASGHASTAVGAMSYAQGHFSNAFGTRATA THIS III I I I I I I I I I I I I I I I I	GAIALGAGTR	LSIGSNSIK           ::  VSIGDVSSTNLK	DNTLTIKGGAETNALTDNNI	SSSTTAELLSI	IGFARDGDVDEKQAPYLDKKQLKVGSVAIT	DAVIIEQLKAAKPILNAGAGISVIPTEISVDAKSG 	NSDGTSDKFSVKGSGTNNSLVTAEH :	DDANAITVAKDTTKNAGAVSILKLKGKNG DOGWTLTASGSNGSKVASGGTVDLKNTDG	TLNNDGLTVKDINEQIQVGANGIKFTN 1	SNPGTGIANT	GLSP	IDILNTGFNLF	STAVDOGWTLI	DTTIHLTGT
Zago M.A "The gen Nature 4 EMBL; AE	Query Match Best Local Matches 54	86 SGTA      86 SGTA	2 4					ω o	4 4				703	732	791	826	747	882
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1794 IAIGDNAQATGDQSIAIGTG-----NVVAGKHSG------ALGDPSTVKADNSY 1836 1659 SDVSLGAMGLFIANGPSVTASGFNAGDK---VISHVAVGMADTDAVNVSQLKQAVQSVTV 1715 1604 VVSGGTVDLKNTDGNLAISKSGDSNDVVFNLSKDFKVDEVTAG-----NTVVNTDGVKVG 1658 1682 VDKDGNANG----DLSNVWVKTQKDGSKKALLATYNAAGQTNYLTNNPA---EAIDRINE 1734 1735 QGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGRQTQA-GNQS 1793 1521 GQTDTNKLTDNNIGVVAGTDGF----TVKLAKDLTNLNSVNAGGTKIDDKGVSFVDSSGQ 1576 1486 VKVSSNVLLDSNELVITSHSSTSSVKTLANGESVVNRTVVNGDGVNIDD--VVVVNDLGL 1543 AKANTPVLSANGLDLGGKVISNVGKGTKDTDAANVQQLNEVRNLLGLG-NAGNDNADGNQ 1635 V---NIADIKK-DPN---SGSSSNRTVI-----KAGTVLGGKGNNDTEKLATGGIQVG 1681 1448 INKEQ-----VKGLEKAASDNKTK 1482 1483 NAAVTVG------DL-NAVAQTPLTFAGDTGTTAKKLGETLTIK-------G 1520 1426 TASGANGSKVASGGTVDLKNTDGNLTISKSGDSNDVVFNLSEDLKEKSITVGNTQLDKDG 1485 1261 D---GVKVGSDVALGTTGLTIANGPAVTASGIDAGSKVISHV------AAGAVSETS 1308 DKKLGVKTTTLTSTGTGANKFALSNQATGÖALVKASDIVAHLNTLSGDIQTAKGASQANN 1387 1126 ------GESSTAGTYSGGN-LKSVVDEAAGRIHLQLA---DSPKFGNVVINNGGK--- 1170 1218 IDSQNGQNTITGLSNTLANVTNDKGSVRTTEQGNIIKDEDKTRAASIVDVLSAGFNLQGN 1277 1278 GEAVDFVSTYDTVNF--ADGNATTAKVTYDDTSKTSKVYYDVNVD------DTTIEVK 1327 DGVKFAK--VNNNGV-VGAGID-GTTRITRDEIGFTGTNGSLDKSKPHLSKDGINAGGKK 1099 1100 ITNIQSGEIAQNSHDAVTGGKIYDLKTELENKISSTAKTAQNSLHEFSVADEQGNNFTVS 1159 1160 NPYSSYDTSKTSDVITFAGENGITTKVNKGVVRVGIDQTKGLTTPKL--TVGNNNGKGIV 1217 990 LKGENGLNIKTDKNGTVTFGINTTSGLKAGKSTLNDGGLSIKNPTGSEQI-----QVGA 1043 TSTDAVNGSQLNAVQVQASQPVTFTGNEGAVKRSLGQSVVISGESSTAGTYSGGNLKSVV 920 GMT---SGTTVVNNDGVKVGSDVALGTTGLTITDGPAVTASGIDAGSKVISHVAAGVVSE 860 1716 KATRYKSTNDGG----TQGGNYDGDGATGSKAIAAGVGTQASGEGAAAVGSGAAASGKGS SAGYVDADGNKVIYDSTDNKYYQAKNDGTVDKTKEVAKDKLVAQAQTPDGTLAQMNVKSV DTALQTFTVKKVDEN-----NNADDANAITVGQK-------NANNQVNTLT SDEDAL----VNAKDIAEN------LNTLAKEI-----HTTKGT-----1636 1577 1544 1206 1328 1388 1171 951 1026 861 921 804 921 δλ Db g ò q οy qq qq Dp ò ρý qq δ qq ò qq δy ò g à q g & Q.y D.b δ Qy Db g Q Dp QΥ ద δ Ob

273 TSATDNTDE 306	319 GPLSIGSNSIKRKIINVGAGVNKTDAVNVAQLEAVVKWAKERRITFQGDDNST 371 1	372	365 NGNGITVKYDAKVGDGLKFDSDKKIVADTTALTVTGGKVAEIAKEDDKKKLVNAGDLVTA 387AETNALTDNNI-GVVKEADNSGLKVKLAKTLNN 1:	DD 425 LGNLSWKARAEADTDGALEGISKDQEVKAGETVTFKAGKNLKVKQDGANFTYSLQDALTG 484  QY 419 LTEVNTTLNATTTVKVGSSSSTAELLSDSLFTQPNTGSQSTSKTV-YGVNGVKFTNN 477  DD 485 LTSITLGGTTNGGNDAKTV-INKDGLTTTPAGNGGTTGTNTISVTKDGIKAGNK 537	478 AETTAAIGTTRITRDKIGFARDGDVDEKQAPYLDKKQLKVGSV	OY 521 AITIDNGIDAGNKKISNLAKGSSANDAVTIEQLKAAKPTLNAGAGISVTPTE 572	573 ISVDAKSGNVTAPTYNIGVKTTELNSDGTSDKFSVKGSGTNNSLVTAEHLASYLNE 628 1	629 VNRTADSALQSFTVKE-EDDDDANAITVAKDTTKNAGAVSILKLKGKNGLTVATKKDGTV 687   1   1   1   1   1   1   1   1   1	OY 688 TF7LSQDSGLTIGKSTLNNDGLTVKDTNEQIOVGANGIKFT728	QY 729NVNGSNPGTGIANTARITRDKIGFAGSDGAVDTNKPYLDQDKLQ 772 	QY 773 VGNVKITNTGINAGGKAITGLSPTLPSIADQSSRNIELGNTIQDKDKSNAASINDI 928 	QY 829 LNTGFNLKNNNNPIDFVSTYDIVDFANGNATTATVTHDTANKTSKVVYDVNVDDTTIHLT 888	QY 889 GTDDNKKLGVKTTKLNKTSANGNTATNFNVNSSDEDALVNAKDIAEN 935   :  :	QY 936 LNTLAKEIHTTKGTADTALQTFTVKKVDENNNADDANAITVGOKNANNQVNTLTLK 991	OY 992 GENG-LNIKTDKNGTVTFGINTTSGLKAGKSTLNDGGLSIKNPTGSEQIQ 1040 :	QY         1041VGADGVKFAKVNN	QY 1054	QY 1090 KDGINAGGKKITNIQSGEIAQNSHDAVTGGKIYDLKTELENKISSTAK 1137   1   1   1   1   1   1   1   1   1
	NS 1866 	1926 1944	1986 1998	2046 2058	<i>δ</i> α	da da	ko a	da	da -	nfluenzae	40 40	. Gans 110.	. 4. C.	104	157	202	258	318
	1837 SYGNNNQFTDATT	1867 VALGSNSAISAGTHAGTQAKKSDGTAGTTTTAGATGTVKGFAGQTAVGAVSVGASGAERR : : : : :	1927 IQNVAAGEVSATSTDAVNGSQLYKATQSIANATNELDHRIHQNENKANAGISSAMAMASM :		2047 F 2047 2059 W 2059	FRESULT 2 P71401 D P71401 PRELIMINARY; PRT; 2353 AA.	01-FEB-1997 (TrEMBLrel. 02, Created) 01-FEB-1997 (TrEMBLrel. 02, Last sequence update) 01-7UN-2000 (TrEMBLrel. 14, Last annotation update) HSF PROMFIN	HSF. Haemophilus influenzae. Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;	NCBL_TAXID=727; [1] SEQUENCE FROM N.A.	MEDLINE=9704, MEDLINE=9704, MEDLINE=9704, MEDLINE=9704, Cutter D. III, Barenhamp S.J.; Geme J.W., Cutter D. III, Barenhamp S.J.; Characterization of the genetic locus encoding Haemophilus in the profession of the genetic locus encoding Haemophilus in the profession of the genetic locus encoding Haemophilus in the profession of the genetic locus encoding Haemophilus in the profession of the genetic locus encoding Haemophilus in the profession of the genetic locus encoding Haemophilus in the profession of the genetic locus encoding Haemophilus in the genetic locus encoding Haemophilus encodin	Cype D Sutter 100115; J. Bacteriol. 178(281-6281-6296). EMBL; U41852; AAC44560.1; SEQUENCE 2353 AA; 243844 MW; 53E491B51A897B77 CRC64;	Query Match         10.9%;         Score 1123;         DB 2;         Length 2353;           Best Local Similarity         23.0%;         Pred. No. 7.98-39;         Matches 607;         Conservative 318;         Matches 838;         Todals 874	MNHIKKVIFNKATGTFWAVAEYAKSHSTGGGSCATGQVGSVCTLSFARIAALA		AQGQAIAIGSSNKTVNGSSLDKIGTDATGQESIAIGGDVKASGD-ASIA 	DLHLLDQHGNPKHPKGTLINDLINGHAVLKEIRSSKDNDVKYRRT		TSSSLGAIALGAGTRAQLQGSIALGQGSVVTQSDN

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Ouery Match 10.2%; Score 1046.5; DB 2; Length 2712; Best Local Similarity 22.9%; Pred. No. 1.5e-35; Matches 591; Conservative 348; Mismatches 917; Indels 725; Gaps 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                              67 AQKKDTK-----HIAIGEQNQPRRSGTAKA------DGDRAIAIGENANAQGGQAI 111
                                                                                                                                                                                                                                                                                                                                                                                     7 VIFNKATGTFMAVAEYAKSHSTGGGSCATGQVGSVCTLSFARIAALAVLVIGATLSGSAY 66
                                         387 AETNALTDNNIGVVK-EADNSGLKVKL-----AKTLNNLTEVNTTTLNATTTVKVG
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Pasteurella multocida.
Bacterrai, Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
NCBI_TaxID=747;
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MAPB PROTEIN.
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	INTRADSA				NGONTITGLSNTLANVTNDKGSVRTTEQGNIIKDEDKTRAASIVDVLSAGFNLQGNGEAV
827 496 884 556 921 594 630	630 1032 671 1085 722	779 1203 836 1258 894	1318 948 1374 995 1434 1043	1073 1548 1110 1605 1162	1222 1689 1282 1742 1325
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1913 KTDGSVVALKDAEGSVLTNGVNVGDLKNAIKDVTSATNGGFGLKDKAGAEFKQDLGTTAQ 1972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2300 NEGLKAGDVIVTTAĞINAĞNKKVTĞVADĞDISPNSTDAVNGSQLNAVKETAEAĞMHLTAN 2359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2471 KNANAIIGVNDSVKGLDGNDGKDGNSKTRIVYTKPNGEEEQV-ATMNDGLVFGADKGTEH 2529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1930 ---VAAGEVSATSTDAVNGSQLYKATQSI---ANATNELDHRIHQNENKANAGISSAMAM 1983
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                                    1371 TLSGDIQTAKGASQAN-----NSAGYVDADGNKVI-----YDSTDNKYYQA-----1411
                                                                                                                                                                                                                                                                                                                                  1496 QTPLTFAGDTG-TTAKKLGETLTIKGG-----QTDTNKL,TDNNIG-------- 1534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1632 DGNQVNIA-DIKKDPNSGSSS-----NRTVIKAG-TVLGGKGNNDTEK-----
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                                                                                                          1412 KNDGTVDKTKEV------
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AmbDLINE-20365717; Pubbed-10910347;
AmbLINE-20365717; Pubbed-10910347;
Alvarenga R., Alves L.M.C., Arruda P., Abreu F.A., Acencio M.,
Alvarenga R., Alves L.M.C., Arraya J.E., Bala G.S., Baptista C.S.,
Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
Bueno M.R.P., Candargo A.A., Ferreira D.M.C. R., Costa M.C. R., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Fraga J.S., Franco M.C., Frohme M., Furial L.R.,
RA Frieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Machado M.A., Madeira A.M.B., Madeira H.M.F., Marino C.L.,
RA Machado M.A., Madeira A.M.B., Madeira H.M.F., Marino C.L.,
RA Mannak C.F.M., Martins E.A.L., Martins E.M.F., Marsukuma A.Y.,
RA Mannak M. J., Nascimento A.L.T.O., Netto L.E.S.,
Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA Oliveira M.C., de Oliveira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA Ge Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sandsaki H.E.,
RA de Silve A.C., R., Salvestri M.L.Z., Siqueira M.J., de Souza A.A.,
RA de Silveira M.C., and Silva F.R., Silva W.A., Truffi D., Tsai S.N., Tsunako M.H.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.N., Tsunako M.H.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
REMEL, AEGONGOT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      379 NTLTIKGGAETNALTDNNIGVVKEADNSGLKVKLAKTLNNLTEVNTTTLNATTTVKVGSS 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 GHASTAVGAMS---YAQGHFSNAFGTRATAKSAYSLAVGLAATAEGQSTIAIGSDATSSS 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 LGAIALGAGTRAQLQGSIALGQGSVVTQSDNNSRPAYTPNTQALDPKFQATNNTKAGPLS 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       248 ANGIALGASSSVTTRGGVALGQGSLAATASGIT--GYDPVTKSTSTLSTSMWRSTLGAVS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 AQVYVNSDSTENCVEILGDSSQTSFIHSASNDKCKPDFTQTEYSLFYDYRNLVLGG---- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 SGDASIAIGSDDLHLLDQHGNPKHPK-GTLINDLINGHAVLKEIRSSKDNDVKYRRTTAS 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 IAIGENANAQGGQAIAIGSSNKT--VNGSSLDKIGTDATGQE-----SIAIGGDVKA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.6%; Score 778; DB 2; Length 1190;
ilarity 20.5%; Pred. No. 8.1e-25;
Conservative 185; Mismatches 432; Indels 1044; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 SAYAQKKDTKHIAIGEQNQPRRSG---TAKAD------GDRA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
01-MAR-2001 (TrEMBLrel. 16, Last annotation update) SURFACE PROTEIN.
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Matches 429; Conserv
                                                                  Xylella fastidiosa
                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                               NCBI_TaxID=2371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                 xylella
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QQ	348	WNLTASGANSSNVALGESVDLKNSDGNLLITKTTDSNDVTFNLATALKV 390
Οy	439	SSTTAELLSDSLTFTQPNTGSQSTSKTVYGVNGVKFTNNAETTAALGTTRITRDKIGFAR 498
QQ	397	RVTLDSTG423
οy	499	KP 55
QQ	424	LQAV
οy	559	SLVT 61
QQ	466	48
Qy	619	
qq	484	20
Qγ	619	VATKKDGTVTFGLSODSGLTIGKSTLNNDGLTVKDTNEQIQVGANGIKFTNVNGS 733
qq	501	54
Qy dd	734	NPGTGIANTARITRDKIGFAGSDGAVDTNKPYLDQDKLQVGNVKITNTGINAGGKAITGL 793
λŏ	794	PTLPSIADQSSRNIELGNTIQDKDKSNAASINDILNTGFNLKNNNN
qq	571	NVAAGTADTDAVNFSQLQAVSSTASKGWNL600
QY	851	HLTGTDDNKKLGVKTTKLNKTSANG 91
qq	601	
Qy	911	NTATNENVNSSDEDALVNAKDIAENLNTLAKEIHTTKGTADTALQTFTVKKVDENNNADD
q	635	
Οý	971	ANAITVGGKNANNQVNTLTLKGENGLNIKTDKNGTVTFGINTTSGLKAGKSTLNDGGLSI ::
QQ	658	TDGVTVGVITDG 679
QY	1031	KNPTGSEQIQVGADGVKFAKVNNNGVVGAGIDGTTRITRDEIGFTGTNGSLDKSKPHLSK 10
QQ	089	P84 SALAS
٥y	1091	DGINAGGKKITNIQSGEIAQNSHDAVTGGKIYDLKTELENKISSTAKTAQNSLHEFSVAD
qq	685	SGISAGNOKITHVVAGTADTDAVNFSQLQAVSSTASKGWNLL 726
Qy	1151	EQGNNFTVSNPYSSYDTSKTSDVITFAGENGITTKVNKGVVRVGIDQTKGLTTPKLTVCN
QD	727	
δλ	1211	NNGKGIVIDSQNGONTITGLSNTLANVTNDKGSVRTTEQGNIIKDEDKTRAASIVDVLSA 12
qq	750	IVISKESGSNDVL 76
Qy	1271	GFNLQGNGEAVDFVSTYDTVNFADGNATTAKVTYDDTSKTSKVYYDVNVDDTTIEVKDKK
QQ	763	1 - FNLSSS
δλ	1331	LGVKTTTLTSTGTGANKFALSNQATGDALVKASDIVAHLNTLSGDIQTAKGASQANNSAG 139C
qq	774	4 LTVGDIVMTING785
Qγ	1391	1. YVDADGNKVIYDSTDNKYYQAKNDGTVDKTKEVAKDKLVAQAQTPDGTLAQMNVKSVINK 145(
q	786	9
δλ	1451	EQVNDANKKQGINEDNAFVKGLEKAASDNKTKNAAVTVGDLNAVAQTPLTFAGD
5	786	SQVTLG 79TT SQVTLG

VDSSGQAKANTPVLSANGLDLGGKVISNVGKGTKDTDAANVQQLNEVRNLLGLGRAGNDN   :::: :: :	ADGNQVNIADIKKDPNSGSSSNRTVIKAGTVLGGKGNNDTEKLATGGIQVGVDKDGNA		IAIGTGNVVAGKHSGAIGDPSTVKADNSYSVGNNNQFTDAT:	1849 -QTDVFGVGNNITVTESNSVALGSNSAISAGTHAGTQAKK 1887	1888 SDGTA-GTTTTAGATGTVKGFAGQTAVGAVSVGASGAERRIQNVAAGEVSA 1937	1938 TSTDAVNGSQLYKATQSIANATNELDHRIHQNENKANAGISSAMAMASMPQAYIPGRSWV 1997 	1998 TGGIATHNGQGAVAVGLSKLSDNGQWVFKINGSADTQGHVGAAVGAGFHF 2047 	RESULT 5 . OPF3X6	9F3X6 PRELIMINARY; PR. 9F3X6; 1-MAR-2001 (TrEMBLrel. 16, Crear 1-MAR-2001 (TrEMBLrel. 16, Last	(TrEMBLrel.	Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae; Pasteurella. NCBI_TaxID=747;	SEQUENCE FROM N.A. STRAIN=PM70;	<pre>Henderson I.R., Nataro J.P., Cappello R., Stein C.; "Evolutionary origins of the autotransporter proteins."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases. EMBL: AJ277635; CAC14202.1;</pre>	SEQUENCE 1299 AA; 130963 MW; 8BCCEOEB66CDB428 CRC64;	Query Match 7.2%; Score 739; DB 2; Length 1299; Best Local Similarity 20.8%; Pred. No. 3.9e-23; Matches 443; Conservative 231; Mismatches 545; Indels 908; Gaps 84;	<pre>1 MNHIYKUIFNKATGTFMAVAEYAKSHSTGGGSCATGQVGSŸCTLSFARIAALAVLVI 57                                      </pre>

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AGKSTLNDGGLSIKNPTGSEQIQVG---- 1042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAGGKAITGLSPTLPSIADQSSRNIEL--GNT 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGTAKADGDRAIAIGENANAQGGQAIAIGSSN 117
                                                                                                                                             SHASTAVGAMSYAQGHFSNAFGTRATAKSAYS 237
                                                                                                                                                                                -----KPAKS 106
                                                                                                                                                                                                                  IALGAGTRAQLQGSIALGQGSVVTQSDNNS-- 295
                                                                                                                                                                                                                                                   IAIGDNAKALDNQAIAIGQNATANSDWDISIG 166
                                                                                                                                                                                                                                                                                         SSNSIKRKIINVGAGVNKTDAVNVAQLEAVVK 355
                                                                                                                                                                                                                                                                                                                KGGAETNALTDNNIGVVKEADNSGLKVKLAKT 415
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------NNIALGTSAGD-----RLAGT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                          AELLSDSLIFTQPNTGSQSTSKTVYGVNGVKF 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTLNAGAGISVTPTEISVDAKSGNVTAPTYNI 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSSIAIGGTVNGNDTARTLASDNFTIA---M 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAEHLASYLNEVNRTADSALQSFTVKEEDDDD 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGLTVATKKDGTVTFGLSQDSGLTIGKSTLNN 706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLNKTSANG-NTATNFNVNSSDEDAL-VNAKD 931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKVDENNNADDANAITVGQ--KNANNQVNTLT 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : |:|| | | | :::
-SIGYNSNAKGYQAIAFGSEAKTTENAGSSIA 665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GYNAGVTKTAD------EAQSDP 384
                     PGTGIANTARITRDKIGFAGSDG------
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1096 GNAONTNGNVAMTDIGGTGKNNINDAIKASRNEVKQCKNMVVTPTTGANGQTIYEVATAD 1155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1961 ELDHRIHQNENKANAGISSAMAMASMPQAYIPGRSMVTGGIATHNGQGAVAVGLSKLSDN 2020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1682 VDKDGNANGDLSNVWVKTQKDGSKKALLATYNAAGQTNYLTNNPAEAIDRINEQGIRFFH 1741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1742 VNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGRQTQAGNQSIAIGDNAQ. 1801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SFVDSSGQAKANTPVLSANGLDLGGKVISNVGKG--TKDT-DAANVQQL----NEVRNLL 1621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1622 GLGNAGNDNADGNQVNIADIKKDPNSGSSSNRTVIKAGTVLGGKGNNDTEKLATGGIQVG 1681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGYVDADGNKVIYDSTDNKYYQAKNDGTVDKTKEVAKDKLVAQAQTPDGTLAQMNVKSVI 1448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NKEQVNDANKKQGINEDNAFVKGLEKAASDNKTKNAAVTVGDLNAVAQTPLTFAGDTGTT 1508
                                                                                                                                                                                                                                                                                                  1269 SAGFNLQGNGEAVDEVSTYDTVNFADGNATTAKVTYDDTSKTSKVVYDVNVDDTTIEVKD 1328
                                                                                                                                                                                                                                                                                                                                                                                                              1329 KKLGVKTTILISIGTGANKFALSNQATGDALVKASDIVAHLNTLSGDIQTAKGASQANNS 1388
                                                                                                                                                                                   1209 GNNNGKGIVIDSQNGQNTITGLSNTLANVTNDKGSVRTTEQGNIIKDEDKTRAASIVDVL 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----TIHDA-----IEAVN 852
                                                                       ADEQGNNFTVSNPYSSYDTSKTSDVITFAGENGITTKVNKGVVRVGIDQTKGLTTPKLTV 1208
                                                                                                                                                                                                                                               827
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EMBL; U38617; AAC43721.1; EMBL; U38617; AAC43721.1; EMBL; U38617; AAC43721.1; CAPATION MY; D977335A89F7333D CRC64; CAPATION MY; D977335A89F7333D CRC64; CAPATION MY; D977335A89F7333D CRC64; CAPATION MY; D977335A89F7333D CRC64; CAPATION MY; D977335A89F7335D CRC64; CAPATION MY; D97735A89F7335D CRC64; CAPATION MY; D97735A89F7735D CRC64; CAPATION MY; D97735A8745D CRC64; CAPATION MY; D97735A8745D CRC64; CAPATION MY; D97735A8745D CRC64; CAPA
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Yersinia.
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Henderson I.R., Nataro J.P., Cappello R., Stein C.;
"Evolutionary origins of the autotransporter proteins.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ277631; CAC14227.1;
SEQUENCE 3705 AA; 370756 MW; 714FDF16455968C9 CRC64;
                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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Best Local Similarity 21.1%; Pred. No. 7.4e-18;
Matches 487; Conservative 329; Mismatches 876;
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1343 T------GANKFALSNQATGDALVKASDIVAHLNTLSGDIQTAKGASQANN 1387 SFSGAHQIGTDGELTV-----GQASNLGASSATVNL------GTLTSHLI 1354 1445 KSYINKEQVNDANKKQGINEDNAFVKGLEKAASDNKT-----KNAAVTVGDLNAV- 1494 VGIDQTKGLTTPKLTVGNNNGKGIVIDSQNGQNTITGLSNTLANVTNDKGSVRTTEQGNI 1252 ILGANGAFGQTSLLDIASGASANINGYSQTVGAVTNVGTVTLGSGGVLTSGLLTNGGILD 1211 1212 LTGGALNLTXGGASTVAGGLTGAGTLNINGGNLSVSAANSGLSGQTHIADVASVTLTDTG 1271 NSLHEFSVADEQGNNFTVSNPYSSYDTSKT-----SDVITFAGENGITTK--VNKGVVR 1192 LNDGGLSIKNPTGSEQIQVGADGVKFAKVNNNGVVGAGIDGTTRITRDEIGFTGTNGS-L 1081 NNADDANAI-TVGQKNANNQVNTL--TLKGENGLNIKTDKNGTVTFGINTTSGLKAGKST 1022 812 ATLGAGTGSALVNNSAN-----VSLEQASM-FAGTWQVNQGGALTASNSNQLGSAKI 862 852 853 FANGNATTATVTHDTANKTSKVVYDVNVDDTTIHLTGTDDNKKLGVKTTKLNKTSANGNT 912 664 DHIINNNGTLDGTLTTGAGNDT-LVLDSSSQSNDVINLGDGNNSVTIQNGATVSSIITGN 722 793 782 -----KVTYDDTSK-----TSKVVYDVNVDDTTIEVKDKKLG-----VKTTTLTSTG S---AGYVDADGNKVIYDSTDNKYYQAKNDGTVDKTKEVAKDKLVAQAQTPDGTLAQMNV 863 GLOGILN-LDNIALENHVLTGNGTLNVAKNLATTAFDFGSTVGGAFSGIVNLT--KTTFA DKSKPHLSKDGINAGGKKITNIQSGEIAQNSHDAVTGGKIYDLKTE-LENKISSTAKTAQ 723 GNDTFTINGMSVGSTYLGSLDAGTGLNTXNXXASTDELAAATSLQGFTNINLVDSHITLV 794 SPTLPSIADQSSRNIELGNTIQDKDKSNAASINDILNTGFNLKNNNNPIDFVSTYD-IVD 134 NPGTGIANTARITRDKIGFAGSDGAVDTNKPYLDQDKLQVGNVKITNTGINAGGKAITGL 913 ATNFNVNSSDEDALVN-----AKDIAENLNTLAKEIHTTKGTADTALQTFTVKKVDEN ALQI------TDGIDNTTTIGNEIQLNAENATAINFLGSSSSKTLNNNGTIKGSVIFAGVA ------DGTVTFGLSQDSGLTIGKSTLNNDGLTVKDTNEQIQVGANGIKFTNVNGS -----DDNIGSGMVNIDSSSELLFGSTFDGILH 468 GVNGVKETNNAETTAAIGT--TRITRDKIGFARDGDVDEKQAPYLDKKQLKVGSVAITID AGTGVNVLASAILNLFGGTINTSATANGITFA-----GTEGGHTLTDLTINLLGTGIALS DAKSGNVTAPTYNIGVKTTELNSDGTSDKFSVKGSGTNNSLVTAEHLASYLNEVNRTADS DAEALDINVNGAGIGIQAT------GGGVNLS-----ASNLIINVANTLGT ALQSFTVKEEDDDDANALTVAKDTTKNAGAVSILKLKGKNGLTV---ATKK-----NGIDAGNKKISNLA----KGSSAND--AVTIEQLKAAKPTLN---AGAGISVTPTEISV-IKDEDKT-RAASIVDVLS-AGFNLQGNGEAVDFVSTYDTVNFADGNATTA---ò

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1515 GIVNLTNTTFALSADNAAALARATLKLSDDSVTTVGATDRTLHGLDLNGGTLIFDGS--- 1571
                                                                                                                                                                                                                                                IADIKKDPNSGSSSNRTV----IKAGTV-LGGKGNNDTEKLAT-------GGIQVG 1681
                                                                                                                                                                                                                                                                             -----PPOSQANGVVTVTDLALNSGTISITGAGNWENEHPVTPPNVSLLEQDRGDILLE 1625
                                                                                                                                                                                                                                                                                                               VDKDGNANGDLSNVWVKTQKDGSKKALLATYNAAGQTNYLTNNPAEAIDRINEQGIRFFH 1741
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                                                AQTPLTFAGDTGTTAKKLGETLTIKG-GQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNL 1553
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STRAIN=MADRID E:
BEDLINE=99039493,
Andersson S.G.E., Zonorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
Eriksson A.-S., Winkler H.H., Kurland C.G.,
"The genome sequence of Rickettsia prowazekii and the origin of mitochondria."
                                                                    NGVSNAVTIDIADATLNLDDIA----LFNHVLTGNGLLNVAKNDASTAFDFGSTVGGAFS
                                                                                                                                                                                                                                                                                                                                              LINAANVTGNANNLDLLV - - DGT - - - - AITSGTQGVESAIQQGGSTVANAIHNYGLTSSN
                                                                                                               NSV-NAGGTK I DDKGVSFVDSSGQAKANTPVLSANGL------DLGGKV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1839 TGAGTLNINGGDLAVSATNSGLSG-QTHIADVASVTLTGTGTLGTSAVEVLGTL----
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Rickettsiaceae; Rickettsieae; Rickettsia.
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EMBL; AJ235271; CAA14908.1; -.
SEQUENCE 2340 AA; 247862 MW; CC4070F93C165F26 CRC64;
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                                                                                                                           84 RRSGTAKADGDRAIAIGENANAQGGQAIAIGSSNKTVNGSSLDKIGTDATGQESIAIGGD 143
                                                                                                                                                                                          144 VKASGDASIAIGSDDLHLL---DQHGNPKHPKG-TLINDLINGHAVLK----EIRSSKDN 195
                                                                                                                                                                                                                                                        254
                                                                                                                                                                                                                       LNFKGNATLNGNINNLNILKFSGGHGKTLNLQGNTKVDNLVFADSVLDSGTISVNGLLDT 407
                                                               SHSTGGGSCATGQVGSVCTLSFARIAALAVLVIGATLSGSAY-AQKKDTKHIAIGEQNQP 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAMIDGSVLCNGGVAGTLDFIGDGNVTQNIGADNANSI--STINIQG----DNTKNVTI-
                                                                                                                                                 GSDATSSSLGAIALGAGTRAQLQGSI-ALGQGSVVTQSDNNSRPAYTPNTQALDPKFQAT
                                                                                                                                                                                                                                                                                                                                                                                       NN-----KIINVGAG---VNKTDA
                                                                                                                                                                                                                                                                                                                                                                                                         345 VNVAQLEAVVKWAKERRITFQGDDNSTDVKIGLDNTLTIKGGAETNALTDNNIGVVKEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TKLLSINSTGQITFNRTLDLGAGGN---IAFGKHGTLVVNGVTGSITTSENNQGIL--TI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NSGLKVKLAKTLNNLTEVNTTTLNATTTVKVGSSSSTTAELLSDSLTFTQPN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---TGSQSTSKTVYGVNGVKFTNNAETTAAIGTTRITRDKIGFARDGDVDEKQAPYLDKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | :| :| :| :| XILTGEVITHNNTKGV--LSLGTGSNITGQIGTNSAALEKI--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QLKVGSVAITIDNGIDAGNKKISNLAKGSSANDAVTIEQLKAAKPTLNAGAGISVTPTEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVDAKSGNVTAPTYNIGVKTTELNSDGTSDKFSVKGSGTNNSLVTAEHLASYLNEVNRTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIFTGNGGITG---NIGANGAALQ------EVVFNGTTN------IGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NS--QNFTVAH---SAANVVITGLTTGALKYKDTGTIIAHGGLVGDIDFNNKAGKFILGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANGIKFTNVNGSNPGTGIANTARITRDKIGFAGSDGAVDTNKPYLDQDKLQVGNVKITNT
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                                                                                                                                                                                                                                                        D-VKYRRTTASGHASTAVGAMSYAQGHFSNAFGTRATAKSAYSLAVGLAATAEGQSTIAI
                                                                                                                                                                                                                                                                                                                                                     -ADNTIYTIDA------KNGNVNLLNNNAKIIFEGADSMLALINTGVTADRTFTIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----NGLTVATKK---DGTVTFGLSQDSGLTIGKSTLNNDGLTVKDTNEQIQVG
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                               658;
                                                                                 Length 2340;
                               Conservative 313; Mismatches 879; Indels
DB 2;
                Pred. No. 3e-16;
Score 582;
 5.6%;
                Similarity
                               488;
Query Match
Best Local 5
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                               Matches
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KNAN 982 	-SSTAKTAONS 1142		VUDAD-GNKVIY 1401	3A 1822 AA 1609 1878 -S 1647   AS 1932 AV 1695	SVVGLNG: 1992 RINEQGIR 1738IN 2041 NQSIALGD 1798 GGIGFDY 2098
ALQTETVKKVDENNNADDANALTVGGKNAN		GSVNESNFEKSGNIVISDGATMOVNNNVIALDISGRNANNSTERLANVTNDKGSVRT	KASDIVAHLNTLSGD-IQTAKGASQAN-NSAGYVDAD-GNKVIY  :	DTK  RDD 	::
IABNLNTLAKEIHTTKGTADTALQTFTVKKVDENNNADDANAITVGQKNAN	HLSKDGINAGGKKITNIQSGEIAQNSHDAVTGGKIYDLKTELENKISSTAKTAQNS	IINAGSVNFSNFLKSGNIVISDGATMQVNNNVTATDIDSGANAMANG LIMINATIA TATALY VGNNNGKGIVIDSGNGQNTIT	SNQATGDALVKASDIVAHLNTLSGD-IQTAKGASQAN-NSAGYUDAD-GNKVIY    KNLDIPDALIDLDVLPRSLSLFNYFTDIKADNLNFADDTATANFKDAVVIDAHIDNGGIL   STONKYYQAKNDGTVDKTKEVAKDKLVAQAQTPDGTLAQMNVKSVI   STONKYYQAKNDGTVDKTKEVAKDKLVAQAQTPDGTLAQMNVKSVI   STONKYYQAKNDGTVDKTKEVAKDKLVAQAQTPDGTLAQMNVKSVI   STONKYYQAKNDGTVDKTKEVAKDKLVAQAQTPDGTLAQMNVKSVI   STONKY	LOKG GGTK I IYTP NVQQ	
932 I 1116 - 983 N 1165 I 1028 I		1391 1208 1451 1247 1510 1296	1351 1621 1402 1681 1449 1728	1772 1559 1823 1610 1879	1933 1696 1993 1739 2042
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Qy	1799 NAQATGDQSIAIGTGNVVAGKHSGAIGDPSTVKADNSYSVGNNNQFTDA-	-
OD	2099	2154
QY	1848	1883
qq	2155 VYGRNKIKNYEKRITTITDQIAIGKFINTFYSYELLGGYNYLISHRTTITPMFGMRY	2211
ογ	1884 QAKKSDGTAGTTTTAGATGTVKGFAGQTAVGAVSVGASGAERRIONVAAV 	1941
qq	2212 ATEKNNGYKENNTIFQNLSIKKNYYDKFETILGLNSV	•
Qy	1942 AVNGSQLYKATOSIANATNELDHRIHQNENKAN	1996
qά	2256 IIIKPELHWFINYQCKNKLPNIDARLDGIDEPLTIRFKPAKITYN	2301
Qy	1997	
QO	b 2302 LGGGISTKN 2310	
RES	RESULT 10	
Z60 QI	O9ZHLO PRELIMINARY; PRT; 4919 AA. ID Q9ZHLO PRELIMINARY;	
AC DT	09ZHLU; 01-MAY-1999 (TrEMBLrel. 10, Created)	
TO TO		
D C	LARGE	
SO		
888	Haemophilus.	
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RP RC		
RA	(X) MEDLINE-99030326; PubMed-9811062; (A) Ward C.K., Lumbley S.R., Latimer, J.L., Cope L.D., Hansen E.J.; (A) Ward C.K., Lumbley S.R., Latimer, J.L., Cope L.D., Hansen E.J.;	
RT	"Haemophillus ducies.";	
RE SO RE		
0	Query Match 5.5%; Score 570.5; DB 2; Length 4919; Best Local Similarity 19.2%; Pred. No. 2.5e-15; Similarity 19.2%; All Similarity 1	Gaps 109
•	Matches total components by several components of the total components of the	43
à à	2 NHIYKIENKAIGIEMAAABIAACABAAGAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	9
20	· ;	98
oy.	ACAGAA 10011111111111111111111111111111111	
ad	63 LGLHNHSPLNVFNGRNLSVVLLSLIFE	126
δδ	OY 87GTAKADGDRAIAIGENANAUG-CUAIALCSSNALYNGSSGUD 	4 -
qu	Db 122 EKVVVINIAKPD-EQGISDNHFSKFNIPNSAVFNNSIKEGNSQLVGLLGENKNLGSQAA	D ·
Qy	ä	18
qa	Db 181 TIFNQVTGDQESKİSGGLEVFGEKADLFIINPNGVTLNGVKTINTDR	77
ΟY	TAKSAYS	24
đ	Db 228 FVASTSEVVEPHIKOLNVQRGKVIIGKDGVATNGLSHFD	26
δλ	QY 241 GLAATAEGQSTIAIGSDATSSSLGAIALGAGTRAQLQGSIALGQGSVVTQSDNNSRPAYT	30
οp	Db 267 VVAKNIEQQGKVSIEGDSKPAKLANVTFAAGNLTYDVNTRDV-N	309

301   PHYOALDPKFQATNNTRACELSIGNSIKRKIINVGAGVN
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δ, ξ	10 NNNGKGIVIDSQNGQNTITGLSNTLANVTNDKGSVRTTE 124
<b>Q</b>	45 NANNSSNPHYLNTALKHILGNGWQDDLKKQENIKVLKQKWEDFKKDKGASKML
oy D	1249 QGNIIKDEDKTRAASIVDVLSAGFNLOGNGEAVDFVSTYDTVNFADGNATTAKVTYD 1305 1299LYPNDVKEKAKIFAGIIRNDVIISDVESEDFKKKSKRQNGFWAKNDTGTDSYD 1353
δy	Ēr.
С	1354 STKASEKYKKVENVDHKE-NIDEHKLNIGKHEITVPGVSFENLNNKNMDHQPDKLGEI 1410
δλ	366 VAHLNTLSGDIQTAKGASQANNSAGYVDADGNKVIYDSTDNKYYQAK 141
QQ	1411 DKSIISELLAQPVYTEKSAARDSDPRVNQNDKEALDNLYRTRLSYINQNNYLGAKYFFNQ 1470
δŏ	3 NDGTVDKTKEVAKDKLVAQAQTPDGTLAQMNVKSVINKEQVNDANKKQGIN 
QQ	1471 LDTEDDKLKGIKRIGDNYFEHQLITRLIEKVADNHLTLKHGLH-DIALVKKL 1521
δλ	ONKTKNAAVTVGDLNAVAQTPLTFAGDTGTTAK :
QO	1522 IDSASIQAKDLNLKVGEALTKEQKDNLKEDIVWYV 1556
δy	1518
qq	1557 KTEVNGQEVLVPQVYLAKQTIEEVEKQRGVGTGQIRAGIIDVKVDDVRNTGTIAGYAVGL 1616
δλ	1543 TVKLAKDLTNLNSVNAGGTKIDDKGVSFVDSSG1575
qq	ESTGVT
Óγ	1576GKVISNVGKGTKDTDA 1608
qq	1673 TDKDKNVDLTASELKGNTGQIKAKDLNLNDIYETSYKYKYEKLFGKNGGEIGDRVTQTSQ 1732
δλ	1609 ANVQQLNEVRNLLGLGAAGADAADGAQVNIADIKKDPNSGSSSNRTVIKAG 1659
qq	1733 AKSVGTDASFDHLHLSLEGDVNQTGSNLKANRTTGVVKGDFNTKAGKDLFHRQIDTVTSG 1792
οy	LGGKGNNDTE
Q	1793 TVYSASASGGGGSAGISLTDQGVETYTNKTATAGANADVTNFWKRTRETETSLTHRNSEF 1852
οy	1702
QQ	1853 NALSGELYVMGKADIGGVDINRDVEVIKTPEEIAAEQKAAEEAKKAEVKENEASETAAKE 1912
δy	1718 TNYLTNNPAEAIDRINEQGIRFFHVNDGNQEPVVQGRNGIDSSA 1761
Dp	1913 TEEAENDNVAEKDKTKPKFKKLTDEEIAAAFETKGEDFFAAYKAREEEDRKKGFTLSA 1970
Οy	1762 SGKHSVAIGEQAKADGEAAVAIGRQTQAGNQSIAIG 1797
qq	1971 EQIESTKARDEKETTYYELKVGVGAEAEAHSAAADAISNKARQIIDTQNGLKQDGTVALQ 2030
δλ	QSIAIGTGNV
qq	2031 EASDVLNLATGDLAGASAKLKFELSTIEKKSRGASDGRSILGGRLNLAAR 2080
Qy	1849 QTDVFGVGNNITVTESNSVALGSNSAISAGTHAGTQAKKSDGTAGTTTAGATGTVKGFA 1908
qq	2081 GGDITLNNVETTENSHLSLKARDNVNVNSGV-TEQKDESNSQSLKVTAGASSGCGVMA 2137
ΟY	RRIQNVAAGEVSATSTD
qq	NTESTSHTNSLLRGKSLRVEAGKDFNLISSNVD
δλ	966 IHQNENKANAGISSAMAMA
qq	2 LHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      442 ----TAELLSD---SLTFTQPNTGSQSTSKTVYGVNG-VKFTNNAETTAAIGTTRITRDK 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           309 VIKATTTKLTDNASAVTFTNPVVVTGAIDNTGNANNGIVTFTGDSTVTGNIGNTNAL--- 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ATVNVGAGLLQVQGGVVKAN--TINLTDNASAVTFTNPVVV 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMSYAQGHFSNAFGTRATAKSAYSLAV--GLAATAEGQSTIAI--GSDATS---SSLGAI 266
                                                                                                                                                                                                                  STRAIN=MALISH 7:
MEDLINE=94171067; PubMed=8125327;
MEDLINE=94171067; PubMed=8125327;
Crocquet-Valdes P.A., Welss K., Walker D.H.;
"Sequence analysis of the 190-kDa antigen-encoding gene of Rickettsia conorii (Malish 7 strain).";
Gene 140:115-119(1994).
BENBL; U01028; AAA17405.1; -.
SEQUENCE 2021 AA: 203366 WW; BE943FBA3BDD5C43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          ENANAQGGQAIAIGSSNKTVNGSSLDKIGTDATGQESIAIGGDVKASGDASIAIGSDDLH 160
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             494 IGFARDGDVDEKQAPYLDKKQLKVGSVAITIDNGIDAGNKKISNLAKGSSA----NDAVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKAIQQGLKAALFTTSTAAIMLSSSGALG-----IAVSGVIATNNNAAFS-----
                                                                                                                                                                                                                                                                                                                                                                                   589;
                                                                                                                                                                                                                                                                                                                                                       Length 2021;
                                                                                                                                               Rickettsia conorii.
Bacteria: Proteobacteria: alpha subdivision; Rickettsiales:
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=781;
                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                         Similarity 23.6%; Score 567.5; DB 2; Similarity 23.6%; Pred. No. 1e-15; 72; Conservative 198; Mismatches 745;
                                                                       2021
                                                                                                  Created)
                                                                        PRT;
                                                                                                 (TrEMBLrel. 01, (TrEMBLrel. 01, 1) (TrEMBLrel. 08, 1)
                                                                       PRELIMINARY;
                                                                                                                                           190-KDA ANTIGEN (ROMPA).
        2251 IV 2252
                                                                                                                             01-NOV-1998
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                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Q52657;
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1600 1277 1278 ATTANVVLFKDAVQLTQTGNIGGFLDF-NAKNGTVTLNNNVNVAGTVK--NTGGTNNGTL 1334 IKAGTVLGGKGNNDTEKLA---TGGIQVGVDKDGNAN-GDLSNVWVKTQKDGSKKALLAT 1711 1544 1391 YV--DADGNKVIYDS-----TDNKYYQAKNDGTVDKTKEVAKDKLVAQAQTPDGTLAQ 1441 1076 LVAPGVDEGTVVFDGGVNGLNIGSNVAGAARNIGDVGGNK------1115 1442 MNVKSVINKEQVNDANKKQG----INEDNAFVKGLEKAASDNKTKNAAVTV----GDLN 1492 TTTLTSTGTGANKFALSNQATGDALVKASDIVAHLNTLSGDI----QTAKGASQANNSAG 1390 981 DGGGKAIPY---YFKGAIANGN------NAILNVNTKSLTA----SHLTIG 1018 1162 YSSYDTSKTSDVITFAGENGITTKVNKGVVRVGIDQTKGLTTPKLTVGN-NNGKGIVIDS 1220 1221 QNGQNTITG-LSNTLANVTNDKGSVRTTEQGNIIKDEDKTRAASIVD-----VLSAGFNL 1274 NIQSGEIAQNSHDAVTGGKIYDLKTELENKISSTAKTAQNSLHEFSVADEQGNNFTVSNP 1161 987 TLTLKGENGLNIKTDKNGTVTFGINTTSGLK-----AGKSTLNDGGLSIKNPTGSEQIQV 1041 1042 GADGVKFAKVNNNGVVGAGIDGTTRIJRDEIGFTGTNGSLDKSKPHLSKDGINAGGKKIT 1101 928 FTGDSTVTGNIGNTNALATVNVGAGVTLQAGGSLD-----ANNIDFGARSTLEFNGPL 980 724 NIN-ALAIISVGAGKATLGGAVIKATTTKLIDNASAVTFTNPVVVTGAIDNTGNANNGIA 782 TISVGAGKATLGGAIIKATTTKLTD-------NASAVTFTNPVVVTGAI 624 -NLKNNNNPIDEVSTYDIVDFANGNATTATVTHDTANKTSKVVYDVNVDDTTIHLTGTDD 892 724 GIKFTN----VNGSNPGTGIANTARITRDKIGFAGSDGAVDTNKPYLDQDKLQVGNVKITN 780 KGTKDT----DAANVQQLNEVRNLLGLGNAGNDNAD-GNQVNIADIKKDPNSGSSSNRTV -----AVAQTPLTFAGDTGTTAKKLGETLTIKGGQTDTNKLTDNNIGVVAGTDGFTV 1545 KLAKDLTNLNSVNAGGT-KIDD----KGVSFVDSSGQAKANTPVLSANGLDLGGKVISNVG 1224 TAGKKLTIAGGKTFGGAHKLQDIVFKGEGDFGTAGTTFNTTNIV---LDITGQL--ELG 1176 IPAGNIQFAHADAQLILQNSSGN----DRTITL-GANIDPD---NDBEGIVILN---SV NALA-TISVGAGKATLGGAIIK-----ATTTKLTYN-----QGNGEAVDFVSTYDTVNFADGNATTAKVTYDDTSKTSKVVYDVNVDDTTIEVKDKKLGVK 893 NKKLGVKTTKLNKTSANGNTATNFNVNSSDEDALVNAKDIAE----NLNTLAKEIHTTKG NASAVTF---TNPVVVTGAIDNTGNANNGIVTFTG-------DSTVTGNIGNT 539 AVTETNPVVVTGAIDNTGNANNGIVT----FTG-DSTVTGN------IGNTNALA TGINAGGKAITG---LSPTLPSIADQSSRNIELGNTIQDKDKSNAASI----NDILNTGF-949 TADTALQTFTVK------KVDENNNADDANAITV----

347 338 392

451 438

617 570 666 622 724

834 757 891 811 951

1230 1079 1286

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L---ATYNAAGQTNYLTNNPAEAIDRINEQGIRFFHVNDGNGEPVVQGRNGIDSSASGKH 1765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVAIGFQAKADGEAAVAIGRQTQAGNQSIAIGDNAQAT----GDQSIA---IGTGNVVAG 1818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GTAANSVGDITTTGTTNFASSVNAKGAATLCGTTSFADTFTNTGAVTLA 1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1819 KHSGAIGDPSTVKADNSYSVGNNNQFTDATQTDVFGVGNNITVTESNSVAL----GSNS 1873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KAS------ITNFAKNVTATSF--AANNATINFGNSLAFNSNITGSGT 1590
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                                                                                                                                                                                                                                                                                                                                                                                               GVNGT-TIATGASTI-----NGHITNIAMLKVGAGAVSITOGGNTSITEIQGNGTAL 1466
                                                                                                                                                                                                                                                                                                                                                                            NEVRNLLGLGUAA-----GNDNAD---GNQVNIADIKKDPNSGSSSNRTVIKAGTVLGGK 1665
                                                                                                                                                                                                   EDNAFVKGLEKAASDNKTKNAAVTVGDLNAVAQTPLTFAGDTGTTAKKLGETLTIKGGQT 1523
                                                                                                                                                                                                                       1404 TDNKYYQAKNDGTVDKTKEVAKDKLVAQAQTPDGTLAQMNVKSVINKEQVNDANKKQGIN 1463
                                                                                                     YDTVNFADGNATTAKVTYDDTSKTSKVVYDVNVDDTTIEVKDKKLGVKTTTLTSTGTGAN 1346
----NAQAIDFKGA 1128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLTLGASQVTYTGTGSFTDTLTLNTTFDGAAKSDGHILIKSGSTLDLSGVSTLALVVTAT
                                                                                                                                                                                                                                                             1524 DINKLTDNNIGVVAGTDGFTVKLAKDLTNLNSVN--AGGTKI------DDKGVSFV
                                                                                                                                                                                                                                                                                                                                      D-SGXAGGRVILASVRNATYGTAVNKLKLLEFRGNGTFQIDTDIFANNLELPVPAAITYN
                                                                                                                                                                                                                                                                                                                                                                                                                                        -----TQKDGSKKAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSSGQAKANTPVLSANGLDLGG----KVISNVGKGT--KDTDA-ANVQQL------
                                                                                    KFALSNQATGDALVKASDIVAHLNTLSGDIQTAKGASQANNSAGYVDADGN----KVIYDS
                                                       -----DDRVVTIKN------DLPAFATGGG
                                                                                                                                                                          -----IINTTOFVD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1998 TGGIATHNGQGAVAVGLSKLSDNGQWVFK----INGSADTQGHVGAAVGAG 2044
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   1080 -NTLGLVTABNAXIGTVAQINI--QDNKTFAINVKNADIEIL-
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                                                                                                                                                                                1202 IDTTNVLAFN-----
                                                                                                                         MLLLFG-----
                                                               NSKLFLVNNSAT
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O9VTK8:
O9VTK8:
O1-MAX-2000 (TrEMBLrel. 13, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last seque
O1-MAR-2001 (TrEMBLrel. 16, Last annot
CG183131 PROTEIN.
CG18331.
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                            Created)
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REDLINE-20196006; Pubbed-10731132;
RADAMS M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Holt G., Nalong Q., Chen L.X.,
RA Gutchan J.R., Yandall M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D.,
RA Abril J.F., Agbayal A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayal A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayerakaroqui L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Brokstein P., Brottler P.,
RA Bernan B.P., Buller H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davengort L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davengort L.B., Davies P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischman W.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorell J.H., Gu Z., Gelbart W.M., Glasser R.,
RA Jalai M., Kalush F., Karpen G. H., Ke Z., Kunp D., Lal Z.,
RA Jalai M., Kalush F., Karpen G. H., Ke Z., Kunp D., Lal Z.,
RA Jalai M., Kalush F., Karpen G. H., Ke Z., Kunp D., Lal Z.,
RA Merkluck G. Milshina N.V., Mobbarry C., Morris J., Mosher G. A.,
RA Melson D.R., Natel B., McIntoon T.C., McIeod M.P., Purk N. Rasser M.G.,
RA Relact B., McIntoon T.C., McIeod M.P., Purk N. Rasser M.G.,
RA Spier E., Spradling A.C., Stapheton M., Stupski M.P., Wang X.,
RA Spier E., Spradling A.C., Stapheton M., Stupski M.P., Wang X.,
RA Spier E., Spradling A.C., Stapheton M., Stupski M.P., Wang X.,
RA Spier E., Spradling A.C., Stapheton M., Stupski M.P., Wang X.,
RA Walliams S.M., Woodage T., Worley K.C., Wurts D., Wang X., Yang S., Yang S., Yang X., Yang S., Yang X., Yang S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
     Metazoa; Arthropoda; Tracheata; нехароцы, мизсомогрha;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
n; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175 LINDLINGHAVLKEIRSSKDNDVKYRRTTASGHASTAVGA---MSYAQGHFSNAFGTRAT
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ilarity 18.7%; Pred. No. 9.1e-15;
Conservative 318; Mismatches 992; Indels 632;
Arthropoda; Tracheata; Hexapoda; Insecta;
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                                                                                                                               SEQUENCE FROM N.A.
STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE003544; AAF50040.2; -.
FlyBase; FB9n0036181; CG18331.
SEQUENCE 2586 AA; 260194 MW;
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                                                      Ephydroidea; Dro
NCBI_TaxID=7227;
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us-09-361-619-7.rspt

337 378 389	432	474	534 525	591 579	649 639	709	767	819	874 845	922 901	982	1015	1063	1091	1151	1200	1254
TISSDPVVEVAQGS-SSNGDGNSTQSSTTTTTTTTSSDGGQSTTLSDPVVEVSQGTNG GPLSIGSNSIKRKIINVGAGVNKTDAVNVAQLEAVVKWAKERRITFQGDDNSTDVKIGLD		SSSDPVSEVAQGSSSIGGEN STATELLSDSLTFTQPNTGSQSTSKTVYGVNGVKF	TNNAETTAALGTTRITRDKIGFARDGDVDEKQAPYLDKKQLKVGSVAITIDNGIDAGNKK  :	ISNLAKGSSANDAVTIEQLKAAKPTLNAGAGISVTPTEISVDAKSGNVTAPTYNIGV : : :  :	KTTELNSDGTSDKFSVKGSGTNNSLVTAEHLASYLNEVNRTADSALQSFTVKEEDDDD :   :	ANAITVAKDTTKNAGAVSILKLKGKNGLTVATKKDGTVTFGLSQDSGLTIGKSTLNNDGL :   :	TVKDTNEQ1QVGANGIKFTNVNGSNPGTGIANTARITRDKIGFAGSDGAVDTNKPYLD	QDKLQVGNVKITNTGINAGGKAITGLSPTLPSIADQSSRNIELGNTIQDKDK	SNAASINDILNTGFNLKNNNNPIDEVSTYDIVDFANGNATTATVTHDTANKTSKV :	VYDVNVDDTTIHLTGTDDNKKLGVKTTKLNKTSANGNTATNFNVNSSD   :	EDALVNAKDIAENLMTLAKEIHTTKGTADTALQTFTVKKVDENNNADDANAITVGQKNAN	NQVNTLTLKGENGLNIKTDKNGTVTFGINTTSG	SAPVVDISQGSSSNGDGNSTQRNPTGSEQIQVGADGVKFAKVNNNGV-VGAGIDGSI   :   :     :     :   SAPVVDISQGSSSNGDGNSTQSSTTTTTTTSSDGDQSTTSSDPVVEVSQGTNGGNSST			QGNNFTVSNPYSSYDTSKTSDVITFAGENGITTKVNKGVVRVGIDQTKG  :	LTTPKLTVGNNNGKGIVIDSQNGONTITGLSNTLANVTNDKGSVRTTEQGNIIK
279 319 338	379	433	475	535	592	650	710	768	. 820 788	875	923	983 958	1016	1064	1092	1152	1201
90 Q	Oy Db	ογ Dp	OY Dp	Oy Op	oy Op	Oy Db	oy op	oy Op	QY	Qy Db	Oy Dp	oy D	oy Op	Oy Op	Qy Dp	Qy Db	ΟΥ Db

1289 GDNSSTQSSSSTTTTTSSDEGQTTSSAPVEVEVTQGSSSNGDGNSTQSSTTTTTTTTTSS 1348 : | : | : | : | : | : | 1469 SAPVVDISQGSSSNGDGNSTQSSTTTTTTTTTTSSDGGSSTT---LSDPVVEVSQGTNGDN 1525 1583 DGGESTISSDPVVEVSQGINGDNSSTQSSSSTITITSSDEGQTISSSDPVVEVAQGSSSN 1642 1592 GG-----KVISNVGKGTKDTDAANVQQLNEVRNLLGLGNAGNDNADG--- 1633 1813 SSTTTTWEVSLKDWRSPKWNRTTKTYSSRTIRIPNSGRKLNSSSSETSTTV---TSSSSS 1869 1870 KPQTKYSWSSSSKKSNNGGKNKKYWTKRWTKKSRKNNNGSSTIVGE------ESSDS 1920 1981 VPKSNGQSSISASKTTKTVTTSTSSTPNVKSSSKK----TSN--SGK---SVKTSSTTI 2030 2031 ITTSSDPGQSSSITQGIPQNDIKSL-NQVTTTTSSVSQVGVPSSPVVKVTKETSVSKDGK 2089 2090 TTRSSTTTTTTTTTKGSNQSGTLTLPAVD-GLKSSTKTTTTSTKGTKLSDILSLPEVDAS 2148 2149 I--AVNGDESRSASIKDTNILSKIDLSLPKLDASLNVNGGKSSSKSSTTTTTTSTKGNKV 2206 -DEDKTRAASIVDVLSAGFNLQGNGEAVDFVS-TYDTVNFADGNATTAKVTYDDTSKTSK 1312 1349 DGGESTISSDPVVEVSQGTNGDNSSTQSSSSTTTTTSSDEGQTISSSGPVVDISQGSSSN 1408 1365 IVAHLNTLSGDI-------1388 :: : | | : | | 1409 VLDNDNNYNDDIFRWMANPPPYLTPLWKSVKEQMAITAPLSLRRPPQQQTSSDEGQTISS 1468 1389 AGYV------DADGNKVIYDSTDNKYYQAKNDGTVDKTKEVAKDKLVAQAQTPDG-- 1437 --TLAQMNVKSVINKEQVNDANKKQGINEDNAFVKGLEKAASDNKTKNAAVTV----- 1488 1526 NSTQSSSSTITITSSDEGQITSSSDPVVE---VAQGSSSNGDGNSTQSSTITITITITSS 1582 1489 -GDLNAVAQTPLTFA-----GDTGTTAKKLGETLTIKGGQTDTNKLTDNNIGVVAGT--- 1539 1540 -DGFTVKLAKDLTNLNSVNAGG---TKIDDKGVSFVDSSG------- 1575 | | | : : : | | : :: | | 100 | | 100 | | 100 | | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | -----ANGLDL 1591 1703 PMVANPPPHLTPLWKSVKEQTAITAPLSLRRPPQQRHLQMRAKLPLLSDPVVEVAQGSSS 1762 -----NQVNIADIK------KDPNSGSSSNRTVIKAGTVLGGKGNNDTE 1671 1672 KLATGGIOVGVDKDGNANGDLSNVWVKTQKDGSKKALLATYNAAGQTNYLTNNPAEAIDR 1731 1732 INEQGIRFFHVNDGNQE------PVVQGRNGIDSSASG-----KHSVAIGF 1771 1921 LTDAGVDVTQGNGLNDEGNSSQSTVTSSLPVVDTSADVQNSESSLTSTENTTKYSSKSFK 1980 1772 QAKADGEAAVAIGRQTQAGNQSIAIGDNAQATGDQSIAIGTGNVVAGKHSGAIGDPSTVK 1831 1832 ADNSYSVGNNNQFTDA-TQTDVFGVGNNITVTESNSVALGSNSAISACTHAGTQAKKSDG 1890 1891 TAGTTTTAGATGTVKGF--AGQTAVGAVSVGASGAERRIQNVAAG------EVSAT 1938 1939 STDAVNGSQLYKATQSIANATNELDHRIHQNEN--KANAGISSAMAMASMPQAYIPGRSM 1996 1313 VVYD-VNVDDTTIEVKDKKLGVKTTTLTSTGTGANKFALSNQATGD-----ALVKASD 1364 -----VTGGIATHNGQGAVAVGLSK---LSDNGQWVFKINGSADTQG 2035 2207 SLSLPEVDASIAV-NGDDARSASIKDTNILSKIDLSLPKLDASLNVNG 2253 RESULT 14 Q55582 ID Q55582 1576 1255 1438 1634 q ò ολ g δλ Q g qq ŏ g δ g ò q õ g ŏ ò g δ οp δ g q ð ó

PRT; 3029 AA.

PRELIMINARY;

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1004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TFQGDDNSTDVK----IGLDNTLTIKGGAETNALTDNNIGVVKEADNSGLKVKLAKTLNN 418
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                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97061201; PubMed-8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      783 GSATDNQTYTVDTTAPIPIITVNDVTADNIINAAESGQAIPITGTVGGEFNVGDTVTLTV 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GQESI----AIGGDVKASGDASIAIGSDDLHLLDQHGNPKHPKGTLINDLINGHAVLKEI 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIGATL----SGSAYA-----QNQPR 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Sequence analysis of the genome of the unicellular cyanobacterium Synachocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NGK PFTGTVDANGDFSIDVLGGDLVNGSDLTIAASVATTDAAGNPGSASDNQTYTVDTTA
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                                                                                                                                                                                                                                               MEDILNE=96127529; March 250279; March 2520ka T., Miyajima N., MEDILNE=96127529; March 27. Tanaka T., Tanaka S., Kotani H., Sazuka T., Miyajima N., Sugiura M., Tabata S.; Squence analysis of the genome of the unicellular cyanobacterlum "Sequence analysis of the genome of the unicellular cyanobacterlum region from map posttions 64% to 92% of the genome."; In the 1 Mb region from map posttions 64% to 92% of the genome.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -------YAQGHFS-----NAFGTRATAKSAYSLAVGLAATAEGQSTIAIGSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 518; DB 2; Length 3029;
Pred. No. 2e-13;
5; Mismatches 901; Indels 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BEE0BB57E822A4FB CRC64;
                                                                                                                                                                                                        Tabata S.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                         Cyanobacteria; Chroococcales; Synechocystis.
          01, Created)
01, Last sequence update)
16, Last annotation update)
                                                                                           Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Res. 3:109-136(1996).

EMBL. D63999; BAA10087.1; -.

Hypothetical protein.

SEQUENCE 3029 AA; 308789 MW;
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Matches 521; Conservative 256;
                          01-NOV-1996 (TrEMBLrel. 01, Las 01-MAR-2001 (TrEMBLrel. 16, Las HYPOTHETICAL 308.8 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.0%;
              (TrEMBLrel.
                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=PCC6803; Tabata S.;
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SEQUENCE FROM N.A.
                                                                                                                                NCBI_TaxID=1148;
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                                                                                                                  Bacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---SKTSKVVYDVNVDDTTIEVKDKKLGVKTTTLTSTGTGANKFALSNQATGDALVKASD 1364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIDGNTYTATVTGNAWTFNIPVADIANFEATEEVVATVSDLAGNPATPATRNITVDTAP 1199
                                                                                                                                                                                                                                                                                        1200 TVTINAIAVDDIINAVEAGSPVAVSGTTTGVEDGQVVTVTIDGNTYTATVTGNAWTFNIP 1259
                                                                                                                                                                                                                                                                                                                                                         1260 VADIANFEATEEVVATVSDLAGNPATPATRNITV----DTVAPAVTIDSISDDTGAQAND 1315
                                                                                                                                                     1098 TAPTVTINAIAVDDIINAVEAGSPVAVSGTTTG-VEDGQV---------VTV 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                             719 QVGANGIKFTNVNGSNPGTGIANTARITRDKIGFAGSDGAVDTNKPYLDQDKLQVGNVKI 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVTID---GNTYTATVTGNAWTFNIPVADIANFEAT----EEVVATVSDLAGNPATPATR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDALVNAKDIAENLNTLAKEIHTTKGTADTALQTFTVKKVDENNNADDANAITVGQKNAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1715 AVSGTTTGVEDGQVVTVTIDGNTYTATVTGNAWTFNIPVADIANFEATERVA-----T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1148 VADEQGN-----NFTVSN--PYSSYDTSKTSDVITF--AGE----NGITTKVNKG-VV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSDLAGNPATPATRNITVDTTAPTVTINAIAVDDIINAVEAGSPVAVSGTTTGVEDGQVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1566 EEVVATVSDLAGNPATPA----TRNITVDTVAPAVTIDSISDDTGAQANDFIT
                                                                                                                                                                                                                                                                                                                                                                                                                     1316 FITNDDTLVF-----NGTAEA---DSTVVYSL---DGIEIGTVTANGAGEWTLDYTGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GFNLKNNNNPIDFVSTYDIV----DFANGNATTAT--VTHDTANKTSKVVYDVNVDD---
                                                                                                                                                                                                                                                                                                                          GSGTNNSLVTAEHLASYLNEVNRTADSALQSFTVKEEDDDDANAITV-----AKD
                                                                                                                                                                                                                                                                                                                                                                                            TTKNAGAVSILKLKGKNGLTVATKKDGTVTFGLSQDSGLTIGKSTLNNDGLTVKDTNEQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 779 INTGINA--GGKAITGLSPTLPSIADQSSRNIEL-GNTIQDKDKSNAASIN----DILNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----TITIHLIGIDDNKKLGVKTTKLNKTSANGNTAT-----NFNVNSSD-----
                                                                                                                                                                                                                                                           ---AKSGNVT-----APTYNIGVKTTELNSDGTSDKFSVK
                                                                              1046 -IEIGTVTAN-----GAGEWILDYTGTLLADGDYELSVTATNPTGNSATATQTIVVDT
                                                                                                                                                                                       523 TID----NGIDAGNKKISNLAKGSSANDAVTIEQLK-----AAKPTLNAGAGISVTPT--
                                               LTEVNTTTLNATTTVKVGSSSST---TAELLSD----SLTFTQPNTGSQSTSKTV----
                                                                                                                    ---- YGVNGVKFTNNAETTAAIGTTRITRDKIGFARDGDVDEKQAPYLDKKQLKVGSVAI
1005 TIDSISDDJGAQANDFIINDDJLVFNGTAEADST-----VVVSLDG-
                                                                                                                                                                                                                                                            ----EISAD-----
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Submitted (JUN-1999)
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 SEQUENCE FROM N.A. STRAIN-ATCC14028;
                                                                         SEQUENCE FROM N.A.
                                                                                   STRAIN=ATCC14028;
                                                                                                                                                                                                                             469;
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Best Local Si
Matches 4699
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                                                                                                                                NAVAQTPLTFAGDTGTTAKKLGETLTIKGCQTDTNK-----LTDNNIGVVAGT--DGFTV
                                                                                                                                                                    KLAKDLTNLNSVNAGGT---KIDDKGVSFVDSSGQ------AKA
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                  1365 IVAHLNTLSGD--IQTAKGASQANNSAGYVDADGNKVIYDSTDNKYYQAKNDGTV----
                              PTVTINAIAVDDIINAVEAGSPVAVSGTTTGVEDGQVVTVTIDGNTYTATVTGNAWTFNI
                                                      --- AKDKLVAQAQTPDGTLAQMNVKSVINKEQVN-
                                                                                           ------ASDNKTKNAAVTVGDL
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                                                                        2048 PVADIANFEATEEVVATVSDLAGNPATPATRNITVDTTAPTVTINAIAVDDIINAVEAGS
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Salmonella.
NCBI_TaxID=602;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDDTS-----QWNMTDPSTVGNL-----TNDGDITLGNASGSTGTLLTVDNTLT
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                                                                                                                                                                                                                                               Baumler A.J.;
"Complete sequence of the xseA-hisS intergenic region of the S. enterica serotype Typhimurium genome and its distribution within genus Salmonella.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 ARIAALAVLVIGATLSGSAYAQKKDTKHIAIGE------QNQPRRSGTAKADG-----
Kingsley R.A., van Amsterdam K., Baumler A.J.;
"The presence of a pathogenicity island specific to Salmonella enteries subspecies I correlates with adaptation to warm blooded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2035;
                                                                                                                                                                                                                        Kingsley R.A., van Amsterdam K., Edwards E.W., Hargis B.M.,
                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AF140550; AAD25110.2; -. Interprise of PRO02173; -. Interprise pso/0584; PFKE_KINASES_2; UNKNOWN_2. SEQUENCE 2035 AA; 207031 MW; 295DBB2FFCA84FAB CRC64;
                                                                                                            to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.0%; Score 514.5; DB 2;
ilarity 21.7%; Pred. No. 1.7e-13;
Conservative 270; Mismatches 808;
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Qy Db	646	78
Qy Dp	699	IGKSTLNNDGLTVKDTNEQIQVGANGIKFTNVNGSNPGTGIANTARITRD 748
ργ	749	
qq	843	
٥y	808	IELGNTIQDKDKSNAASINDILNTGFNLKNNNNPIDFVSTYDIVDFANGNATTATVTHDT
qq	968	TIIGGTLTADHADSLGTGAVANSGVLQVGEGELENTLSGSGS
δy	898	ANKTSKVVYDVNVDDTTIHLTGTDDNKKLGVKTTKLNKTSANGNTATNFNVNSSDEDALV
Op	938	
Οy	928	NAKDIAENLNTLAKEIHTTK-GTADTALQTFTVKKVDENNNADDANAITVGQK 979
QQ	980	
Qy	980	NANNQVNTLTLKGENGLUIKTDKNGTVTFGINTTSGLKAGKSTLNDGG-LSIKNPT
QQ	1040	
Qy	1035	GSEQIQVGADGVKFAKVNNNGVVGAGIDGTTRITRDEIGFTGTNGSLDKSKPHLSKDG 109
QQ	1096	
Qy	1093	INAGGKKITNIQSGEIAQNSHDAVTGGKIYDLKTELENKISSTAKTAQNSLHEFSVAD
qq	1153	MNREDVDFLTI-DGKVDEADNTHYDLTASLSWYADRDNATTD
ογ	1151	EQGNNFTVSNPYSSYDTSKT-SDVTK 118
QQ	1194	AHG-TFTLSDPDGSFNVAATLTDVDDTLDPGSRWDGKSLTKEGAG
Qy	1186	VNKGVVRVGIDQTKGLTTPKLTVGNNGKG- 1
QQ	1253	
Qy	1216	
qq	1312	SALIQQDGSTLNVELNSDSVQPLITGSSATLGGDLVVSDASLQARASDAEFQSFKLMDMT 1
Qy	1260	O RAASIVDVLSAGFNLQGNGEAVDFVSTYDTVNFADGNATTAKVTYDDTS 1308
qq	137	2 SDIS-GDFTSLTMNLTDKPDYLTVTGTINPEDASEYLLTEGLSWNATATSAT 1422
Qy	1309	9 KTSKVVYDVNVDDTTIEVKDKKLGVKTTTLTSTGTGANKFALSNQATGDALVK 1361
QQ	1423	
Οy	1362	ASDIVAH
qq	148	0
Qy	1421	KEVAKDKLVA
QQ	1519	KVTNEGTLVFGNSEETGAIFTFNGDLINMGTMTSGSSSSTPGNTLYVDG
QY	1472	LEKAASDNKTKNAAVTVGDLNAVAQTPLTFAGD-TGTTAKKLGETLTIKGGQ
q	1568	NYTGNGGSLYLNTVLGDDDS-ATDKLVITGDASGTTDLYINGIGDGA 161
δy	152	3 TDTNKLTDNNIGVVAGTDGETVKLAKDLTNLNSVNAGGTKIDDKGVS
q	1614	OTTNGIEVVDVGGVSTSDAFELKNEVNAGLYTYRLYWNESD

1942	£	1898	qq
895	1838 VGNNNQFTDATQTDVFGVGNNITVTESNSVALGSNSAISAGTHAGTQAKKSDGTAGTT 1895	1838	٥y
1897	1855 GAYVDSWYQYGFYNNSVESGDAGSESYDSTANAVSLETGYRYD 1897	1855	g
1837	1790 GNOSIAIGDNAQATGDQSIAIGTGNVAGKHSGAIGDPSTVKADNSYS 1837	.1790	οy
1854	1804TVGVMASYINADTDSTGNRGADGSQFTSSGNVDGYNLGVYATWFADAQTHS	1804	qq
1789	RINEGGIRFEHVNDGNQEPVVQGRNGIDSSASGK-HSVAIGFQAKADGEAAVAIGRQTQA 1789	1731	δy
1803	EGSO	1749	Ob
1730	1685 DGNANGDLSNVWVKTQKDGSKKALLATYNAAGQTNYLTNNPAEAID 1730	1685	ΟŸ
1748	1699 TPPDDGGDGGDVTPPDHGGDVAPQYRADIGAYMGNQWMARNLQMQTLYDR 1748	1699	qq
1684	1629DNADGNOVNIADIKKDPNSGSSSNRTVIKAGTVLGGKGNNDTEKLATGGIQVGVDK 1684	1629	οy
1698	1666 DDDDSGGDDTPSDGGDDGGNVTPPDDGGDGGNV 1698	1666	QQ
1628	1570 FVDSSGQAKANTPVLSANGLDLGGKVISNVGKGTKDTDAANVQQLNEVRNLLGLGNAGN-	1570	Qy

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Copyright (c) 1993 - 2000 Compugen Ltd.
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RESULT 1
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Matches 5063; Conservative 0; Mismatches 1009; Indels 156; Gaps 1 atgatcacatctataaagtcatctttaacaaagccacaggcacatttatggccgtggcg 60	DD 121 GTATGCAGCTTTGCCGGGGTGGGTGGTGGTGGATGGTGGAAGG 180  Qy 181 ctcaatggcagtgcttatgctcaacaattactaccaagatcgaaattggtcaaaca 237	Qy       358 gatcctaataatggtagtaatgtaatgtaggttcccacgccaaaggtaacgagtccatc 417	523 cttattcatggcatgaaatattaaaaaaaatacaaacctcaaccgatggtaaaatcaaa	caggictattiticaaagoctitiggiaaataggaacagotgaagicgicatticitig 70	ttgatagggata 	Db 949 AAGGCGCGCCCTTCCATTGCTAA
Oy 5521 agttacagtgtgggtaataacaaccagtttaccgatgccactcaaaccgatgtctttggt 5580	Qy         5701 accaccaggtggccacaggtacggttaaaggctttgctggacaaacggcgttggt         5760           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		Oy over tegagetegeraatggccaarggtcaarcaarggtcaaccaa b120  J	AX079918 6141 bp DNA Sequence 6 from Patent W00107619. AX079918 AX079918.1 GI:13159439 Moraxella catarrhalis. Moraxella catarrhalis Bacteria; Proteobacteria; gamma subdivis: Moraxella to 6141)	Loosmore, S.M., Sasaki, K., Yang Recombinant high molecular wel moraxella Patent: WO 0107619-A 6 01-FEB- CONNAUGHT LABORATORIES LIMITED Location/Qualifiers 16141 /Organism="Moraxella /Ob_xref="taxon:480"	.01.6; 0.0;

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oy B	481	tacggttagtaaccettactccagttatgacacctcaaagacctct 354	Qy	4561 ctgggcgagactttgaccatcaaaggtgggc 
O.y D.b	41	aaggtgtggtg 360 	Qy	4621 aacatcggtgtggtagcaggtactgatggcl 
O.y Db	- 4*	9tgggcattgaccaaaccaaaggcttaaccacgcctaagctgaccgtgggtaatat 366 	Ολ Dp	4681 aatcttaacagcgttaatgcaggtggcacca 
Oy Db	3661 aat     3634 AAT	₩ <u>-</u> ₩	QY	4741 gacgcaaacggtcaagccaaagcaaacaccc 
Qy Dp	3721 aac           3694 AAC	accaatgataaaggtagcgtacgcaccacagaacaggcaat 378 	Oy Dp	4801 ggtggcaaggtcatcagtaatgtgggcaaa. 
Oy Op	781		Qy	4861 caacagitaaacgaagtacgcaacitgitgc 
O.Y Db	3841 ttt     3814 TTT	cacttatgacaccgtcaac 390 	QY	4912 gacggcaatcaggtaaacattgccgacatca 
Oy Db	3901 ttt     3874 TTT	ggcaataccaccaccgctaaggtgacctatgatgacacaagcaaaccagt 396 	Qy	4972 aaccgcactgtcatcaaagcaggcacggtar 
Oy Db	961	atgatgtcaatgtggatgatacaaccattgagttaaagataaaaactt 402 	Oy Db	5032 aaacttgccactggtgtgtgtacaagtgggcc 
QY Dp	021	ttgaccagtactggcacaggtgctaataaatttgccctaagc 408 TTGACCAGAGACACAGGTGCTAATAAATTGCCCTAAGC 405	Qy	5092 ttaagcaatgtttgggtcaaaacccaaaag 
Qy Dp	081 054	gegettgtcaaggecagtgatatcgttgctcatctaaacacc 414	Qy Dp	tataacgccgcaggtcagaccaac! 
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9ggtct-----tggtaatgataacgct 4911
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|CGTCTTGGTAATGCTGGTAATGATAACGCT 4893 AGAAGTTGCCAAAGACAAACTGGTCGCCCAA 4293 CAAAAAAGACCCAAATTCAGGTTCATCATCT caaaaaagacccaaattcaggttcatcatct

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/organism="M /db_xref="ta /db_x	Local Similarity 81.3% es 5063; Conservative  1 atgaatcacatctataaagtc  1	Oy 61 gaatatgccaaatcccacagtacggggggggggtagctgtgctacagggcaagttggcagt 120	181 722 238	298	Oy 358 gatcctaataatggtagtaatgaggtagtccacaggcaaggtcargggggggggg	τ,	DD 1070 CITAITARCSCCATSCANDING TO THE CONTROLL OF SB3 tatcgacgcacaagagcacaagggcacgccagtactgcagtgggagccatgtcatatgca 642  Qy 583 tatcgacgcacaagagcacaagggcacgccagtactgcagtgggagccatgtcatatgca 642  Db 1136 TATAGACGCACAACCGCAAGCGGACACGCCAGTACTGCAGTGGCATGCCATGTCATATGCA 1195	Oy 643 cagggcattttccaacgcctttggtacatacgcaacagctgaagctgcctattccttg 702  1196 CAGGGTCATTTTCCAACGCCTTGGTACACGGCAACAGCTAAAGTGCTATTCTTG  Db 1196 CAGGGTCATTTTCCAACGCCTTTGGTACACGGCAACAGCTAAAGTGCCTATTCTTG  Oy 703 gcagtaggtcttgcccaagccaaacaatcttcaatcgqttggttccaatga 762
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	REFERENCE 1 (bases 1 to 6973)	
1316		
Oy 762 aaaagc	VERSION AROA0716.1 GI:5960079 KEYWORDS	
Oy 702 ggcagta               Db 1256 GGCAGT	AR040716  LOCUS AR040716 6973 bp DNA  DEFINITION Sequence 1 from patent US 5808024. ACCESSION AR040716	
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Db 956 CGCCATC	Oy 5932 aaagccaatgcagggatttcatcagcgatggcgatggcgtccatgccacaagcctacatt 5991	
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Best Local Simi Matches 5063;	Oy 5452 acaggcaatgtggtagcaggtaagcactctggtgccatcggcgacccaagcactgttaag 5511	
W.	QY 5552 caatcocategecategecateaegecaegeqeaegeatcaatccategeateget55154 Db 5915 CAATCCATCGCCATCGTGATAACGCACAGGCGGCGATCAATCCATCGCCATCGGT 5974	
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	5795 CAAGGGGGTAACGGCATTGACTCAAGTGCCTCAGGCAAGCACTCAGTGGCGATAGGTTC	
AUTHORS Sasal	Qy 5272 caaqqqcqtaacqqcattqactcaaqtqcctcaqqcaaqcactcaqtqqcqataqqtttc 5331	

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                                                                                                            66.4%; Score 4090.6; DB 9; Length 6973;
larity 81.3%; Pred. No. 0;
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aki, K., Harkness, R.E., Loosmore, S.M. and Klein, M.H. leic acids encoding high molecular weight major out tein of moraxella ent: US 5808024.A 1 15-SEP-1998; Location/Qualifiers
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protein

1 (bases 1 to 6973) Loosmore, S.M., Sasaki, K., Yang, Y.P. and Klein, M.H. Recombinant high molecular weight major outer membrane

moraxella Patent: WO 0107619-A 1 01-FEB-2001; CONNAUGHT LABORATORIES LIMITED (CA)

Location/Qualiflers

catarrhalis"

gamma subdivision; Moraxellaceae;

Moraxella catarrhalis. Moraxella catarrhalis Bacteria; Proteobacteria;

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Moraxella.

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	0 RESULT 6 AX067457 LOCUS AX067457	DEFINITION Sequence 32 ACCESSION AX067457 VERZION AX067457.1 KEYWORDS	O ONGANISM	REFERENCE 1 (bases 1 to 62 AUTHORS Lagace, R.E., Patt TITLE Nucleotide sequer JOURNAL Patent: WO 007896	FEATURES SOURCE	50 BASE COUNT 18449 a 13798 ORIGIN	Query Match Best Local Similarity 81. Matches 5068; Conservative	570 Qy 1 atgaatcacatctataaag 	030 0y 61 gaatatgccaaatcccace	690 Qy 120 tgtacgcactctaagcttt	09 180 gctcaatggcagtgcttat 	0y 240 caagataaacaacagctc 	870 Qy 300 tggtagtcttctaaggcs   1   1   1   1   1   394   Db 42909 TGGTGAAAAGCTGTTGCA	. Qy 360 Db 42969	990 QY 420 catcggtggtgatgtttc 	O50 QY 480 atatttgcctaagaa 574 Db 43083 ATATTGGAGAGTAAAGG	10 Qy 534 ccatgaaatattaaaaaa   10   11   1   11   1   1   1   1   1	0y 591 cacaagagcacaagggcac
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6072	4 6	4850		ACCESSION AX079914 VERSION AX079914.1 GI:1. KEYWORDS ACTRICE Moraxella catarr	ORGANISM MOTAXELLA CATATTY BACTETIA: Protect MOTAXELLA.  1 (Asaes 1 to 5	ACTIVE Recombinant high TITLE MOTAX BOURNAL PATENT WO 01076	CONNAUGHT LABORA FEATURES LOCATIO SOURCE 1597	/db_xre BASE COUNT 1972 a 1360 ORIGIN	Query Match Best Local Similarity 86 Matches 4905; Conservativ	Oy 166 gtgatcggtgcgacgctc	Oy 223 gaaattggtcaaacaaa 	Oy 283 gaagcatccattgcttt                         Db 115 GATCGAGCCATTGCTAT	Oy 343 ggtagtgtcaaaccaga	Qy 403 ggtaacgagtccatcgc	Oy 463 aloggtaglgatgactt	Oy 510tgaatttcacaaact	Qy 568 gatggtaaaatcaaata                  	Oy 628 gccatgtcatatgcace
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	Qy 4992	* <	<del>,</del> 4	. 5 4	, ,	DD 47664	4	4		4	Qy 5 Db 47	0y 5 0b 48	Oy 5 Db 48	Oy :	Oy Db 46	4	Oy Db 4	Qy Db 4

20; ), ), ), Sasaki, K., Yang, Y.P. and Klein, M.H. Sasaki, K., Yang, Y.P. and Klein, M.H. molecular weight major outer membrane protein of gcatoggtggtgatgtattggctgaggtgatgcctcgattgcc 462 64.1%; Score 3947.8; DB 10; Length 5976; 80.9%; Pred. No. 0; 1ve 0; Mismatches 1002; Indels 156; Gaps 22-FEB-2001 obacteria; gamma subdivision; Moraxellaceae; PAT nism="Moraxella catarrhalis" ref="taxon:480" 50 c 1355 g 1289 t 7619-A 2 01-FEB-2001; RATORIES LIMITED (CA) 76 bp DNA Patent WO0107619. sttttcacttt 6159 13159437 rhalis.

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/db_xref="taxon:480"
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Patent: WO 0107619-A 10 01-FLL
CONNAUGHT LABORATORIES LIMITED (CA)
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CONNAUGHT LABORATORIES LIMITED (CA)
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qq	6055 CANGGCGTAACGGCATTGACTCAAGTGCCTCAGGCAACACTCAGTGGCGGTAGGTTTC 6114	TILE RECOMBINANT LIGH MOLECULAR WELL MOLAKELLA JOHNAN PAPENT WO 0107619-A 47 01-FFR
Qy Db	5332 caggccaaggcagatggtgaagccgcttgccataggcagacaaacccaagcagcaac 5391 	CONNAUGH
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Qy Dp	4354 a	aatgtcaaatcagtcattaacaaagaacaagtaaatgatgccaataaaaagcaaggcatc 4413 
γς	4414 a	aatgaagacaacgctttgttaaaggacttgaaaagccgcttctgataacaaaaccaaa 4473 
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ογ	654	CAGACACCAAIANACIANACCAAACCAACCAACCAACCAACCA
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δ	4714	attgatgaaaaaggcatctctttgtagacgcaaacggtcaagccaaagccaaacaccct 4773 
6 6	4	traagtgccaatgggctggacctgggtggcaaggtcatcagt
a a	738	ijGCCAATGGGCIGGACCIGGGIGGGGGGGGGCCAACGAACGAACGAGCTGGGGGGGGGG
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Qy Dp	4894	cttggtaatgataacgctgacggcaatcaggtaaacattgccgacatcaaa 4944 
δλ	94	Jacccaaattcaggttcatcatctaacgcactgtcatcaaagcaggcacggtactt 50
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MapA protein.
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El-Sayed, N.M., Khalak, H. and Adams, M.D.

Direct Submission

Submitted (28-10199) The Institute for Genomic Research, 9712

Medical Center Dr., Rockville, MD 20850, USA

On Feb 12, 2001 this sequence version replaced gi:6707792.

* NOTE: This is a "working draft" sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                       El-Sayed, N., Zhao, H., Mason, T., Wanless, D., Fujii, C., Barnstead, M., Boman, C., Peterson, J., Khalak, H., Ullu, E., Melville, S., Donelson, J., White, O., Fraser, C. and Adams, M.
Trypanosoma brucel GUTatl0.1 RPC193-3415 BAC genomic sequence
                                                                                                                                                                                                                                 Trypanosoma brucei chromosome II clone RPCI93-3H15, *** SEQUENCING IN PROGRESS ***, I ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1458 aaagaaaattggttttgctggtactaatgatggagttgatgaaagcaaaccttatcttga 1517
                                1518 caacgaaaagctaaaaagttggcaacagcaccctaaacagtggtagcttgactgttaataa 1577
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               5365 ataggcagacaaacccaagcaggcaaccaatccatcgccatcggtgataacgcacaagcc
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1 149789: contig of 149789 bp in length.
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tive 0; Mismatches 385;
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Submitted (25-APR-2000) Henderson I.R., Center for Vaccine
Development, University of Maryland School of Medicine, 685
Baltimore St, MD 21202, USA
                                                                                                                                 1758 acttaaagtgggtcgtgttgaaattaccacagatagtggtattaatgctggtaatcacaa
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Henderson, I.R., Nataro, J.P., Cappello, R. and Stein, C.
Evolutionary origins of the autotransporter proteins
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Pasteurella.
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Henderson, I.R.
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                                                                                        2. (bases 1 to 10533)
2. (bases 1 to 10533)
2. Lang, Q. and Kapur, V.
Direct Submission
Submitted (24-0CT-2000) Department of Veterinary Pathobiology,
University of Minnesota, 1971 Commonwealth Ave., St. Paul, MN
Complete genomic sequence of Pasteurella multocida,Pm70
Proc. Natl. Acad. Scl. U.S.A. 98 (6), 3460-3465 (2001)
21145866
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/organism="Pasteurella multocida"
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/db_xref="taxon:747"
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/product="YfkJ"
/protein_id="AAK03653.1"
/db_xref="G1:12721962"
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/gene="PM1568"
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/gene="PM1568"
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/transl_table=11
/product="unknown"
                                                                                                                                                                                                                                                                  Location/Qualifiers
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/gene="hsf_2"
/codon_start=1
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/transl_table=11
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/gene="fkpA"
/note="PM1567"
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91. .804
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/gene="fkpA"
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                                                                                                                                                       DAVEIGNRAGYK SOUNDRAGVSLIGKDSGEGVYGTENYTIGNSAGKNIYKGNITHNISTSRA
GONVEGHDNFAALIEAGONIKGSDALAIGKRAGRSADPNTKLNINNTISLGKESVSLK
GONVEGHDNFAALIEAGONIKGSDALAIGKRAGRSADPNTKLNINNTISLGKESVSLK
NEGLAGORKAKTOGLASIATGRNARAVGGETANIAIGDSASADASGAIVLGTKAQAKS
ILTVDGKKYGAYSAIYGTEARAIAQAAPAGKNENPKDALAIGTKARATALGYR
AKSDTKAQAVSIGYNNAKGYQALAEGSRKTRENAGSSIARGTKAQTRASAIALGY
GTNEATVNEKKYSGRAIKTRANAAGKTAAAAGKAAAAAG
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AKSTTVKREDNITYTERAAADGSRTYTYATKKDOKDANAGGOLFAGGEGVKNIIGGDTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NLATLLGGNAQNTNGNVAMTDIGGTGKNNINDAIKASRNEVKOGKNMVYTPTTGANGO
TIYEVATADKVAFDEVKVGGITIDATINKISGIAKGDISENSTDAVNGSQLYELQOKI
AKSGDNYNILNNRINKVDKDLRAGIAGANAAAGLPQAYIPGKSMVAVAAGTYKCQNAI
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                                                  WDISIGROAGAEOTEVSAEGRNIAIGDGALKRCKGVNNNIALGTSAGDRLAGTHNVLM
GTYVNADEAVRSALTAGSTTKEINAKETTDNKYYIEASNTVALGTRALATQLAAVAIG
QQAKAFGNQSVAVGNGTKASGQTAIATGSNAHATGSSSIAIGGTVNGNTARTLASDN
FTIAMGLSAQATKSDAIAVGRNAKAAGINTVSIGYNAGYTKTADEAOSDPNNKLEPAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YTVATAKEVTFDKTTVGSVVTDKNTNDITGLSNKTLGGDNFAKNGRAASEEQLNATQT
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Pasteurella multocida PM70 section 161 of 204 of the complete
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Pasteurella.
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May, B.J., Zhang, Q., Li, L.L., Paustian, M.L., Whittam, T.S. and
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Pred. No. 8.1e-10;
0; Mismatches 151; Indels
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AE006194.1 GI:12721958
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Pasteurella multocida
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Best Local Similarity 55.8%;
Matches 202; Conservative
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Kapur, V.

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/protein_id="ARK03658.1"
/db_xref="G1:12721967"
/db_xref="G1:1272196
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Pred. No. 8.9e-10;
0; Mismatches 151; Indels
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St. Geme, J.W. III and Barenkamp, S.J.
DNA encoding haemophilus adhesion proteins
Patent: US 5646259-A I 08-JUL-1997;
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Sequence 1 from patent US 5646259.
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9420. .10412
/gene="asnA"
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NNLISLCEOLGKLGYWVRLHYYYPYHVDOLIPLMAEGKILLPYLDIPLCHASPKILKA
KRRGSIERTLERIKKWREICPDLILRSTFIVGFPGESEBDFOLLLDFLKRALLDRVG
CKRSSPYBGALATBWDQVPEEVKRARFHREWQLQQEISAARLQQKYGKVFTVLVDEV
DEEGIIARSIADAPELDGVVYIDNPNRVAVKAGQFIEVKITRADAYDLYASLLN"
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/db_xref="G1:12721965"
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GDILVTTGAVRLDGAELHFRMEXPRYNNEECTNALVKAATELANQKVYVGITPASDT
FY FOGDERY DTYSGK VY RHFOGSLKOWODLNWNFEMESATLFTMCSALGLRAGWVAGA
IVNRTQQEIPNEAA VKDIEKNAVEIVVKAAAYLL"
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YSFFIKWWHTIAELHSVLASKIOLIDEIQSTETLISMQNPILRDIKP"
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YNBTGGEVARTNIGGTGASTIDAGIKANNTPKRAKTEVVQGBIVVTGSAPGANGNTV
YTVATAKEVTFDKTTYGSVYTDKNTNDITGISNKTLGGDNFAKNGRASEEQIAATOT
NLATLLGGNAQNTNGNVAMTDIGGTGKNNINDAIKASRNEVKQGKNMVVTPTTGANGO
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LVIVNTCGFIDSAVQESLEAIGEALEENGKVIVTGCLGAKEDRIREVHPKVLEVTGPH
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AKSGDNYNILNNRINKVDKDLRAGIAGANAAAGLPQAYIPGKSMVAVAAGTYKGQNAI
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                                                                                                                                                                                           PAKSVVIGFGATNDGETNVALGAKSKSSKAASTALGDNAKALDNQALALGQNATANSD
WDISIGRQAGAEQTEVSAEGRNIALGDGALKRGKGVNNNIALGTSAGDRLAGTHNVLM
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/product="Udp"
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/note="PM1572"
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200kDa outer membrane protein; antibacterial; immunogenic; infection;
otitis media; detection; ds.
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Database

New nucleic acid encoding Moraxella catarrhalis outer membrane protein, useful in protective vaccines and for diagnosis

720 3030

S N Result

The present invention describes an isolated and purified nucleic acid (I) that encodes a 200 kDa outer membrane protein of Moraxella catarrhalis. The 200 kDa outer membrane protein (II) has antibacterial activity and can be used in vaccines. (II), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarrhalis infections, particularly office and in humans. (II) is also used as infections, particularly office media in humans. (II) is also used as carried in mununoasys for detecting specific antibodies (Ab), and to affice an probes for identifying/Cloing 200 kDa protein fragments are used as probes for identifying/Cloing 200 kDa protein fragments are used as probes for identifying/Cloing 200 kDa protein fragments are used as probes for identifying/Cloing 200 kDa protein fragments are used as probes for identifying/Cloing 200 kDa protein fragments of truncated versions of (II) reduces toxicity of the protein Expression of truncated versions of (II) reduces toxicity of the protein constants the Escherichia coli host. The present sequence represents the manual carrier invention.

M. catarrhalis strain OB 200kDa gene, which is given in the exemplification of the present invention. English 247pp; 1; Claim

BP; 2035 A; 1386 C; 1385 G; 1353 T; 0 other; 6129 Sequence

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Qy	5161 g	caggtcagaccaactatgtgaccaacaacccccagaagaccattgacagaaadaaaatgaa 322 
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QQ	5221 c	anggtatecegettettecatgteaacgatggeaateaagageettgtggtaeaagggegt 528
Qy	5281 a	acggcattgactcaagtgcctcaggcaagcactcagtggcgataggtttccaggccaag 53
QQ	5281 a	acggcattgactcaagtgcctcaggcaagcactcagtggcgataggtttccaggccaag 334
Qy	5341 g	gcagatggtgaagccgttgccataggcagacaaacccaagcaggcaaccaatccatc 3400
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ογ	5461	52
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Qy	5581	tgggcaataacatcaccgtgaccgaaagtaactcggttgccttaggttcaaactctgcc 5640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes an isolated and purified nucleic acid (I) that encodes a 200 kpa outer membrane protein of Moraxella catarrhalis. The 200 kpa outer membrane protein (II) has antibacterial activity and can be used in vaccines. (II), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarrhalis infections, particularly otitis media in humans. (II) is also used as antigen in immunoassays for detecting specific antibodies (Ab), and to generate Ab. (I) are used for recombinant production of (II) and its fragments are used as probes for identifying/cloning 200 kba protein genes from other strains, and for diagnostic detection of M. catarrhalis. (I) makes possible production of large amount of recombinant immunogens. Expression of truncated versions of (II) reduces toxicity of the protein towards the Escherichia coll host. The present sequence represents the minor of the contraction of the protein coll to can be contracted to the protein contraction of the protein contraction of the protein contraction of the protein contraction of the protein contraction of the protein contraction of the protein contraction of the protein contraction of the protein contraction of the protein contraction of the protein contraction of the protein contraction of the protein contraction of the protein contraction of the protein contraction contracti
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                                                                                                                                                                                                                                                                        Moraxella catarrhalis strain 4223; major outer membrane protein;
200kDa outer membrane protein; antibacterial; immunogenic; infection;
otitis media; detection; ds.
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                                                                                                                                                                                                                        catarrhalis strain 4223 genomic 200kDa
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                                                     ВР
                                                     DNA; 6144
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                                                  AAF59103 standard;
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c acid encoding Moraxella catarrhalis outer membrane protein, protective vaccines and for diagnosis
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200kDa outer membrane protein; antibacterial; immunogenic; infection;
otitis media; detection; ds.
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                         5751
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catarrhalis strain 4223 genomic 200kDa gene SEQ ID NO:5.
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P-PSDB; AAB69134.
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The present invention describes an isolated and purified nucleic acid (I)
that encodes a 200 kba outer membrane protein of Moraxella catarrhalis.
that encodes a 200 kba outer membrane protein of Moraxella catarrhalis.
The 200 kba outer membrane protein (II) has antibacterial activity and
can be used in vaccines. (II), and its truncated versions, are used as
immunogenic compositions and vaccines to protect against M. catarrhalis
immunogenic compositions and vaccines to protect against M. catarrhalis
cantigen in immunoasays for detecting specific antibodies (Ab), and to
antigen in immunoasays for detecting specific antibodies (Ab), and its
generate Ab. (I) are used for recombinant production of (II) and its
canning as probes for identifying/Cloining 200 kba protein
fragments are used as probes for identifying/Cloining 200 kba protein
canning application of large amount of recombinant immunogens.
Clomates possible production of large amount of recombinant immunogens.
Charcaston of truncated versions of (II) reduces toxicity of the protein
towards the Escherichia coli host. The present sequence represents the
constant and the present invention.
Cexemplification of the present invention.
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                                                                                                                                                                                                                                                                                   brane protein; OMP; immunogen; vaccine; otitis media;
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Moraxella catarrhalis strain 4223; major outer membrane protein; 200kba outer membrane protein; antibacterial; immunogenic; infection; otitis media; detection; ds.
                                                                                    M. catarrhalis strain 4223 lambdaEMBL3 clone 200kDa
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The present invention describes an isolated and purified nucleic acid (I) that encodes a 200 kba outer membrane protein of Moraxella catarrhalis. The 200 kba outer membrane protein of Moraxella catarrhalis. The 200 kba outer membrane protein of Moraxella catarrhalis. The used in vaccines. (II), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarrhalis infections, particularly offitis media in humans. (II) is also used as antigen in immunoasays for detecting specific antibodies (Ab), and to generate Ab. (I) are used for recombinant production of (II) and its fragments are used as probes for identifying/cloning 200 kba protein genes from other strains, and for idagnostic detection of M. catarrhalis. (I) makes possible production of large amount of recombinant immunogens. Expression of truncated versions of (II) reduces toxicity of the protein towards the Escherichia coli host. The present sequence represents the M. catarrhalis strain 423 lambdabEmblas clone 200kba gene, which is used in the exemplification of the present invention. 2A-W; 247pp; English Fig 3, Example 

Sequence 6973 BP; 2265 A; 1555 C; 1533 G; 1620 T; 0 other;

21; 1015 1075 119 236 356 476 641 781 601 acagggtcatttttccaacgcctttggtacatacgcaacagctgaagctgcctattcctt 701 Gaps .09 gaatatgccaaatcccacagtac-gggggggggtagctgtgctacagggcaagttggcag geteaatggeagtgettatgeteaacaaattactacea---agategaaattggteaaae getcagtggcagtgcttatgctcaaaaaaaaaagataccaaacatatcgcaattggtgaaca aaacaagataaacaacacgctgaaaggcgatgccctagcgacaggtgaagcatccattgc ttttggtagtctttctaaggcacaaggctctcaagctattgctatcggtagtgtcaaacc agatectaataatggtagtaatggtaatgtaggtteecaegeeaaaggtaaegagteeat 1 atgaatcacatctataaagtcatctttaacaaagccacaggcacatttatggccgtggcg aaaccagccaagacgctc----aggcactgccaaggcggacggtgatcgagccattgc tattggtgaaaatgctaacgcacagggcggtcaagccatcgccatcggtagtagtaataa cgccatcggtggtgatgtattggctgagggtgatgcctcgattgccatcggtagtgatga ---tgaatttcacaa atatcgacgcacaagagcacacgccagtactgcagtgggagccatgtcatatgc acttattcatggccatgaaatattaaaaaaaatacaaacctcaaccgatggtaaaatcaa Length 6973; 157; Indels 22; 0; Mismatches 1009; DB cttatatttgcctaagaatcttgatctgaagaa----66.4%; Score 4090.6; 81.3%; Pred. No. 0; Query Match 66.4' Best Local Similarity 81.3' Matches 5063; Conservative 1196 542 1016 1076 61 502 120 662 722 782 836 968 926 522 1136 180 237 297 357 417 477 582 ò q οy a οy QQ ò Dp ò g ò q ò g ò ద ó g οy g ò g ò q

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                                                                                                                                                      Genomic library; bacteria; human upper airway; otitis media; sinusitis;
bronchopulmonary; endocarditis; meningitis; ss.
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            0; Mismatches 785;
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The present invention describes an isolated and purified nucleic acid (I) that encodes a 200 kba outer membrane protein of Moraxella catarrhalis. The 200 kba outer membrane protein of Moraxella catarrhalis. The 200 kba outer membrane protein (II) has antibacterial activity and can be used in vaccines. (II), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarrhalis infections, particularly outtis media in humans. (II) is also used as antigen in immunoassays for detecting specific antibodies (Ab), and to generate Ab. (I) are used for recombinant production of (II) and its fragments are used as probes for identifying/Cloning 200 kba protein genes from other strains, and for diagnostic detection of M. catarrhalis. (I) makes possible production of large amount of recombinant immunogens. Expression of truncated versions of (II) reduces toxicity of the protein towards the Escherichia coll host. The present sequence represents the M. catarrhalis strain 423 lambdaEmBal3 clone 200kba coding sequence, which is used in the exemplification of the present invention.
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200kDa outer membrane protein; antibacterial; immunogenic; infection;
otitis media; detection; ds.
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BP. 6229

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RESULT

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that encodes a 200 kDa outer membrane protein of Moraxella catarrhalis.

The 200 kDa outer membrane protein (I) has antibacterial activity and the can be used in vaccines. (II), and its truncated versions, are used as can be used in vaccines. (II), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarrhalis infections, particularly otitis media in humans. (II) is also used as infections, particularly otitis media in humans. (II) is also used as infections, particularly otitis media in humans. (II) is also used as infections as protes for recombinant production of (II) and its generate Ab. (I) are used for recombinant production of (II) and its generate Ab. (I) makes probes for identifying/cloning 200 kDa protein fragments are used as probes for identifying/cloning 200 kDa protein genes from other strains, and for identifying/cloning 200 kDa protein consersation of truncated versions of (II) reduces toxicity of the protein towards the Escherichia coll host. The present sequence represents the complification of the present invention.

C exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding Moraxella catarrhalis outer membrane protein, useful in protective vaccines and for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                          present invention describes an isolated and purified nucleic acid
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                                         Moraxella catarrhalis strain Q8; major outer membrane protein;
200kba outer membrane protein; antibacterial; immunogenic; infection;
otitis media; detection; ds.
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                            M. catarrhalis M56 200kDa gene in
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80.9%;
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                                                                                                            Moraxella catarrhalis
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P-PSDB; AAB69127.
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Matches 4904; C
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The present invention describes an isolated and purified nucleic acid (I) that encodes a 200 kDa outer membrane protein of Moraxella catarhalis. The 200 kDa outer membrane protein (II) has antibacterial activity and can be used in vaccines. (II), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarhalis infections, particularly ofitis media in humans. (II) is also used as antigen in immunoassays for detecting specific antibodies (Ab), and to generate Ab. (I) are used for recombinant production of (II) and its fragments are used as probes for identifying/cloning 200 kDa protein genes from other strains, and for diagnostic detection of M. catarhalis. (I) makes possible production of large amount of recombinant immunogens. Expression of truncated versions of (II) reduces toxicity of the protein
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200kDa outer membrane protein; antibacterial; immunogenic; infection;
otitis media; detection; ds.
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or diagnosis
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P-PSDB; AAB69136.
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29; 885 879 942 825 705 669 165 759 645 639 522 585 462 417 402 477 present sequence represents the is given in the exemplification 240 237 300 360 180 gttgcctaggttttggttctcagatccttgatagggataataataataggggtgcc attcaaaaccatacagtattacgccaaatacgagactcaa---atggttctcagaaatat ttatatttgcctaagaatcttg-----atctgaagaatgaattcacaaaactt |||||||||| || |||||| ttatattttggataggaatagcactaactctaaatatccaaatggtcttcttagcactctt attoatggccatggaatattaaaaaaaaatacaaacctcaaccgatggtaaaatcaaatat atgaatcacatctataaagtcatctttaacaaagccacaggcacatttatggccgtggcg Indels 1395; Length 0 other; 22; 1471 T; DB 2939.2; No. 0; 0; Mismatches .; G wards the Escherichia coli host. The catarrhalis les1 200kba gene, which the present invention. 1564 Score Pred. ΰ 1621 Query Match 47.7%; Best Local Similarity 70.2%; Matches 5085; Conservative Ä 2286 Sequence 6942 BP; towards t M. catarr of the pr 988 700 160 826 640 991 902 523 286 580 949 478 463 526 343 238 301 283 361 241 21 121 181 61 181 qq QQ ò ò Q D οy qq ò ρος οy Db ad Q Qy Dp Š qq òγ QQ δ qq Dp õ g ò ŏ 888888 õ 8

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Db 4	0y 4	q <sub>Q</sub>	δ	a Ao	g	οy	Db	Οy	QO	QΥ	Dp	QY	qq	Qy	QQ	οy	qq	οy	QQ	Qy	Dp	ΟŸ	QQ	ογ	Op	δλ	qq	QY	qq	ολ	qq	Qγ	qq	Qy	qq
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=	tatege	gcgaa 	gcaad	gala       gata	aaag	aaag	aaat	aaat	gaca	agaca	aaacgccgcagt	cgcaç	gatacage	tacae	Cacc	cacci	caaa		tgaa	L L J I I	aagt	taagt		atgat		ctaaad		agcc	;	tacta		logga		jtggc	-
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	qq	Οy	q	QY Dp	δδ	qq	γo	Dp	Qy	Db	δλ	QQ	οy	qq	δý	QQ	ò	q	δy	qq	οy	qq	οy	QΩ	δ	QQ	Qy	QQ	Qy	Ωp	οy	qq	ογ	QQ	δ

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0y 48	
Db 52	cagacgacctcatgcca 53.
Qy 48	
Db 53	35 aacggetcactaaaagcaggcaaatcagccagtgatgccaaaactccaactyglucaagc 33
2y 4	
Db 5	atgcagtggctcttaataactta 34.
Oy 4	
Ob 5	gtaagctctgatggc 55.
Oy 4	48(
Db 5	atgta 55
Oy 4	807aaggtcatcagtaatgtgggcaaaggcacaaaagataccgacgctgccaatgta 486
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οy	aagggcgtaacggcattgactcaagtgcctcaggcaagcactcagtggcgataggtttc
QQ	gtaacggcattgactcaagtgcctcaggcaagcactcagtggcgataggttt

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Sasaki

2000WO-CA00870

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present invention describes an isolated and purified nucleic acid (I)
                                                                                                                             New nucleic acid encoding Moraxella catarrhalis outer membrane protein, useful in protective vaccines and for diagnosis
                                                                                                                                                     Example 14; Fig 17; 247pp; English
                                                                      (CONN-) CONNAUGHT LAB LTD.
                                                                                                      2001-159722/16.
                                                                                                             P-PSDB; AAB69147
      WO200107619-A1.
                                                                                      Loosmore SM,
                                      26-JUL-2000;
                      01-FEB-2001
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                                                                                                                                                                                                                                                                                                            Moraxella catarrhalis strain 4223; major outer membrane protein;
200kDa outer membrane protein; antibacterial; immunogenic; infection;
                                              aactctgccatcagtgcaggcacacacgcaggcacacaagccaaaaaatctgacggcaca
                                                                                                                                                                                                     gcaggtacaaccaccacagcaggtgccacaggtacggttaaaggctttgctggacaaacg
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                                                                     acaggcaatgtggtagcaggtaagcactctggtgccatcggcgacccaagcactgttaag
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                                                                                                                                                                                                                                                                     gcaggtgaggtcagtgccaccagcaccgatgcggtcaatggtagccagttgtacaaagcc
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otitis media; detection; ds.
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that encodes a 200 kba outer membrane protein of Moraxella catarrhalis. The 200 kba outer membrane protein (II) has antibacterial activity and can be used in vaccines. (II), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarrhalis infections, particularly otitis media in humans. (II) is also used as antigen in immunoassays for detecting specific antibodies (Ab), and to generate Ab. (I) are used as probes for identifying/cloning 200 kba protein genes from other strains, and for diagnostic detection of M. catarrhalis. (I) makes possible production of large amount of recombinant immunogens. Expression of truncated versions of (II) reduces toxicity of the protein towards the Escherichia coli host. The present sequence represents a M. catarrhalis strain 423 200kba partial nucleotide sequence, which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hia; adhesin; Haemophilus influenzae adhesin; NTH1; infection; vaccine; non-typeable Haemophilus influenzae; antiinflammatory; auditory; antibacterial; meningitis; epiglottitis; septicaemia; otitis media; diagnosis; immunogenic; antigen, ds.

    gaatatgccaaatcccacagtacggggggggggtagctgtgctacagggcaagttggcaqt 120

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22; Length 720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 720 BP; 201 A; 142 C; 140 G; 237 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.7%; Score 166.2; DB 22; Best Local Similarity 95.5%; Pred. No. 2.2e-33; Matches 171; Conservative 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                 used in an example from the present invention.
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Claim 1; Fig 21; 275pp; English.
                                              Klein MH;
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Best Local Similarity 58.2%;
Matches 280; Conservative (
                    2000WO-CA00289
                             99US-0268347
                                     (CONN-) CONNAUGHT LAB LTD.
                                               Loosmore SM, Yang Y,
                                                        WPI; 2000-618897/59.
                                                             P-PSDB; AAB23857
  WO200055191-A2
                    16-MAR-2000;
                             16-MAR-1999;
            21-SEP-2000
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gene from the non-typeable Haemophilus influenzae (NTHi) strain M47.

gene from the non-typeable Haemophilus influenzae (NTHi) strain M47.

Ha genes and proteins have antiinflammatory, auditory and antibacterial

activities, and can be used in the production of a vaccine. An

activities, and can be used in the propaptide la useful for inducing

by an Hia gene, or a recombinant Hia polypeptide is useful for inducing

by an Hia gene, or a recombinant Hia polypeptide is useful for inducing

protection against disease caused by Haemophilus strains in a

protection against disease caused by the infection of Haemophilus

for other immunogenic preparations including vaccines, as a carrier

antigen, in immunogenic preparations including vaccines, as a carrier

for other immunogenic acused by the infection of Haemophilus

influenzae such as meningitis, epiglotitis, septicaemia and ottics

media. Recombinant production of Hia favours high recovery of the

media. Recombinant production of Hia favours high recovery of the

protein compared to the low recovery of native protein from Haemophilus

influenzae species. A truncated protein has a significantly higher

amount of recovery than a full-length protein.
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                                                                                                                                                                                                                Novel nucleic acid encoding Hemophilus influenzae adhesin protein, fuse as antigens and vaccines and for treating Hemophilus influenzae infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 144.6; DB 21; Length 3030;
Pred. No. 2.2e-27;
0; Mismatches 189; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3030 BP; 965 A; 596 C; 786 G; 683 T; 0 other;
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The present sequence represents a Haemophilus influenzae adhesin (Hia)

Gene from the non-typeable Haemophilus Influenzae (NTH1) strain 33.

Gene from the non-typeable Haemophilus Influenzae (NTH1) strain 33.

Gene from the non-typeable Haemophilus Influenzae (NTH1) strain 33.

Activities, and can be used in the production of a vaccine. An activities, and can be used in the production of a vaccine. An immunogenic composition comprising an Hia gene, a polypeptide concoded immunogenic composition and Haemophilus strains in a protection against disease caused by Haemophilus strains in a susceptible host, preferably a human. An Hia protein is useful as an antigen, in immunogenic preparations including vaccines, as a carrier antigen, in immunogenic preparations including vaccines, as a carrier for useful for treating diseases caused by the infection of Haemophilus influenzae such as meningitis, epiglotitis, septicaenia and otitis media. Recombinant production of Hia favours high recovery of the meninging of the infection of protein compared to the low recovery of native protein from Haemophilus in the species. A truncated protein has a significantly higher
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  His; adhesin; Haemophilus influenzae adhesin; NTH1; infection; vaccine; non-typeable Haemophilus influenzae; antlinflammatory; auditory; antibacterial; meningitis; epiglottitis; septicaemia; otitis media; diagnosis; immunogenic; antigen; ds.
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Pred. No. 5.7e-27;
0; Mismatches 190;
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The present sequence represents a Haemophilus influenzae adhesin (Hia)
gene from the non-typeable Haemophilus influenzae (NTH1) strain K9.
Hia genes and proteins have antiinflammatory, auditory and antibacterial
cutivities, and can be used in the production of a vaccine. An
immunogenic composition comprising an Hia gene, a polypeptide encoded
by an Hia gene, or a recombinant Hia polypeptide is useful for inducing
protection against disease caused by Haemophilus strains in a
susceptible host, preferably a human. An Hia protein is useful as an
antigen, in immunogenic preparations including vaccines, as a carrier
for other immunogens, and in the generation of diagnostic reagents. Hia
is useful for treating diseases caused by the infection of Haemophilus
influenzae such as meningitis, epiglottitis, septicaemia and otitis
media. Recombinant production of Hia favours high recovery of the
media. Recombinant production of Hia favours high recovery of the
protein compared to the low recovery of native protein from Haemophilus
influenzae species. A truncated protein has a significantly higher
amount of recovery than a full-length protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   2.2%; Score 138.2; DB 21;
llarity 57.4%; Pred. No. 1.1e-25;
Conservative 0; Mismatches 193;
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Best Local Similarity
Matches 276; Conserv
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gene from the non-typeable Haemophilus influenzae (NTHI) strain K22.

gene from the non-typeable Haemophilus influenzae (NTHI) strain K22.

Hia genes and can be used in the production of a vaccine. An activatives, and can be used in the production of a vaccine. An immunogenic composition comprising an Hia gene, a polypeptide encoded by an Hia gene, a polypeptide is useful for inducing by an Hia gene, a polypeptide is useful for inducing protection against disease caused by Hemophilus strains in a protection pagainst disease caused by Hemophilus strains in a mannogenic preparations including vaccines, as a carrier antigen, in immunogenic preparations including vaccines, as a carrier of for other immunogens, and in the generation of diagnostic reagents. His for other immunogens, and in the generation of diagnostic reagents. His is useful for treating diseases caused by the infection of Haemophilus influenzae such as meningitis, epiglottitis, septicaemia and ofthis media. Recombinant production of Hia favours high recovery of the compared to the low recovery of native protein from Haemophilus influenzae species. A truncated protein has a significantly higher mount of recovery than a full-length protein.
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use as antigens and vaccines and for treating Hemophilus influenzae
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 23; 275pp; English.
                                                                                                                                                                                                                                                                                         Klein MH;
                                                                                                                                                                                                                      99US-0268347.
                                                                                                                                                                                     16-MAR-2000; 2000WO-CA00289.
                                                                                                                                                                                                                                                     (CONN-) CONNAUGHT LAB LTD.
                                                                                   Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                          WPI; 2000-618897/59.
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                                                                                                                       WO200055191-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6097 atcaatggttcagccgatacccaaggccatgtaggggcggcagttggtgcaggtttcac 6156 | 6097 atcaatggttcagccatgtaccac 6156 | 6097 atcaatggtaaaacaggcgttgcagcaggtgttgcagcaggtaacaaggtaaaacaggcgttgcagcaggtgttggttagcag 3322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Electron-transfer group; ETM; mismatch; genotyping;
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480; Mismatches
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17-MAR-2000; 2000US-0190259.
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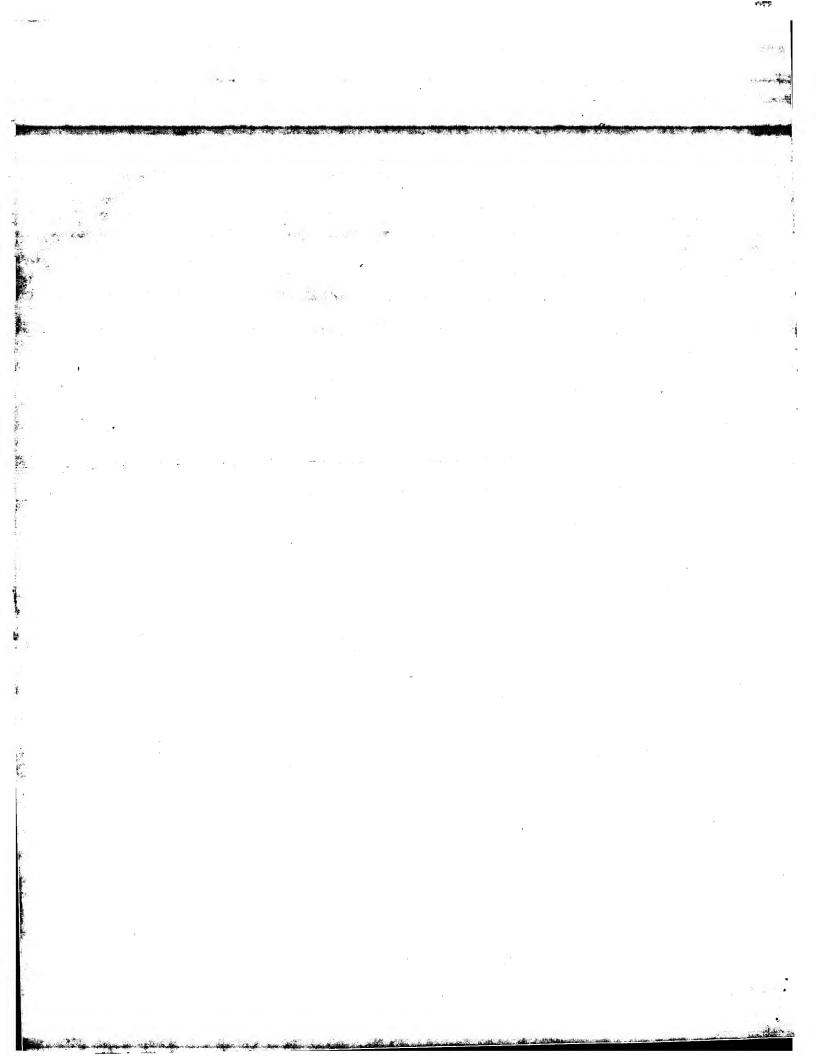
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Search completed: September 12, 2001, 13:39:40 Job time: 3602 sec



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18,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,370
FILING DATE: 07-UN-1995
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
RECESTRACTION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 24,973
TELEPHONE: (416) 595-11-7
TELEPHONE: (416) 595-11-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SASAKI, Ken
APPLICANT: HARKNESS, Robin E.
APPLICANT: LOSOWORE, Sheena M.
APPLICANT: LOSOWORE, Sheena M.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER
TITLE OF INVENTION: MEMBRANE PROTEIN OF MORAXELLA
NUMBER OF SEQUENCES:
ADDRESSEE: SIM & MCBULNEY
US-08-750-532-8

US-08-728-323A-1

US-08-770-370-370-370-370-300

US-08-801-898A-23

US-08-801-898A-23

US-08-802-690-12

US-08-630-822A-65

US-08-630-822A-65

US-08-630-822A-71

US-08-005-069-65

US-08-98-416-186

US-08-98-416-186

US-08-98-416-186

US-08-455-829-3

US-08-455-829-3

US-08-455-836C-69

US-08-235-836C-69

US-08-235-836C-69
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Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 1, Application US/08478370; Patent No. 5808024; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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nucleic acid
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Best Local Similarity 81.3
Matches 5063; Conservative
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COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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                                 Compugen Ltd
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US-09-377-155-6
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US-08-676-974-2
US-09-098-487-2
                GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Listing first 45 summaries

    nucleic search, using sw model

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Sequence 9, Application US/08968685A

Patent No. 6714981

GENERAL INFORMATION:

APPLICANT: TUCKER, KENNETH

APPLICANT: PLOSILA, LAURA

TITLE OF INVENTION: MORAXELLA CATARRHALIS OUTER MEMBRANE

TITLE OF INVENTION: MORAXELLA CATARRHALIS GENE SEQUENCE AND USES THER.

CORRESPONDENCE ADDRESS:

ADDRESSEE: PENNIE & EDMONDS LLP

STREET: 1155 Avenue of the Americas

CITY: New York
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
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0; Mismatches
 JMBER: US/08/968,685A
No. 6214981ember 12, 1
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APPLICATION NUMBER: US/08/968, FILING DATE: No. 6214981ember CLASSIFICATION: O. 6214981ember CLASSIFICATION: O. 6214981ember CLASSIFICATION: NUMBER: 31,232 REFERENCE/DOCKET NUMBER: 7969-TELEPHONE: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERICS: LENGTH: 9542 base pairs TYRE: nucleic acid STRANDEDNESS: single
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Best Local Similarity 79.7°
Matches 5115; Conservative
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4852 gocaatgtacaacagttaaacgaagtacgcaacttgttgggtcttggtaat 4902		*ATAAGGCGGAGGTCAGACCAACTATTTGACCAACAACCCGGCAGAAGC taaatgaacaaggtatccgcttcttccatgtcaacgatggcaatcaaga	323 ataggtttccaggccaaggcagatggtgaagccgttgccataggcagacaaacccaa 538	5443 gccatcggtacaggcaatgtggtagcaggtaagcactctggtgccatcggcgacccaage 5502	5563 caaaccgatgtctttggtgtgggcaataacatcaccgtgaccgaaagtaactcggttgcc 5622	5683         gacggcacagcaggtacaaccaccacagcaggtgccacaggtacggttaaaggctttgct         5742           111111111111111111111111111111111111	03 aatgtggcagc 
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                                                                                                     3043 GGCAAAGTGAATAAAGTGGGCAAACGTGCAGATGCAGGTACAGCAAGTGCATTAGCGGCT 3102
---aaagccacccaaagcattgccaacgcaaccaatgagcttgac 5907
                                 2983 CAGIIGIAIGCIGIGGCAAAAGGGGIAACAAACCIIGCIGGACAAGIGAAIAAICIIGAG 3042
                                                                       5908 catcgtatccaccaaaacgaaaataaagccaatgcagggattcatcagcgatggcgatg
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STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
US-08-685-467-1
Sequence 1, Application US/08685467
; Sequence 10, 6060059
; GENERAL INFORMATION:
; APPLICANT: St. Geme III, Joseph W.
APPLICANT: Barenkamp, Stephen J.
; APPLICANT: Barenkamp, Stephen J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/685,467 FILING DATE: 22-JUL-1996 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: S11va, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61053-2/RFT/RMS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.4%; Score 84.4;
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APPLICATION NUMBER: US 08/409,995
FILING DATE: 24-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: DNA (genomic) US-08-685-467-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
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STRANDEDNESS: unkno
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50.0%; Pred. No. 8.3e-13;
cive 0; Mismatches 236; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400 CITY: San Francisco STATE: CA
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Barenkamp, Stephen I.
APPLICANT: St. Geme III, Joseph W.
TILE OF INVENTION: Haemophilus Adhesion Proteins
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/409,995 FILING DATE: 24-MAR-1995 CLASSIFICATION:
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: S11va, Robin M.
REGIGSTRATION NUMBER: 38,304
REFRENCE/DOCKET INFORMATION:
TELEPHONE: (415) 781-1989
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08409995
Patent No. 5646259
GENERAL INFORMATION:
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nucleic acid
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Best Local Similarity 50.00
Matches 245; Conservative
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US-08-409-995-1
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APPLICANT: St. Geme, Joseph
APPLICANT: St. Geme, Joseph
APPLICANT: Barenkamp, Stephen J.
TITLE OF INVENTION: HAEMOPHILUS ADHESION PROTEINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr Hobbach Test Albritton & Herbert LLP
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STREET: California
COUNTRY: United States
21P: 9411-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OMEDIUM SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                  Indels
8.3e-13;
thes 236;
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Pred. No. 8.3e); Mismatches
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FILING DATE: 29-DEC-1997
CLASSIPRICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,995
FILING DATE: 24-MR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/4031
FILING DATE: 22-MR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Vance, DOlly A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08913942
Patent No. 6200578
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Best Local Similarity 50.0%;
Matches 245; Conservative
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Patent No. 6200578
CENERAL INFORMATION:
APPLICANT: Barenkamp, Stephen J.
TITLE OF INVENTION: HAEMOPHILUS ADHESION PROTEINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr Hobbach Test Albritton & Herbert LLP
                                                                                                                                                                                                                                                                                                                          Score 84.4; DB 4; 1 pred. No. 8.3e-13; 0; Mismatches 236;
                       A-61053-1/RFT/RMS/DAV
              REFERENCE/DOCKET NUMBER: A-61(
REFERENCE/DOCKET NUMBER: A-61(
TELEPHONE: (415) 781-1989
TELEPHONE: (415) 781-1989
TELERA: 910 277299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3294 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPPOLOGY: unknown
39,054
                                                                                                                                                                                                                                                                                                                            1.4%;
                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 50.0 Matches 245; Conservative
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COUNTRY: United States
ZIP: 94111-4187
      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
STATE: California
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US-08-913-942-1
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US-08-913-942-14
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                                                                                                                                                                              PRIOR APPLICATION DATA:

APPLICATION DATA:
APPLICATION NUMBER: US 08/409,995
FILING DATE: 24-MAR-1995
FILING DATE: 24-MAR-1995
PRIOR APPLICATION NUMBER: PCT/US96/4031
FILING DATE: 22-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Vance, Dolly A.
REGISTRATION NUMBER: A-61053-1/RFT/RMS/DAV
REFERENCE/DOCKET NUMBER: A-61053-1/RFT/RMS/DAV
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1899
TELECOMMUNICATION 10199
TELECOMMUNICATION 10109
TELECOMMUNICATION 10109
TELECOMMUNICATION 1010 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2017 base pairs
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC: compatible
COMPUTER: IBM PC: compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,942
FILING DATE: 29-DBC-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08913942
Patent No. 6200578
GENERAL INFORMATION:
APPLICANT: St. Geme, Joseph
APPLICANT: Barenkamp, Stephen J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
1.4%;
Best Local Similarity 54.1%;
Matches 198; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
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5964 gatggcgtccatgccacaagcctacattcctggcagatccatggttaccgggggtattgc 6023
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                                                                                                                        ADDRESSEE: Flehr Hobbach Test Albritton & Herbert LLP STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/913,942 FILING DATE: 29-DEC-1997 CLASSIFICATION NUMBER: US/08/913,942 FILING APPLICATION NUMBER: US/08/913,942 FILING DATE: 24-MAR-1995 FILING DATE: 24-MAR-1995 FILING DATE: 24-MAR-1995 FILING DATE: 22-MAR-1996 ATTORNEY/AGENT INFORMATION: NAME: Vance, DOLly A. REGISTRATION NUMBER: 39,054 REGISTRATION NUMBER: 39,054 REGISTRATION NUMBER: 39,054 REGISTRATION NUMBER: 39,054 REGISTRATION NUMBER: 39,054 REGISTRATION NUMBER: 34,054 REGISTRATION NU
TITLE OF INVENTION: HAEMOPHILUS ADHESION PROTEINS NUMBER OF SEQUENCES: 19 CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Flehr Hobbach Test Albritton & Herber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 39,054
REFERENCE/DOCKET NUMBER: A 61053-1/RFT/RMS/DAV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 77.2; DB 4;
Pred. No. 1.2e-10;
0; Mismatches 243;
                                                                                                                                                                                                          CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUH TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.3%;
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TELEFA: (415) 398-3249
TELEX: 910.277299
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 7291 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: unknown
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Best Local Similarity
Matches 242; Conserv
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COCATION:
US-08-913-942-3
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2558 CTTTAACT---GAGCCAAGCGCGGGGGGAGTCTTCACACGTTGATTTAAATGTGGATG 2614
                                           2735 ACAGCACAGGTACAACAACGGTAAC-----CGTAACCCAAAAAGCAGATGGCAAAGGTG 2788
                                                                                                                                                     2675 AAGGTAATGGTAATGTTGATTGTAGCGACGATGACGACAGAAACTTTACCGATG
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                                                                                                                               2543 aaaataatggcaaagacaaagactttgtctccacttatgacactgttgactttatcgatg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: St. Geme III, Joseph W.
APPLICANT: Barenkamp, Stephen J.
TITLE OF INFORMATION: HAEMOPHILUS ADHESION PROTEINS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,467
FILING DATE: 22-Jul-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILIG DATE: 24-MAR-1995
ATTORNEY/ACENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tch 1.1%; Score 66; DB 3; La Similarity 49.4%; Pred. No. 1.1e-07; 233; Conservative 0; Mismatches 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08685467
Patent No. 6060059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic) US-08-685-467-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5738 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
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Best Local S
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6024 cacccacaacggicaaggigcggiggcagigggacigicgaagcigicggaiaaiggica 6083
                            2378 TTGAGGTGAAAACTGCGAAAGTGAGTGATACTTTAACGATTGGCGGGAATACACCTACAG 2437
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                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08409995
Pattent No. 5646259
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bt. Geme III, Joseph W.
TITLE OF INVENTION: Haemophilus Adhesion Proteins
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Datentin Pc-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61053/RFT
TELECOMUNICATION INFORMATION:
TELEPAN: (415) 781-1989
TELEPAN: (415) 398-3249
TELERX: 910 277299
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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24-MAR-1995
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                                                                                                                                                                                                           7206 TGTTGGTTACCAGT 7219
                                                                                                                                                                        tgcaggttttcact 6157
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EDNESS: double
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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TOPOLOGY:
US-08-409-995-3
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                                                                                                                                                                                                                                                                                               US-08-409-995-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
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us-09-361-619-8.rni

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NAME/KEY: CDS
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SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                         cactgectageattgecagtecaagtggeegeaacatageactgggeaatacaategaag 2482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2735 ACAGCACAGGTACAACAACGGTAAC-----CGTAACCCAAAAAGCAGATGGCAAAGGTG 2788
                       2438 GTGGCACTACTGCGACGCCAAAAGTGAATATTACTAGCACGGCTGATGTTTGAATTTG 2497
                                                                                                                             2498 CAAAAGAAACAGCCGATGCCTCGGGTTCTAAGAATGTTTATTTGAAAGGTATTGCGACAA 2557
                                                                                                                                                                                                                                                                                                                                       2543 aaaataatggcaaagacaaagactttgtctccacttatgacactgttgactttatcgatg
gictcaccacgcctaagctgaccgtgggtagcgatacaaatggtaatcgattggttattg
                                                                                   2363 agcaagtccctagcgctgacggtaacagcaccaaaaacatcattaaaggattgtcccaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SASAKI, Ken
APPLICANT: HARKNESS, Robin E.
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER
TITLE OF INVENTION: MEMBRANE PROTEIN OF MORAXELLA
CORRESPONDENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,370 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-502
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08478370 Patent No. 5808024 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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TYPE: nucleic acid
STRANDEDNESS: single
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US-08-478-370-4
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                                                                           Gaps
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Pred. No. 6.4e-06;
0; Mismatches 121;
  DB 1; Le
3.2e-07;
                                                                                                                                                                                                                                                                             APPLICANT: PEAK, IAN RICHARD ANSelm APPLICANT: JENNINGS, Michael Paul APPLICANT: MONON, E. RICHARD TITLE OF INVENTION: NOVEL SURFACE ANTIGEN FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: 1999-08-19
CURRENT FILING DATE: 1999-08-19
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VENTION NUMBER: 2007-13-12
Query Match 1.0%; Score 60; DB Best Local Similarity 100.0%; Pred. No. 3.2 Matches 60; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, MICHAEL Paul
APPLICANT: MOXON, E. Richard
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
                                                                                                                                                                                                                         Sequence 12, Application US/09377155 Patent No. 6197312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09377155 Patent No. 6197312
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Matches 131; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (1)..(1794)
US-09-377-155-12
                                                                                                                                                                                                                                                  ; Patent No. 6197312
; GENERAL INFORMATION:
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                             accatcgtatccaccaaaacgaaaataaagccaatgcagggatttcatcagcgatggcga
                                                                                                           5966 tggcgtccatgccacaagcctacattcctggcagatccatggttaccgggggtattgcca
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Pred. No. 4.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Security 10. Application US/09377155
Patent No. 6197312
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER: OF SEQ ID NOS: 33
SCOTTWARE: PETENTING DATE: 1097-12-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.9%;
Best Local Similarity 51.2%;
Matches 129; Conservative
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1760 tcggttatcagt 1771
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US-09-377-155-10
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US-09-377-155-10
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                                                                                                                                                                                                                                                                                                                                                                       Length 1797;
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                                                                                                                                                                                                                                                                                                                                                                  Score 56.8; DB 4;
Pred. No. 1.7e-05;
0; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: PERK, Ian Richard Anselm
APPLICANT: PENNK, Ian Richard Anselm
APPLICANT: BURNINGS, Michael Paul
SPELICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REPERENCE: 065064/0129
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-14
SPRIOR FILING DATE: 1997-12-12
SOFTWARE: PATCHIN VOT: 2.0
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
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                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.9%;
Best Local Similarity 51.6%;
Matches 130; Conservative
                                                                                                      NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENCTH: 1797
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Best Local Similarity 51.2
Matches 129; Conservative
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; LOCATION: (1)..(1794)
US-09-377-155-4
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; LOCATION: (1)..(1767)
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LENGTH: 1770
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US-09-377-155-18
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0.9%; Score 55.2; DB 4; Length 1776;
Best Local Similarity 51.2%; Pred. No. 4.7e-05;
Matches 129; Conservative 0; Mismatches 123; Indels 0
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; Sequence 20, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PERK, IEN Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; TITLE OF INVENTION: NOVEL: SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR FILING DATE: 1999-12-14
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PATENTIN VET: 2.0
; SEQ ID NO 20
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NAME/KEY: CDS
LOCATION: (1)..(1773)
US-09-377-155-20
RESULT 15
US-09-377-155-20
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Welssenbach, J.  TITLE Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis JOURNAL Unpublished REFERRNCE 2 (bases 1 to 806)		Unpublished 3 (bases 1 to 806) Genoscope. Direct Submission	JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.	rce	/cloud_lib_s /note="Genoscope sequence ID : COBGO95BD12LP1-end : T7" BASE COUNT 247 a 87 c 99 g 333 t 40 others ORIGIN	Query Match 1.3%; Score 83; DB 221; Length 806; Best Local Similarity 43.5%; Pred. No. 6.5e-11; Matches 273; Conservative 19; Mismatches 335; Indels 0; Gaps 0;	Qy 1407 tactaatgatagtaatagtatagcaactaaaggtactactcgtattaccaaaagaaaat 1466 	OY 1467 tggttttgctggtactaatgatggagttgatgaaagcaaaccttatcttgacaacgaaaa 1526 	Oy 1527 gctaaaagttggcaacagcacctaaacagtggtagcttgactgttaataacaccactgg 1586 	Oy 1587 taataaacaaatccaagtcggtgctaatggcattaaatttgccacagtcgctaataatgt 1646       :	OY 1647 tgcaaatacctcagcaacagtcggcactgctcgtattaccgaagaaaattggttttgc 1706 ::	1707 tggtactaatgatggagttgatgaacaagcaccatatttggataaagaacgacttaaagt		Qy 1887 gcctactttaaacgcaggcgatggcatcagtattaatagtaataacggggatctagttga 1946
SUMMARIES Query e Match Length DB ID	83 1.3 806 221 CNSO4AEE 77.4 1.3 641 236 AQ946120 71.2 1.2 709 236 AQ945248 67.4 1.1 729 236 AQ945618 66.8 1.1 500 107 AU086536	65.8 1.1 621 236 AQ941683 62.4 1.0 469 107 AU076358 62 1.0 541 221 CNSO4KUS 58.2 0.9 827 220 CNSO2156	10 56.8 0.9 520 231 AQ656286 AQ656286 Sheared D 11 56.8 0.9 654 228 AQ411842 AQ411842 CPG0865B 12 56.2 0.9 442 107 AU053378 AU053378 AL197365 Tetraodon 14 55.8 0.9 500 107 AU088475 AU	54.6 0.9 401 231 AQ639568 54.2 0.9 252 156 C93354 54.2 0.9 363 156 C9385 54.2 0.9 363 156 C92885 54.2 0.9 816 245 AZ535744 53 8 0 9 743 234 AZ196612	53.2 0.9 560 231 AQ658275 53 0.9 560 107 AU087658 53 0.9 835 221 CNS046DH 52.8 0.9 595 240 AZ216659 57 0.0 655 240 AZ216659	26 52.6 0.9 558 218 AA2506424 27 52.6 0.9 1042 221 CNSO3YTF 28 52.4 0.9 581 231 AQ658242 29 52 0.8 739 239 AZ166614	52 0.8 989 220 CNS02HA4 51.8 0.8 240 107 AU078556 51.8 0.8 500 107 AU088092 51.4 0.8 500 107 AU088092	51.4 0.8 810 239 A219472 51.4 0.8 856 156 C25694 51.2 0.8 443 258 PT015E15U 51.2 0.8 500 156 C93360	51.2 0.8 639 231 AQ656218 50.8 0.8 410 107 AU037570 50.8 0.8 660 239 AZ212542 50 4 0 8 488 258 PPD03315P	50.4 0.8 702 236 AQ946396 AQ946396 50.2 0.8 407 231 AQ644537 AQ644537 49.8 0.8 302 256 B73937 B77397 T2 49.8 0.8 457 156 C90465	ALIGNMENTS	RESULT 1 CNSOAAEE/C LOCUS CNSOAAEE 806 bp DNA GSS 21-MAY-2000 DEFINITION TELRAOdon nigroviridis genome survey sequence T7 end of clone 095G24 of library G from Tetraodon nigroviridis, genomic survey	386 sequence. dis.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.  REFERENCE 1 (bases 1 to 806) AUTHORS Roest-Croilius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,

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In (base) 100 end sequences from Trypanosoma brucel GUTat 10.1 sheared DNA 1brary

Unpublished (1999)

Other.

Contact: Najib M. El-Sayed

Department of Bukaryotic Genomics

The Institute for Genomic Research

9712 Nedical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208
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Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
alstribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/tdb/mdb/tbdb/.
Seq primer: M13-Forward
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/strain="TRE02774 GUTat 10.1"
/db_xref="taxon:5691"
/clone="Sheared DNA-42E21"
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Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/tdb/mdb/tbdb/.
Seq primer: Ml3-Reverse
Class: shotgun.
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Sheared DNA-46J23.TR Sheared DNA Trypanosoma brucei genomic clone
Sheared DNA-46J23, DNA sequence.
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                       2007 cagtaatggcaccagtggtaataataa 2033
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AQ946120.1 GI:6769385
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/clone_lib="Sheared DNA"
/clone_lib="Sheared DNA"
/note="Vector: pUG18: Site_l: Smal; Constructed at The Institute for Genomic Research (FIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10:1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + 1 method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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Petermination of clone end sequences from Trypanosoma brucei GUTat 10.1 sheared DNA library
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Pred. No. 9.1e-08;
0; Mismatches 238;
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Other_GSSs: Sheared DNA-49K6.TR
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Best Local Similarity 47.3%;
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/note="vector: pucl8; Site_1: Smal; Constructed at The Institute for Genomic Research (TiGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun
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                                                                                                            MD 20850, USA
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/db_xref="taxon:5691"
/clone="Sheared DNA-49K6"
/clone_lib="Sheared DNA"
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Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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                                                                                                                                                                                                             Email: nelsayed@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                            Email: jwatanab@manage.ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
                                                                                                                                    Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 500)
Watanabe, J., Sasaki, M., Suzuki, Y. and Sugano, S.
FULL-malaria: a database for a full-length enriched cDNA library from human malaria parasite, Plasmodium falciparum
Nucleic Acids Res. 29 (1), 70-71 (2001)
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AU086536 Sugano Malaria cDNA library Plasmodium falciparum cDNA
clone XPFn2783, mRNA sequence.
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                                                                                                                                                                                                                                                                                                        Institute of Medical Science
The University of Tokyo, Department of Parasitology
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="3D7"
/db_xref="taxon:5833"
/dboe="xpra783"
/clone=lib="sugano Malaria cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="erythrocytic stage"
43 c 34 g 142 t
                                                                                                                       malaria parasite P. falciparum.
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Contact: Junichi Watanabe
                                                                                    AU086536.1 GI:12388677
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                                                                                                                                                                                                                                                                                                                                                          Tel: 81-3-5449-5378
Fax: 81-3-5449-5410
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/ Organism="Trypanosoma brucel"
/ Strain="Trypanosoma brucel"
/ Strain="TrE0927/4 GUTat 10.1"
/ Ab_ratef="taxon:5691"
/ Clone="Sheared DNA" |
/ Clone="Sheared DNA" |
/ Clone="Sheared DNA" |
/ Clone="Sheared DNA" |
/ Clone="Sheared DNA" |
/ Clone="Sheared DNA" |
/ Clone="Sheared DNA" |
/ Clone="Sheared DNA" |
/ Institute for Genomic Research (TIGR), Rockville, MD.
Institute for Genomic Research (TIGR), Rockville, MD.
Institute for Genomic Research (TIGR), Rockville, MD.
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from a cloned population of
Trypanosoma brucel (TRE0927/4 GUTat 10.1) was mechanically
sheared to give a tight size distribution (approx 2 kb).
The v + i method used for the library construction is
described in detail in Smith, H.O. and Venter, J.C.
(Making small insert libraries for whole genome shotgun
sequencing projects. In Genome Sequencing: A Practical
Approach, eds. M. Vaudin and B. Barell, Oxford University
Press, 1999)."
                                                                                                                                                                                                                                                                                                     Trypanosoma.

Trypanosoma.

Trypanosoma.

Trypanosoma.

El-Sayed, N., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C., Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J., Fraser, C. and Adams, M.

Fraser, C. and Adams, M.

Determination of clone end sequences from Trypanosoma brucei GUTat 10.1 sheared DNA library

Unpublished (1999)

Other GSSs: Sheared DNA-43D2.TF

Contact: Najib M. El-Sayed

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: nelsayed@tigr.org
Clones are derived from the Trypanosoma brucel GUTat 10.1 sheared
Clones are derived from the TIGN. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/tdb/mdb/tbdb/.
Seq primer: M13-Reverse
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A0941683 621 bp DNA GSS 27-JAN-2000
Sheared DNA-43D2.TR Sheared DNA Trypanosoma brucei genomic clone
Sheared DNA-43D2, DNA sequence.
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RESULT AQ941683

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                                                                                                                                                 AU076358 469 bp mRNA EST 27-JUL-1999
AU076358 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
discoideum cDNA clone SSA642, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lone_lib="Dictyostelium discoideum SS (H.Urushihara)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aaacgcaggcgatggcatcagtattaatagtaataacggggatctagttgatagtgg 1955
1776 tgaaattaccacagatagtggtattaatgctggtaatcacaagattaccggacttactaa 1835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tggtatagcaaataccgatgcggttaccatcaaacagctcaaagacgccaagcctacttt 1895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218 TAATAATAATAATAATAATAACAATAANAATAATAANAATAATAATAATAATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: 4007husakura.cc.tsukuba.ac.jp
PROJECT = Dictyostelium discoideum cDNA project in Japan.
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0
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                                                                                                                                                                                                                                 Dictyostelium discoideum.
Dictyostelium discoideum.
Eukaryota: Mycacoideum
Lukaryota: Mycacoa: Dictyosteliida; Dictyostelium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Dictyostelium discoideum"
/strain="Ax4"
/db_xref="taxon:44689"
/clone="SSA642"
/clone="1b="Dictyostelium discoideum
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/dev_stage="slug"
26 g
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                                                                   Unpublished (1999)
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GSS; genome survey sequence.

Tetraodon nigroviridis.

Tetraodon nigroviridis

Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Rutaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetraodontidae; Tetraodon.

E 1 (bases 1 to 541)

S Roest-Crollius, H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,

Bouncau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.

Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 541)
cost.crollius, w. Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
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CNSO4KUS 541 bp DNA GSS 21-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 117023 of library G from Tetraodon nigroviridis, genomic survey
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/db_xref="taxon:99883"
/clone="117023"
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44.9%; Pred. No. 2.5e-05;
ive 26; Mismatches 126;
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Matches 124; Conservative
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RESULT CNS02156

RESULT 8 CNS04KUS/c

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Best Local Similarity 50.4%;
Matches 139; Conservative
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AQ656286.1 GI:5164054
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This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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           CNSO2156 827 bp DNA GSS 12-MAY-2000
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 224F10 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                       Tetraodon nigroviridis

Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Eukaryota; Meopteryqii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopteryqii; Percomorpha; Tetraodontiformes;

Tetraodontidae; Tetraodon.

1 (bases 1 to 827)

1 (bases 1 to 827)

Bouncau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Baurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
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45.2%; Pred. No. 0.0003;
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/organism-"Tetraodon nigroviridis"
/organism-"tetraodon pigroviridis"
/clone="224F10"
/clone_lib="G"
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AL176451.1 GI:7814508
GSS; genome survey sequence.
Tetraodon nigroviridis.
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Jorganism="Trypanosoma brucei" |

Jorganism="Trypanosoma brucei" |

Jorganism="Trypanosoma brucei" |

Job_xref="taxon:5691" |

Job_xref="taxon:5691" |

Johne="Sheared DNA-27K23" |

Johne="Vector: pUC18: Site_1: Smal; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Persex, 1999)."

Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Determination of clone end sequences from Trypanosoma bruce1 GUTat 10.1 sheared DNA 11brary
Unpublished (1999)
Other_GSSs: Sheared DNA-27k23.TF
Contact: Naj1b M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhao, H., Gill, S., Suh, E., Malek, J., Fujil, C., de Jong, P., Ullu, E., Melville, S., Donelson, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: nelsayed@tigr.org
Clones are derived from the Trypanosoma brucel GUTat 10.1 sheared
Clones are derived from the Trypanosoma will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/tdb/mdb/tbdb/.
Seq primer: Ml3-Reverse
Class: Shotgun
                                                                                                                                                                                                                              AQ656286 520 bp DNA GSS 23-JUN-1999
Sheared DNA-27K23.TR Sheared DNA Trypanosoma brucel genomic clone
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Pred. No. 0.0006;
0; Mismatches 137; Indels 0;
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2217 cttaaaactcaaaggtgaaaacggtgttaatattacgaccaat 2259
                                571 CAACAATAACAGTGATRACAACAATGACAGTGATRACRACAAT
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Gerrard, C., Leech, V., de Jong, Fraser, C. and Adams, M.
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397 TAATAATACGACAAATAATCTCAATTCTGGTAGTAATACATCAATTTCTGCTGGAAATAT 456
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/strain="lowa"
/strain="lowa"
/db.ref="taxon:5807"
/clone_lib="CplowAgoNal"
/lab_host="E. col! %L2 Blue MRF'"
/lab_host="E. col! %L2 Blue MRF'"
/lab_host="E. col! %L2 Blue MRF'"
/lab_host="E. col! %L2 Blue Script II ($K-); Site_l: EcoRV; C.
parvum (lowA isolate) genomic DNA was hydrodynamically
sheared to produce fragments having a tight size
distribution between 2-4 kb by Dr. Yvonne Thorstenson of
the Stanford DNA Sequencing and Technology Center
(http://sequence-www.stanford.edu/group/techdev/shear.htm
). The randomly sheared gDNA was chromatographed on
Sephacryl S-400 to remove any small fragments and DNA
eluting in the void volume was subcloned into an EcoR
V-digested, alkaline phosphatase-treated pBlueScript II
($K-) vector and transformed into E. coli strain XL2 Blue
MRF'. Recombinant clones from the first plating of the
library were selected for sequence analysis using T3 and
T7 primers."

3.85 3.140.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: malaria@itsa.ucsf.edu
For Annotation Data see http://medsfgh.ucsf.edu/id/CpTags/home.html
Seg primer: T3
Class: shotgun.
                                                                                                                                                                                                                                                                                                                 AQ411842 854 bp DNA GSS 12-MAY-2000 CG06065B CpIOWAgDNAl Cryptosporidium parvum genomic, DNA sequence. AQ411842.1 GI:4469566
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                                                                                               taacattagcgtgaaaaccactaagcttaacagtaatggcaccagtggtaataataaatt 2036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 854) Strong, W.B. and Nelson, R.G. Preliminary profile of the Cryptosporidium parvum genome: a expressed sequence tag and genome survey sequence analysis Mol. Blochem. Parasitol. 107 (1), 1-32 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Depts. of Medicine & Pharmaceutical Chemistry
San Francisco General Hospital-University of California,
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Pred. No. 0.00073;
0; Mismatches 152; Indels 0;
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Cryptosporidium parvum
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
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Box 0811, 3an Francisco, CA 94143-0811, USA
TTE1: 415 206 8846
Fax: 415 206 3353
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/organism="Cryptosporidium parvum"
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Matches 148; Conservative
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AUTHORS
TITLE
                                                                                             1977
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AQ411842
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AU053378 442 bp mRNA EST 28-APR-1999
AU053378 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium
discoideum cDNA clone SLI507, mRNA sequence.
AU053378 GI:4701860
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/clone_lib="Dictyostelium discoideum SL (H.Urushihara)"
                                                                                                                                                                              2015
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tggtatagcaaataccgatgcggttaccatcaaacagctcaaagacgccaagcctactt 1895
                                                                                      1896 aaacgcaggcgatggcatcagtattaatagtaataacggggatctagttgatagtagtgg 1955
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                                                                                                                                                                              1956 caatattaccaccccaacttataacattagcgtgaaaaccactaagcttaacagtaatgg
                                                                                                                                                                                                                                                                                            Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodal, Tsukuba, Ibaraki 305, Japan
Bmail: 402hu@sakura.cc.tsukuba.ac.jp
PROJECT - Dictyostelium discoideum cDNA project in Japan.
Location/Qualifiers
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Wacarozoa, Dictyostellida, Dictyostellum.
1 (bases 1 to 442)
Yoshino, R., Morio, T. and Tanaka, Y.
Poetlopmental cDNA in Dictyostellum discoideum
Unpublished (1997)
Contact: Hideko Urushihara
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40 c 28
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Email: jwatanabemanage.ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama.K., Suyama.A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library Gene 200 (1-2), 149-156 (1997).
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                                                                                                                                                                                                                                                                                                                                                              AU088475 500 bp mRNA EST 27-JAN-2001 AU088475 Sugano Malaria cDNA library Plasmodium falciparum cDNA clone XPFn7167, mRNA sequence.
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Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 500)
ctaataatgttgcaaatacctcagcaacagtcggcactgctcgtattaccgaagagaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The University of Tokyo, Department of Parasitology 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Watanabe, J., Sasaki, M., Suzuki, Y. and Sugano, S. 
Will.malaria: a database for a full-length enriched 
from human malaria parasite, Plasmodium falciparum 
Nucleic Acids Res. 29 (1), 70-71 (2001)
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/clone="xpEn7167"
/clone_lib="sugano Malaria cDNA library"
/dev_stage="erythrocytic stage"
1 5 2 c 73 g 149 t abothers
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Pred. No. 0.0011
                                                                                                                                                                                1697 ttggttttgctggtactaatgatggagttgatg 1729
                                                                                                                                                                                                              /organism-"Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Junichi Watanabe
Institute of Medical Science
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Fax: 81-3-5449-5410
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Best Local Similarity 52.9
Matches 117; Conservative
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AU088475
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This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
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                                                                                                                                                             AL197365.
AL197365.
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AL197365.
GSS; genome survey sequence.
Tetracdon nigroviridis.
Tetracdon nigroviridis.
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthopterygii; Percomorpha; Tetracdonidae; Tetracdonid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 989)
Roest-Collius, H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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t 41 others
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                                                    CNSOZHA4 989 bp DNA GSS 13-MAY-2000
Tetraodon nigroviridis genome survey sequence T7 end of clone
139021 of library G from Tetraodon nigroviridis, genomic survey
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/db_xref="taxon:99883"
/clone="139021"
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5; Mismatches 249;
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/note="Genoscope sequence
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1 (bases 1 to 590)

Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M., Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H., Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.
The Dictyostelium developmental CDNA project: generation and analysis of expressed sequence tags from the first-finger stage of
               AU039138 590 bp mRNA EST 29-7MAN 12523
AU039138 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum cDNA clone SSM436, mRNA sequence.
AU039138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="AX4" // Ab_xref="taxon:44689" // Ab_xref="taxon:44689" // Clone="SSM436" // Clone_lib="Dictyostellum discoideum SS (H.Urushihara)"
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University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: 402hu@sakura.cc.tsukuba.ac.jp
PROJECT - 'Dictyostellum discoideum cDNA project in Japan'.
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0.9%; Score 55.2; DB 107; Length 590;
Best Local Similarity 49.0%; Pred. No. 0.0017;
Matches 147; Conservative 0; Mismatches 153; Indels 0;
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78 c 39
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New nucleic acid encoding Moraxella catarrhalis outer membrane protein, useful in protective vaccines and for diagnosis
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200kDa outer membrane protein; antibacterial; immunogenic; infection;
otitis media; detection.
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N-PSDB; AAF59104.
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AAB69135
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M. catarrhalis str
Moraxella 200 kba
M. catarrhalis M56
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Haemophilus influe
Haemophilus influe
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Haemophilus influe
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1580.859 Million cell updates/sec
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                                                                                                                                                                                                                      Description
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**Sinsil/gcgdata/geneseq/geneseqp/AA1981.DAT:**

**Sinsil/gcgdata/geneseq/geneseqp/AA1981.DAT:**

**Sinsil/gcgdata/geneseq/geneseqp/AA1983.DAT:**

**Sinsil/gcgdata/geneseq/geneseqp/AA1984.DAT:**

**Sinsil/gcgdata/geneseq/geneseqp/AA1985.DAT:**

**Sinsil/gcgdata/geneseq/geneseqp/AA1987.DAT:**

**Sinsil/gcgdata/geneseq/geneseqp/AA1987.DAT:**

**Sinsil/gcgdata/geneseq/geneseqp/AA1989.DAT:**

**Sinsil/gcgdata/geneseq/geneseqp/AA1989.DAT:**

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**Sinsil/gcgdata/geneseq/geneseqp/AA1993.DAT:**

**Sinsil/gcgdata/geneseq/geneseqp/AA1993.DAT:**

**Sinsil/gcgdata/geneseq/geneseqp/AA1993.DAT:**

**Sinsil/gcgdata/geneseq/geneseqp/AA1999.DAT:**

**Sinsil/gcgdata/geneseq/geneseqp/AA1090.DAT:**
                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                              412676 seqs, 60623988 residues
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Listing first 45 summaries
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AAW04505
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Score

Result . 9 7675 7408 7405 7405 7219.5 1206 1205 1021 1021

Claim 1; Fig 4A-V; 247pp; English.

XX

The present invention describes an isolated and purified nucleic acid (1)

CC that encodes a 200 kba outer membrane protein of Moraxella catarrhalis.

CC The 200 kba outer membrane protein (II) has antibacterial activity and CC an be used in vaccines. (II), and its truncated versions, are used as can be used in vaccines (II), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarrhalis infections, particularly outlis media in humans. (II) is also used as antigen in immunoassays for detecting specific antibodies (Ab), and to generate Ab. (I) are used for recombinant production of (II) and its fragments are used as probes for identifying/cloning 200 kba protein consension of truncated versions of (II) reduces toxicity of the protein towards the Escherichia coli host. The present sequence represents the covards the Escherichia coli host. The present sequence represents the covards the Escherichia coli host. The present sequence represents the covards the strain QB 200kba protein, which is given in the coverement invention.

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Sequence 2053 AA;

ö 540 420 420 480 480 180 240 300 300 360 360 LNGSAYAQQITTKIEIGQTNKINNTLKGDALATGEASIAFGSLSKAQGSQAIAIGSVKPD 120 9 0; Gaps ISVKTTKLNSNGTSGNNKFSVSNAHDNNSLVTAKDLADYLNKVNETADSALPSFKVQNGD TTRITKKKIGFAGTNDGVDESKPYLDNEKLKVGNSTLNSGSLTVNNTTGNKQIQVGANGI · KFATVANNVANTSATVGTARITEEKIGFAGTNDGVDEQAPYLDKERLKVGRVEITTDSGI NRKITFKGDGDNNSNSVERGLGNTLTIKGDAQINALTEANIGVYTDGNCLKVKLAKELTG MNHIYKVIFNKATGTFWAVAEYAKSHGTGGGSCATGQVGSVRTLSFARIAALAVLVIGAT PNNGSNGNVGSHAKGNESIAIGGDVLAEGDASIAIGSDDLYLPKNLDLKNEFHKLIHGHE QATKQSSIAVGSNAKANAFAATAIGGNTVVNLGRGVALGFGSQILDRDNNTDASAYVPLG KTLADQYKATROGDSTDIFSIGNSNNNNSSIRRKIINVGAGSRDTDAVNVAQLKLVEELA Length 2053; 0; Indels 22; DB s; Score 10356; i; Pred. No. 0; 0; Mismatches Ouery Match 100.0%; Best Local Similarity 100.0%; Matches 2053; Conservative 0; 541 601 661 601 181 541 241 301 361 421 421 181 61 61 121 121 181 181 301 361 qq ŏ g ò q δ g οŽ g ò qq g οy δ qq ò g ò Ω ò ð

1020 840 900 QGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGRQTQAGNQSI AIGDNAQATGDQSIAIGTGNVVAGKHSGAIGDPSTVKADNSYSVGNNNQFTDATQTDVFG NENSVNAGGTKIDEKGISFVDANGQAKANTPVLSANGLDLGGKVISNVGKGTKDTDAANV QQLNEVRNLLGLGNDNADGNQVNIADIKKDPNSGSSSNRTVIKAGTVLGGKGNNDTEKLA AQTPDGTLAQMNVKSVINKEQVNDANKKQGINEDNAFVKGLEKAASDNKTKNAAVTVGDL IIKDEDKTRAASIVDVLSAGFNLQGNGEAVDFVSTYDTVNFANGNTTTAKVTYDDTSKTS TALQTFTVKKVDENDKADDTNAITVGKDGTSGKVNTLKLKGKNGLDIKTDKDGTVTFGIN GDNGKKQLGVKTIKLTETSTNGNATTFSTDDDHALVKASDIAGNLNTLAEEIHTTKGTAN NSNNAITVGKDINGKTFNTLKLKGENGVNITTNRATGTVTFGIDQSNGLTTPKLTVGSDT NGNRLVIEQVPSADGNSTKNIIKGLSPTLPSIASPSGRNIALGNTIEEKDKSNAASIDDV 1.681 1681 1741 1501 1561 1621 1621 1441 1501 1561 1261 1321 1321 1381 1381 1021 1081 1141 1141 1201 1201 1261 1441 1081 196 1021 781 901 901 961 781 721 q q ò g qq ŏ ò g ŏ qq ογ Q δý Db δ g ò ò g g ΩŽ οχ õ Q δ Db g οχ g οχ Q 셤 ò q ò δ

us-09-361-619-9.rag

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The present invention describes an isolated and purified nucleic acid (I) that encodes a 200 kba outer membrane protein of Moraxella catarrhalis.

The 200 kba outer membrane protein (II) has antibacterial activity and can be used in vaccines. (II), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarrhalis infections, particularly outlis media in humans. (II) is also used as antigen in immunoassays for detecting specific antibodies (Ab), and to generate Ab. (I) are used for recombinant production of (II) and its fragments are used as probes for identifying/cloning 200 kba protein genes from other strains, and for diagnostic detection of M. catarrhalis.

(I) makes possible production of large amount of recombinant immunogens. Expression of truncated versions of (II) reduces toxicity of the protein towards the Escherichia coli host. The present sequence represents the moral strains of the protein which is given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding Moraxella catarrhalis outer membrane protein, useful in protective vaccines and for diagnosis
                                                                                                                                                                  AVSVGASGAERRIQNVAAGEVSATSTDAVNGSQLYKATQSIANATNELDHRIHQNENKAN 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moraxella catarrhalis strain 4223; major outer membrane protein;
200kDa outer membrane protein; antibacterial; immunogenic; infection;
otitis media; detection.
                                              VGNNITVTESNSVALGSNSAISAGTHAGTQAKKSDGTAGTTTTAGATGTVKGFAGQTAVG
                                                              catarrhalis strain 4223 genomic 200kDa protein SEQ ID NO:7.
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The present invention describes an isolated and purified nucleic acid (I) that encodes a 200 kba outer membrane protein of Moraxala catarrhalis. The 200 kba outer membrane protein (II) has antibacterial activity and can be used in vaccines. (II), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarrhalis infections, particularly otitis media in humans. (II) is also used as antigen in immunoassays for detecting specific antibodies (Ab), and to generate Ab. (I) are used for recombinant production of (II) and its fragments are used as probes for identifying/cloning 200 kba protein genes from other strains, and for diagnostic detection of M. catarrhalis. (I) makes possible production of large amount of recombinant immunogens. Expression of tuncated versions of (II) reduces toxicity of the protein towards the Escherichia coli host. The present sequence represents the M. catarrhalis strain 4233 lambdababbablas force 200kba protein, which is
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200kDa outer membrane protein; antibacterial; immunogenic; infection;
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N-PSDB; AAF59100, AAF59101.
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                                                                                                                                                                                                                                           An approx. 200 kDa outer membrane protein (AAW04505) can be isolated from Moraxella catarrhalis otitis media strain 4223 by electroelution, or expressed from a gene (see also AAT38740) obtd. from a strain 4223 genomic library. Natural or recombinant outer membrane protein is useful as an immunogen to protect against infection by Moraxella, esp. M. catarrhalis. It can also be used to detect antibodies, esp. Go differential diagnosis abtween bacteria that cause similar symptoms, and also useful as a carrier for other antigens and used to raise antitumour antibodies for conjugation to therapeutic agents.
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N-PSDB; AAT38740.
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07-JUN-1995;
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                                           DGISINSNNGDLVDSSGNITTPTYNISVKTTKLNSNGTSGNNKFSVSNAHDNNSLVTAKD
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        DEQAPYLDKERLKVGRVEITTDSGINAGNHKITGLTNGIANTDAVTIKQLKDAKPTLNAG
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                                                                               HSGAIGDPSTVKADNSYSVGNNNQFTDATQTDVFGVGNNITVTESNSVALGSNSAISAGT 1885
                                                                                                                                                                                                                                        HAGTQAKKSDGTAGTTTTAGATGTVKGFAGQTAVGAVSVGASGAERRIQNVAAGEVSATS 1945
                                                                                                                                                                                                                                                                                          The present invention describes an isolated and purified nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moraxella catarrhalis strain Q8; major outer membrane protein;
200kDa outer membrane protein; antibacterial; immunogenic; infection;
otitis media; detection.
                               NTPVLSANGLDLGGKVISNVGKGTKDTDAANVQQLNEVRNLLGL---GNDNADGNQVNIA
                                                                                                                                                       SASGKHSVAIGFQAKADGEAAVAIGRQTQAGNQSIAIGDNAQATGDQSIAIGTGNVVAGK
                                                                                                                                                                                                         TDAVNGSQLYKATQSIANATNELDHRIHQNENKANAGISSAMAMASMPQAYIPGRSMVTG
                                                                                                               QKDGSKKALLATYNAAGQTNYVTNNPAEAIDRINEQGIRFFHVNDGNQEPVVQGRNGIDS
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28; that encodes a 200 kba outer membrane protein of Moraxella catarrhalis. The 200 kba outer membrane protein (II) has antibacterial activity and can be used in vaccines. (II), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarrhalis infections, particularly otitis media in humans. (II) is also used as antigen in immunoasays for detecting specific antibodies (Ab), and to generate Ab. (I) are used for recombinant production of (II) and its fragments are used as probes for identifying/cloning 200 kba protein genes from other strains, and for diagnostic detection of M. catarrhalis. (I) makes possible production of large amount of recombinant immunogens. Expression of truncated versions of (II) reduces toxicity of the protein towards the Escherichia coll host. The present sequence represents the exemplification of the present invention. 114 165 225 174 285 234 345 287 404 345 456 405 515 422 448 635 Gaps 58 56 VIGATLNGSAYAQQITTK-IEIGQTNKINNTLKGDALATGEASIAFGSLSKAQGSQAIAI GSVKPDPNNGSNGNVGSHAKGNESIAIGGDVLAEGDASIAIGSDDLYL-----PKN 226 ATAEAAYSLAVGLAAQATKQSSIAVGSNAKANAFAATAIGGNTVVNLGRGVALGFGSQIL DAVNVAQLKLVEELA-NRKITFKGDGDNNSNSVERGLGNTLTIKGDAQTNALTEANIGVV --TDGNGLKVKLAKELTGLTSV----SATNKITVSNTNNNAELQSGGLTFS-PITGTK -TDKTVYSIDGLKFTNDSNSIATKGTTRITKKKIGFAGTNDGVDESKPYLDNEKLKVGNS TLNSGSLTVNNTTGNKQIQVGANGIKFATVANNVANTSATVGTARITEEKIGFAGTNDGV 576 DEQAPYLDKERLKVGRVEITTDSGINAGNHKITGLTNGIANTDAVTIKQLKDAKPTLNAG LDLKNEFHKLIHGHEILKKIQTSTDGKIKYRRTRAQGHASTAVGAMSYAQGHFSNAFGTY 286 DRDNNTDASAYVPLGKTLADQYKATRQGDSTDIFSIGNSNNNNSSIRRKIINVGAGSRDT Indels 186; Length 1992 Query Match 71.5%; Score 7405; DB 22; Best Local Similarity 74.2%; Pred. No. 0; Matches 1549; Conservative 135; Mismatches 218; 1992 AA; Sequence 115 166 175 346 405 59 288 457 516 423 g QQ QQ ŏ g ò q δ g ò g ò qq ò ò ò g ŏ δ

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                                  ASPSGRNIALGNTIEEKDKSNAASIDDVLNAGFNLKNNGKDKDFVSTYDTVDFIDGNATT
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The present invention describes an isolated and purified nucleic acid (I) that encodes a 200 kDa outer membrane protein of Moraxella catarrhalis. The 200 kDa outer membrane protein (II) has antibacterial activity and can be used in vaccines. (II), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarrhalis infections, particularly otitis media in humans. (II) is also used as cantigen in immunoassays for detecting specific antibodies (Ab), and to generate Ab. (I) are used for recombinant production of (II) and its fragments are used as probes for identifying/cloning 200 kDa protein genes from other strains, and for diagnostic detection of M. catarrhalis. (I) makes possible production of large amount of recombinant immunogens. Expression of truncated versions of (II) reduces toxicity of the protein towards the Escherichia coli host. The present sequence represents the catarrhalis lesi 200kDa protein, which is given in the exemplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             membrane protein,
                                                                                                                                                                                                                                                                                                                                                                   strain Q8; major outer membrane protein; protein; antibacterial; immunogenic; infection;
                                                                                                        HSGAIGDPSTVKADNSYSVGNNNQFTDATQTDVFGVGNNITVTESNSVALGSNSAISAGT
              HAGTQAKKSDGTAGTTTTAGATGTVKGFAGQTAVGAVSVGASGAERRIQNVAAGEVSATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding Moraxella catarrhalis useful in protective vaccines and for diagnosis
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ò	HIYKVIENKATGTEWAVAEYAKSHSTGGSCATGOVGSVRTISFARIAAI.VIGAT 60	Qy	105
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qq	:      :	qq	103
Qy	121 P-NNGSNGNVGSHAKGNESIAIGGDVLAEGDASIAIGSDDLYLPKNLDLKNEFHK 174	ογ	116
qq	:	op ::	109
ΟŊ	175 LIHCHEILKKIOTSTDGKIKYRRTRAQCHASTAVGAMSYAQGHFSNAFCTYATAEAAVSL 234	ž d	115
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δo a	AVGLAAQATKQSSIAVGSNAKANAFAATAIGGNTVVNLGRGVALGFGSQILDRDNNTDAS 29	qq	121
<u>a</u> :	avgıtakaekgytialgsnaqaınygalalgadtrvdidyglalgygsqilnnnnnnk 29	QY	134
ò f	295 AYVPLGK TLADQYKATRGDSTDIFSIGNSNNNNSSIRRKIINVGAGSRDTDAVNVAQL 353 297 AVVDAGNAGNIKASKATNAG	QQ	127
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٥y	526 NTTGNKOLOVGANGIKFATVANNVANTSATVGTARITEEKIGFAGTNDGVDEQAPYLD 583	ογ	157
QQ		QQ ,	151
Qy	584 KERLKVGRVEITTDSGINAGNHKITGLTNGIANTDAVTIKQLKDAKPTLNAGDGISINSN 643	δλ	16(
qq	:: :    :    :          :   : :	qa	157
Qy	644 NGDLVDSSGNITTPTYNISVKTTKLNSNGTSGNNKFSVSNAHDNNSLVTAKDLADYLNKV 703	ΟŻ	160
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ò	704 NETADSALPSFKVONGDNSNNAITVGK-DINGKTENTLKLKGENGVNITINRATGTV 759	Οy	160
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Qy	818 RNIALGNTI-EEKDKSNAASIDDVLNAGFNLKNNGKDKDFVSTYDTVDFIDGNATTATVT 876	ΟŊ	160
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٥y	877 YDEANQTSKVAYDVNVDEKTIELTGDNGK-KQLGVKTIKLTETSTNGNATTFSTDDDHAL 935	Οy	161
qq		qq	187
Οy	936 VKASDIAGNINTLAEEIHTTKGTANTALQTFTVKKVDENDKADDINAITVGKDGT-SGK- 993	oy G	167
qo	860 vnakdiaenintlakeihttkgtadtalqtfkvkkdgatddetitvgkdgtgngkt 915	2 2	173
Οy	994 VNTLKLKGKNGLDIKTDKDGTVFFGINTQSGLKAGDSTTLNNNGLSIKNTASNEQIQVGA 1053	i d	199

vntlklkgengltvatnkdgtvtfgintgsglkagdsttlnkdglsiknpasnegiqvga GNNFTVSNPYSSYDTSKTSDVITFAGENGITTKVNKGVVRVGIDQTKGLTTPKLTVGNNN sgaslpfvvtdangkpingtdgkpqkaikgadgkyyhanangvpvdkdgkpitdadklan qsnaasvkdvlnvgfnlqtnhnqvdfvkaydtvnfvngtgaditsvrsadgtmsnitvnt KKLGETLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGTKIDEKGIS alaatdddgnv1ikakdgkfykaddlmpngslkagksasdaktptglslvnpnagkgstg ------GGKVISNVGKGT KDTDAANVQQLNEVRNLLGL --- GNDNADGNQVNIADIKKDPNSGSSSNRTVIKAGTVLG NPAEAIDRINEQGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAI INAGGKKITNIQSGEIAKNSHDAVTGGKIYDLKTELENKISSTAKTAQNSLHEFSVADEQ GKGIVINSQNGQNTITGLSNTLANVTNDKGSVRTTEQGNIIKDEDKTRAASIVDVLSAGF NLQGNGEAVDFVSTYDTVNFANGNTTTAKVTYDDTSKTSKVYYDVNVDDTTIEV-KDKKL GVKTTTLTSTGTGAN--KFALSNQATGDALVKASDIVAHLNTLSGDIQTAKGASQANNSA laahgkpldaghqvvaslggnsdaitltnikstlpgidtpntgnanaggagslpslsaag GKGNNDTEKLATGGVQVGVDKDGNANGDLSNVWVKTQKDGSKKALLATYNAAGQTNYVTN DGVKFAMVNNGVVGAGIDGTTRITRDEIGFTGTNGSLDKSKPHLSKD-FVDANGQAKANTPVLSANGLDL------1 1 1 1 

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                                                                                                                          Haemophilus adhesion protein HA2 (AAR99393) is associated with the formation of surface fibrils involved in adhesion to various host cells; it is also referred to hsf (Haemophilus surface fibrils). Its amino acid sequence was deduced from a genomic DNA clone (AAT41476) derived from Haemophilus influenzae type b strain C65. Large quantities of recombinant HA2 can be produced in transformed prokaryotic or eukaryotic host cells, for use in vaccines against influenzae infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QSSIAVGSNAKANAFAATAIGGNTVVNLGRGVALGFGSQILDRDNNTDA-----SAYVPL 299
                                                                                                                                                                                                                                                                                                                                                    ---vsaynnvefitgdkntldvvltakengkttevkftpktsvikekdgklftgke--- 288
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                                                                                                     59 dpvvrtapvlsfhsdkegtgekevtensnwgiyfdnkgvlkagaitlkagdnlkikgntd
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                                                                                                                                                                                                                                                                                                                 GGDVLAEGDASIAIGSDDL------YLPKNLDLKNEFHKLIHGHEILKK
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                                                                                                                                                                                                                                                                       dstlpdavtntgvlssssftpndvektra---atvkdvlnagwnikgaktaggnvesvdl
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114;

Gaps

Indels 856; Length 2353;

Query Match
Best Local Similarity 23.8%; Pred. No. 4.2e-45;
Matches 627; Conservative 295; Mismatches 853;

1935 1688 1995 1737 2047 1786 2091	2145 adgkv 1898 AGTTT 2183 adkwy 1946 TDAVI 191: 2243 tdain 2003 VTGG	AAB23860 s ID AAB23860 s AAC AAB23860; XX AAB23860; XX AAB23860; XX AAB23860; XX AAB29860; XX AAB29860; XX AAB29860; XX AAB29860; XX Hia, adhes KW AAB150ACE KW AAB150ACE KW AAB150ACE KW AAB150ACE KW AAB150ACE		WPI; 2000 N-PSDB; AA Novel nuc. use as ant infection Claim 1; 1 The preset (Hia) prof Hia genes
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		Sptddgandalkagdtltlkagknlkvkrdgknitfalandlsvksatvsdklsigtngn KGIVINSONGONTITGLSNTLANVTNDKGSVRTTEGGNIIKDEDKTR	DALVKASDIVAHLNTLSGDIQTAKGASQANNSAGIVDADGNKVIYDSTDNKYY	
		1212	1366 DALVKASDIVA 1614 nglrdavid 1619 QAKNDG-TVD 1619   1   1   1668 -kandgsitvk 1468 KQGINEDNAFV 1717 kfv 1528 KGGTDTNKLT	
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The present sequence represents a Haemophilus influenzae adhesin (Hia) protein from the type c Haemophilus influenzae strain APT. Hia genes and proteins have antiinflammatory, auditory and antibacterial activities, and can be used in the production of a vaccine. An
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                                                                                                                                                                                                                                                                                                                         : :: ||:| : | : | : | : | : | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | indicates | 
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hymunogenic composition comprising an Hia gene, a polypeptide encoded by an Hia gene, or a recombinant Hia polypeptide is useful for inducing protection against disease caused by Haemophilus strains in a susceptible host, preferably a human. An Hia protein is useful as an antigen, in immunogenic preparations including vaccines, as a carrier for other immunogenic preparations including vaccines, as a carrier is useful for treating diseases caused by the infection of Haemophilus influenzae such as meninglis, epiglotitis, septicaemia and oitis media. Recombinant production of Hia favours high recovery of the protein compared to the low recovery of native protein from Haemophilus influenzae species. A truncated protein has a significantly higher amount of recovery than a full-length protein. 2411 AA; Sequence \$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$**%** 

115; VNNTTGNKQIQVGANGIKFATVANNVANTSATVGTARITEEKIGF-AGTNDGVDEQAPYL 582 583 DK--ERLKVGRVEITTDSGINAGNHKITGLTNGIANT-----DAVTIKQLKDAKPTL 632 NAGDGISINSNNGDLVDSSGNITTPTYNISVKTTKLNSNGTSGNNKFSVSNAHDNNS--- 689 476 575 674 357 EELANRKITFKGDGDNNSNSVERGLGNTLTIKGDAQTNALTEANIGVVTDGNGLKVKLAK 416 TDGKIKYRRTRAQGHASTAVGAMSYAQGHFSNAFGTYATAEAAYSLAVGLAAQATKQSSI 248 249 AVGSNAKANAFAATAIGGNTVVNLGRGVALGFGSQILDRDNNTDA-----SAYVPLG--- 300 ---angqngdfatvasgtnvtfesgdgttas----vtkdtngng1tvkydakvgdglkf 379 380 dsdkkivadttaltvtggk--vaeiakedd----kkklvnag------dlv 418 188 KGDALATGEASIAFGSLSKAQGSQAIAIGSVKPDPNNGSNGNVGSHAKGN-ESIAIGGDV 145 232 59 dpvvrtapvlsfhsdkegtgekevtensnwgiyfhnkgvlkagaitlkagdnlkikgstn 118 Gaps 62 58 ELTGLTSVSATNKITVSNTNNNNAELQSGGLTFSPITGTKTDKTVYSIDGLKFTNDSNSI 619 kqadeviftgagaatvtsksengkhti---tvsvaetkadsglekdgdtiklkvdngnt-ATKGTTRITKKKIGFAGTNDGVDESKPYL---DNEKLKVGNST---LN-----SGSLT || || || : : : : : : |
pdavtntgvlsssftpndvektra---atvkdvlnagwnikgaktaggnvesvdl---v LAEGDASIAIGSDDL------YLPKNLDLKNEFHKLIHGHEILKKIQTS ----KTLADQYKATRQGDSTDIFSIGNSNNNNSSIRRKIINVGAGSRDTDAVNVAQLKLV | | ::|| | sesftyslkkdltdltsvateklsfgangdkvditsdanglklaktgngnvhlngldstl 1 MNHIYKVIFNKATGTFMAVAEYAKSHSTGGGSCATGQVGSVRTLSFARIAALA-----880; Length 2411; Indels -----VLVIGA-11.6%; Score 1205; DB 21; Similarity 23.6%; Pred. No. 4.8e-45; 30; Conservative 299; Mismatches 863; GSAYAQQI----Query Match Best Local Simi Matches 630; 419 417 477 524 479 328 233 189 301 87 179 146 287 63 54 q qq Qγ g ò qq S B õ ολ Op oy Db QY Db òγ g ò qq οy qq ò Q q ò ò

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::: atdadrgkv	NNAITVCKDTNGKTFNTLKLK-GE :              1  1dednptdngkddalkagdtltfkagk	ta ;	PSIASPSGRNIALGNTIEEKDKSNAASIDDVLNAG    :   : : :                psagaksshvdlnvdatkksnaasiedvlrag	DEANQTSKVAYDVNVDEI : :     : tqkadgkgadvk1ga	ALVKASDI	FTVKKVDEN	NTLKLKGKNGL         ansvnoklvnaeqlatalnnl	TASNEQIQVGADG	knikvkgsekdftyslgdtltgltsi	LSKDGINAGGKKITNIQS ::    :    :   ::  isvtkdgisagnkeitnvks	-NSHDAVTGGK	rraa	rakradnsch :        saktdnngkh	TSDVITFAGENG	fnavttdattaggtn		ativkvenddsatiddsprudgandaik	TPKLTVGNNNGKGIVINSQNGQN	KISIgengnkvnie	LSNTLANVINDKGSVRTTEQGNIRKDEDKIRAASIVOLSAGENEGG 	- 1	:     ::  :veskdngkrtev		vtetdgkdegnglvtak	DGNKVIYDSTDNKYYQAKNDG
 etvktg	FKVQNGDNS   :    vktenltts	-TNRATGTVTFGIDQSNGLT   : :   :   :     ktakvsdtltiggntptggt	TKNI-IKGLSPTLPSIASPSGR    : :  :           sknvylkgiattltepsagakssh	IDGNATTATVTY   :        tddstqtttvtv	TNGNATTESTDDDHALVKASDI	nngalvseddyndrysgrycanar. -EIHTTKGTANTALQTFTVKKVDEN ::                   :   tsvnfkngnattatvskdngn		-NNGLSIKN	agkn1kvkqseko	LDKSKPH-     : aagtdasngnt		tkpatg	TELENKISS  :    : knanevefvgkngatv:	NPYSSYDTSK	vdatkgasvakge		aindaativk		andlsvksatvsd	NDKGSVRTTEGGNI. :  :	NGNTTTA	:  : :      dfvsgdkdttsvt	GAN-KFALSNQAT	kelkdannngvtv	A
  tvgnngtavtkggf	LVTAKDLADYLNKVNETADSALPS 	GVNIT	SSADGNSTKNI-IKGLSPTL-     : :  : :  : -tadasqsknvylkgiattlt	FNLKNNGKDKDFVSTYDTVDFIDGNATTATVTYDEANQTSKVAYDVNVDEKTIELTGDNG	KKQLGVKTIKLTETSTNGNATTFSTDDDH	AGNENTEA	DTNAITVGKDGT	YGDST	gesegetdqevkagdkvtfkag	TRITRDEIGFTGTNGS       :         :   tvinkdgltitlanga	GEIAK	atqpaantaevakq	etgdkefhaav	- EFSVADEOGNNFTVSNPYSSYDTSK	:   :     1klkvdntdgnnllt	LT	tetdkkkvatvgdvak		knlkvkrdgknitfalandl	-TITG	- NGEAYDEVSTYDTV	:   :     :   sannqvenidfvatydtvdfv	KLGVKTTTLTSTGTG	kigaktsvikdhngklftgkelkdannngvtv	IQTAKGASQANNSAGYVD- ::    :  :
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Novel nucleic acid encoding Hemophilus influenzae adhesin protein, for use as antigens and vaccines and for treating Hemophilus influenzae

use as ant infection

Klein MH;

16-MAR-2000; 2000WO-CA00289.

21-SEP-2000.

99US-0268347

16-MAR-1999;

(CONN-) CONNAUGHT LAB LTD. Loosmore SM, Yang Y, WPI; 2000-618897/59. N-PSDB; AAA92495.

7			i	
Q D	<pre>1691 vktt-ganggnddfatvasgtnvtfadgngttaevt</pre>	kandgsitvkynvkvadg	1743	
ογ	1435DKLVAQAQTPDGTLAQMNVKSVINKEQ		48	
DP	1744	fvdasglada	1785	
ò	Qy 1487 DNKȚKNAAVTVGDLNAVAQTPLIFAGDIGTTAKKLGETLIKGGQTDINKLTDNNIGVVA	GOTDINKLTDNNIGVVA	1546	
QQ	1786 lnklswta-tagkegtgevdpansaggevkagdk		1831	
δ	1547	DANGQAKANTPV	1592	
qq	Db 1832 sgkdftyslkkelkdltsvefkdanggtgsestkitkdgltitpangagaagantanti	   pangagaagantantis	1891	
δ	1593 LSANGLDLGGKVISNVGKGTK	-DTDAANVQQLNEVRNLLGLGNDN	1636	
QQ	:: : :	::         aykdltnldekgadnnp	1951	
ολ	Qy 1637ADGNQVNIADIKKDPNSGSSSNRTVIKAGT-	VIKAGTVLGG	1670	
QQ		:   kfksgnginvsgktlng	2011	
ŏ	1671VQVG	VWVKTQ	1706	
QQ	Db 2012 trvitfelakgevvksneftvknadgsetnlvkvgdmyyskedidpatskpmtg	: ::   : idpatskpmtgkte	2068	
δy	1707 K	NEQGIRFFHVNDGNQEP	1755	
QQ	:    :         Db 2069 kykvengkvvsangsktevtltnkgsgyvtgngvadajaksgfel	:   aksgfel	2113	
δ	1756 VVQGRNGIDSSASGKHSVAIGFQAK	ADGEAAVAIGRQTQAGNQSIAIGD	1804	
q	2114		2164	
ò	1805 NAOA	NSY SVGNNNOFTDATOT	1856	
7 g	:     : 2165 stdangdkvtttfv	gkwye1	2210	
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Oy Db	Oy 1962 ANATNELDHRIHQNENKANAGISSAMAMASMPQAYIPGRSMVTGGIATHNGQGAVAVGL         ::::    :  :  :   Db 2320 agqvnnlegkvnkvgkradagtasalaasqlpqatmpgksmvalagssygggnglaigv	GGIATHNGQGAVAVGLS :::    : : :  iagssyqgqnglaigvs	2021 2379	
ΟŊ	2022			
QQ	Db 2380 risdngkviirlsgtnsqgktgvaagvgygw 2411			
REST AABJ ID XX XX XX XX	RESULT 9 AAB23856 ID AAB23856 standard; Protein; 1104 AA. XX XX AC AAB23856; XX XX XX XX XX XX XX XX XX XX XX XX XX			
DE X	DE Haemophilus influenzae adhesin (Hia) protein from NTH1. xx	m NTHi strain 29.	•	
K K K K K	Hia; adhesin; Haemophilus influenzae adhesin; NTH1; in non-typeable Haemophilus influenzae; antiinflammatory antibacterial; meningitis; epiglottitis; septicaemia; diagnosis; immunogenic; antigen.	<pre>Hi; infection; vac atory; auditory; emia; otitis media</pre>	cine; 1;	
×× 00 ××	AX OS Haemophilus influenzae. vy			
A N	AA PN WO200055191-A2.			

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The present sequence represents a Haemophilus influenzae adhesin (Hia) protein from the non-typeable Haemophilus influenzae (NTH1) strain 29. Hia genes and proteins have antiinflammatory, auditory and antibacterial activities, and proteins have antiinflammatory, auditory and antibacterial activities, and can be used in the production of a vaccine. An immunogenic composition comprising an Hia gene, a polypeptide encoded by an Hia gene, or a recombinant Hia polypeptide is useful for inducing protection against disease caused by Haemophilus strains in a susceptible host, preferably a human. An Hia protein is useful as an antigen, in immunogenic preparations including vaccines, as a carrier of or other immunogens, and in the generation of diagnostic reagents. Hia is useful for treating diseases caused by the infection of Haemophilus influenzae such as menigitis, epiglottitis, septicaemia and otitis media. Recombinant production of Hia favours high recovery of the low recovery of native protein from Haemophilus influenzae species. A truncated protein has a significantly higher amount of recovery than a full-length protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 ssflvadntaat----vgnlrklgwvlsskngtrne--ksygvkgade-----
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1264 DEDKTRAASIVDVLSAGFNLQGNGEAVDFVSTYDTVNFANGNTTTAKVTYDDTSKTSKVV 1323

293 gkdtnkvditsdanglklaktgngnggngnvhlngiastl----tdtitgmttgasngva 348

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IGRQTQAGNQSIAIGDNAQATGDQSIAIGTGNVVAGKHSGAIGDPSTV--KADNSYSVGN 1846
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ngastkitkdgltitsangangaaatdadkikvasddisagnkavknvvsglkkfgdanf
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                                                             409 vdvtglpvqyvtedgktvvkvdnkyyeakqdgsadmdkkvengelaktkvklvsasgqnp
                                                                                           1357 FALSNQATGDALVKASDIVA--HLNTLSGDIQTAKGASQANNSAGYVDADGNKVI----
                                                                                                                  469 vkisnvaeg---teendavsfkqlkalq-ekqvtltasnayanggn-dadggkatqtlnn
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Hia; adhesin; Haemophilus influenzae adhesin; NTH1; infection; vaccine; non-typeable Haemophilus influenzae; antiinflammatory; auditory; antibacterial; meningitis; epiglottitis; septicaemia; otitis media;
                                                                                                            Haemophilus influenzae adhesin (Hia) protein from NTHi strain K22
                AAB23859 standard; Protein; 1104 AA
                                                                                   (first entry)
                                                                                  17-JAN-2001
                                                   AAB23859;
AAB23859
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The present sequence represents a Haemophilus influenzae adhesin (Hia)

protein from the non-typeable Haemophilus influenzae (NTH1) strain K22.

protein from the non-typeable Haemophilus influenzae (NTH1) strain K22.

Hia genes and proteins have antiinflammatory, auditory and antibacterial
activities, and can be used in the production of a vaccine. An
activities, and can be used in the production of a vaccine. An
immunogenic composition comprising an Hia gene, a polypeptide encoded
by an Hia gene, or a recombinant Hia polypeptide is useful for inducing
protection against disease caused by Haemophilus strains in a
protection against disease caused by Haemophilus strains in a
autigen, in immunogenic preparations including vaccines, as a carrier
antigen, in immunogenic preparations including vaccines, as a carrier
for other immunogenic acused by the infection of Haemophilus
is useful for treating diseases caused by the infection of Haemophilus
media. Recombinant production of Hia favours high recovery of the
influenzae species. A truncated protein has a significantly higher
amount of recovery than a full-length protein. for Novel nucleic acid encoding Hemophilus influenzae adhesin protein, iuse as antigens and vaccines and for treating Hemophilus influenzae infection Claim 1; Fig 23; 275pp; English. Œ, diagnosis; immunogenic; antigen. Klein 16-MAR-2000; 2000WO-CA00289. (CONN-) CONNAUGHT LAB LTD. Haemophilus influenzae SM, Yang Y, WPI; 2000-618897/59. N-PSDB; AAA92498. 1104 AA; WO200055191-A2. 16-MAR-1999; 21-SEP-2000 Sequence Loosmore 

50; 1044 ASNEQIQVGADGVKFAMVNNGVVGAGIDGTTRITRDEIGFTGTNGSLDKSKPHLSKDGIN 1103 1104 AGGKKITNIQSGEIAKNSHDAVTGGKIYDIKTELENKISSTAKTAQNSLHEFSVADEQGN 1163 NFTVSNPYSSYDTSKTSDVITFAGENGITTKVNKG------VVRVGIDQTKGLTTPKLTV 1217 246 292 925 TTESTDDDHALVKASDIAGNLNTLAEEIHTTKGTANTALQTFTVKKVDENDKADDTNAIT 984 872 TATVTYDEANQTSKVAYDVNVDEKTIELTGDNGKKQLGVKT-----IKLTETSTNGNA 924 985 VGKDGTSGKVNTLKLKGKNGLDI-KTDKDGTVTFGINTQSGLKAGDSTTLNNNGLSIKNT -----vlftgsgaatvssskdgkhtitisvtkgsfaevktdattgg-----Indels 390; Length 1104; 99 ssflvadntaat----vgnlrklgwvlsskngtrne--ksyqvkqade-----9.9%; Score 1021; DB 21; llarity 27.5%; Pred. No. 2.3e-37; Conservative 163; Mismatches 402; ----gvnadrgkvkaeden--gadvd-----Similarity Best Local Sin Matches 363; Query Match 183 141 q g δλ 셤 ò g δ g ò õ

Hia; adhesin; Haemophilus influenzae adhesin; NTH1; infection; vaccine; non-typeable Haemophilus influenzae; antiinflammatory; auditory; antibacterial; meningitis; epiglottitis; septicaemia; otitis media; diagnosis; immunogenic; antigen.

Haemophilus influenzae adhesin (Hia) protein from NTHi strain M407.

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GNNNGK------GIVI-----NSQNGQNTITGLSNTLANVTNDKGSVRTTEQGNIIK 1263
                                                                DEDKTRAASIVDVLSAGFNLQGNGEAVDFVSTYDTVNFANGNTTTAKVTYDDTSKTSKVV 1323
                                                                                                                                  -----VNVDDTTIEVK-----DKKLG----VKTTTLTSTGTGANK 1356
                                                                                                                                                                                                   1357 FALSNQATGDALVKASDIVA--HLNTLSGDIQTAKGASQANNSAGYVDADGNKVI---- 1409
                                                                                                                                                                                                                                                                                                                                                                                                        GTTAKKLGETLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSV----- 1565
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                                                                                                                                                                    409 vdvtglpvgyvtedgktvvkvdnkyyeakgdgsadmdkkvengelaktkvklvsasgqnp 468
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Novel nucleic acid encoding Hemophilus influenzae adhesin protein, f use as antigens and vaccines and for treating Hemophilus influenzae

Claim 1; Fig 21; 275pp; English.

infection

Klein MH;

N-PSDB; AAA92496

(CONN-) CONNAUGHT LAB Loosmore SM, Yang Y, WPI; 2000-618897/59.

16-MAR-1999;

16-MAR-2000; 2000WO-CA00289.

Haemophilus influenzae.

WO200055191-A2

21-SEP-2000

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The present sequence represents a Haemophilus influenzae adhesin (Hia) protein from the non-typeable Haemophilus influenzae (NTHi) strain M407. His genes and proteins have antiinflammatory, auditory and antibacterial activities, and can be used in the production of a vaccine. An immunogenic composition comprising an Hia gene, a polypeptide encoded by an Hia gene, or a recombinant Hia polypeptide is useful for inducing protection against disease caused by Haemophilus strains in a susceptible host, preferably a human. An Hia protein is useful as an antigen, in immunogenic preparations including vaccines, as a carrier for other immunogenic preparations including vaccines, as a carrier for other immunogenic preparations including vaccines, as a carrier is useful for treating diseases caused by the infection of Haemophilus influenzae such as meningitis, epiglottitis, septicaemia and otitis media. Recombinant production of Hia favours high recovery of the low recovery of native protein from Haemophilus influenzae species. A tunncated protein has a significantly higher amount of recovery than a full-length protein.
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llarity 28.8%; Pred. No. 3.2e-36;
Conservative 139; Mismatches 341;
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AAB23857 standard; Protein; 1004

RESULT 11

AAB23857

(first entry)

17-JAN-2001 AAB23857;

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RES	RESULT 12	
AAB2 ID	.23854 AAB23854 standard; Protein; 1002 AA.	
X X	AAB23854;	
YY I	17-JAN-2001 (first entry)	
DE	Haemophilus influenzae adhesin (Hia) protein from NTHi strain 33.	
XX	Hia; adhesin; Haemophilus influenzae adhesin; NTHi; infection; vaccine;	

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The present sequence represents a Haemophilus influenzae adhesin (Hia)

protein from the non-typeable Haemophilus influenzae (NTH1) strain 33.

the protein from the non-typeable Haemophilus influenzae (NTH1) strain 33.

Hia genes and proteins have antiinflammatory, auditory and antibacterial activities, and can be used in the production of a vaccine. An activities, and can be used in the production of a vaccine. An immunogenic composition comprising an Hia gene, a polypeptide encoded immunogenic composition compressed by Haemophilus strains in a protection against disease caused by Haemophilus strains in a protection against disease caused by Haemophilus strains in a carrier antigen, in immunogenic preparations including vaccines, as a carrier antigen, in immunogenic preparations including vaccines, as a carrier for to other immunogenic acused by the infection of Haemophilus influenzae such as meningitis, epiglottitis, septicaemia and ottis media. Recombinant production of Hia favours high recovery of the low recovery of native protein from Haemophilus influenzae species. A truncated protein has a significantly higher amount of recovery than a full-length protein.
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use as antigens and vaccines and for treating Hemophilus influenzae
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non-typeable Haemophilus influenzae; antiinflammatory; auditory; antibacteria; meningitis; epiglottitis; septicaemia; otitis media; diagnosis; immunogenic; antigen.
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9.2%; Score 952; DB 21; Length 1002;
Best Local Similarity 28.5%; Pred. No. 2.2e-34;
Matches 324; Conservative 138; Mismatches 319; Indels 356;
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                                                                                      Haemophilus influenzae
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N-PSDB; AAA92493.
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1339 KLGVKTTTLTSTGTGANKFALSNQATGDALVKASDIVAHLNTLSGDIQTAKGASQANNSA 1398

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WO9812331-A1
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Hia; adhesin; Haemophilus influenzae adhesin; NTH1; infection; vaccine; non-typeable Haemophilus influenzae; antlinflammatory; auditory; autibacterial; meningitis; epiglottitis; septicaemia; otitis media; diagnosis; immunogenic; antigen.

Haemophilus influenzae adhesin (Hia) protein from NTH1 strain K9

(first entry)

17-JAN-2001

AAB23858;

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1851 TDATQTDVFGVGNNITVTESNSVALGSNSAISAGTHAGTQAKKSDGTAGTTTTAGATGTV 1910
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                                                                                                                                                    RAASIVDVLSAGFNLQGNGEAVDFVSTYDTVNFANGNTTTAKVTYDDTSKTSKVVYDVNV 1328
                                                                                                                          gskgyngsdslgvmyddgngvfklslnmtalttslan----tfakldasnltddsnke 1533
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|-----dptsavnrgqlntvidnvqnnfngvng
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1103 NAGGKKITNIQSGEIAKNSHDAVTGGKIYDLKTELENKISSTAKT-AQNSLHEFSVADEQ
                GNNFTVSNPYSSYDTSK----TSDVITFAGENGITTKVNKGVVRVGIDQTKGLTTPKLTV
                                                                   GNN - - NGK - - - GIVINSQNG - - - - QNTITGLSNTLANVTNDKGSVRTTEQGNIIKDEDKT
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for

Novel nucleic acid encoding Hemophilus influenzae adhesin protein, fuse as antigens and vaccines and for treating Hemophilus influenzae infection

MH; Klein

Yang Y,

Loosmore SM,

WPI; 2000-618897/59. N-PSDB; AAA92497.

16-MAR-2000; 2000WO-CA00289

Haemophilus influenzae.

WO200055191-A2

21-SEP-2000

99US-0268347

16-MAR-1999;

(CONN-) CONNAUGHT LAB

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The present sequence represents a Haemophilus influenzae adhesin (Hia)

C protein from the non-typeable Haemophilus influenzae (NTH1) strain K9.

C protein from the non-typeable Haemophilus influenzae (NTH1) strain K9.

C Hia genes and proteins have antiinflammatory, auditory and antibacterial

c activities, and can be used in the production of a vaccine. An

c activities, and can be used in the production of a vaccine. An

c immunogenic composition comprising an Hia gene, a polypeptide encoded

c immunogenic composition comprising an Hia polypeptide is useful for inducing

c protection against disease caused by Heemophilus strains in a

c susceptible host, preferably a human. An Hia protein is useful as an

c antigen, in immunogenic preparations including vaccines, as a carrier

c for other immunogenic preparations including vaccines, as a carrier

c for other immunogenic acused by the infection of Haemophilus

is useful for treating diseases caused by the infection of Haemophilus

c influenzae such as meningitis, epiglottitis, septicamila and oithis

c media. Recombinant production of Hia favours high recovery of the

protein compared to the low recovery of native protein from Haemophilus

c influenzae species. A truncated protein has a significantly higher

c amount of recovery than a full-length protein.
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Best Local Similarity 25.1%; Pred. No. 1.1e-23;
Matches 315; Conservative 162; Mismatches 438;
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AAB23858 standard; Protein; 1094

AAB23858 ID AAB2 XX

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Search completed: September 13, 2001, 12:37:48 Job time: 82104 sec

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MORAXELLA CATARRHALIS OUTER MEMBRANE PROTEIN-106 POLYPEPTIDE, GENE SEQUENCE AND USES THEREOF
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Sequence 17,
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/968,685A

FILING DATE: NO. 6214981ember 12, 1997

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: BAIGWIN, GETAIDIN:

REGISTRATION NUMBER: 31,232

REFERENCE/DOCKET NUMBER: 7969-060

TELEPRAN: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 71.0%; Score 7357; DB 4; 18est Local Similarity 70.6%; Pred. No. 0; Matches 1571; Conservative 120; Mismatches 261;
                                 US-08-719-641-2
US-08-169-927-2
US-09-377-155-15
US-09-377-155-9
US-09-377-155-9
US-09-377-155-5
US-09-377-155-5
US-09-377-155-13
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/08968685A Patent No. 6214981 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: TUCKER, KENNETH
APPLICANT: PLOSILA, LAURA
TITLE OF INVENTION: MORAXELL
TITLE OF INVENTION: PROTEIN-
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2123 amino acids
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTER:STICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 11.6%; Score 1206; DB 4; Length 2353; Best Local Similarity 23.8%; Pred. No. 5.1e-64; Matches 627; Conservative 295; Mismatches 853; Indels 856
                                                                                                                                               APPLICANT: DENK, Ian Richard Anselm
APPLICANT: DENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: U5/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1998-12-14
                                                                                                      Sequence 33, Application US/09377155 Patent No. 6197312
                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Haemophilus influenzae US-09-377-155-33
                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 33
                                                                                                                                      GENERAL INFORMATION:
2050 GFHF 2053
                            2120 GFHF 2123
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LKFTNDSNSIATKGTTRITKKKIGFAGTNDGVDESKPYL---DNEKLKVGNST---LN--
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1270 AASIVDVLSAGFNLOG------DTSKT
                QAKNDG--TVDKTKEVAK-----DKLVAQA---QTPDGTLAQMNVKSVINKEQVNDANK
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Sequence 1, Application US/08913942

GENERAL INFORMATION:
APPLICANT: St. Geme, Joseph
APPLICANT: Barenkamp, Stephen J.
TITLE OF INVENTION: HAEMOPHILUS ADHESION PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 DPVVRTAPVLSFHSDKEGTGEKEVTENSNWG1YFDNKGVLKAGAITLKAGDNLKIKQNTD 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MNHIYKVIFNKATGTFMAVAEYAKSHSTGGGSCATGQVGSVRTLSFARIAALA----- 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245 QSSIAVGSNAKANAFAATAIGGNTVVNLGRGVALGFGSQILDRDNNTDA----SAYVPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNTLKGDALATGEASIAFGSLSKAQGSQAIAIGSVKPDPNNGSNGNVGSHAKGN-ESIAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----YLPKNLDLKNEFHKLIHGHEILKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 ---VSAYNNVEFITGDKNTLDVVLTAKENGKTTEVKFTPKTSVIKEKDGKLFTGKE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IQTSTDGKIKYRRTRAQGHASTAVGAMSYAQGHFSNAFGTYATAEAAYSLAVGLAAQATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -- NNDTNKVT------SNTATDNTDEGNG------LVTAKAVID-AVNKAGWRVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2353;
                                ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPERENCE/DOCKET NUMBER: A-61053-1/RFT/RMS/DAV TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                           Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 23.8%; Pred. No. 5.1e-64;
Matches 627; Conservative 295; Mismatches 853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 -TLNGSAYAQQI------TTKIEIG-----
                                                                                                                                                                                                                                                                    29-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/409,995
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/4031
FILING DATE: 22-MAR-1996
                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 GGDVLAEGDASIAIGSDDL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39,054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 22-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 2353 amino acids
amino acid
                                                                                                                       COUNTRY: United States ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Vance, Dolly A. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS LENGTH: 2353 amino ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein US-08-913-942-4
                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr Hoh
                                                                                   San Francisco
California
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linea
                                                                                                                                                                                                                                                                                                                            FILING DATE: 29
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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419	VTD 406     KQD 470	IDG 466    KDG 508	N 518     NRH 567	GTN 572   STK 610	DAVTI 622        DGDTI 667	SVS 682 :  TVK 712	GKT 736   LKA 765	TVG 777 : NIT 825	SNA 834     SNA 879	VDE 894 : IGA 937	941 SGW 991	974 DVN 1047	1005 NLS 1103	VKF 1058 : ITL 1163	TNI 1112    : TNV 1219	NSL 1152   NGK 1270	TSDVI 1183  :  TTDAT 1330	1211
:: ::  ::    :DDKKKLVNAG	SNSVERGLGNTLTIKGDAQTNALTEANIGVVTD 	INAELQSGGLTFSPITGTKTDKTVYSIDG 	DESKPYLDNEKLKVGNSTLN- 	ANNVANTSATVGTARITEEKIGF-AGTN:: :       -	KADCGLEK	TTPTYNISVKTTKLNSNGTSGNNKFSVS 	SALPSFKVQNGDNSNNAITVGKDTNGKT 	-TNRATGTVTFGIDQSNGLTTPKLTVG   : :   :	'LPSIASPSGRNIALGNTIEEKDKSNA         :   :       'LTEPSAGAKSSHVDLNVDATKKSNA	DGNATTATVTYDEANQTSKVAYDVN 	STNGNATTESTDDDHALVKASDI 	AGNLNTLAEEIHTTKGTANTALQTFTVKKVDEN      :	GTSGKVNTLKLKGKNGL	NGLSIKNTASNBOIQVGADGVKF   :         :   KNLKVKQSEKDFTYSLQDTLTGLTSITL	GTTRITRDEIGFTGTNGSLDKSKPHLSKDGINAGGKKITNI 	-EIAKNSHDAVIGGKIYDLKTELENKISSTAKTAQNSL         : :         : :	-EFSVADEGGNNFTVSNPYSSYDTSKTS :   :         : IKLKVDNTDGNNLLTVDATKGASVAKGEFNAVTT	
:   :   :   :   :   :   :   :   :   :	LKLVEELANRKITFKGDGDNNSNSVERGLGNTLTIKGD 	GNGLKVKLAKELTGLTSVSATNKITVSNTNNNNAELQSGGLTFSPITGTKTDKTVYSIDG 	LKFTNDSNSIATKGFTRITKKKIGFAGTNDGVDESKPYLDNEKLKVGNSTLN 	SGSLTVNNTJGNKQIQVGANGIKFATVANNVANTSATVGTARITEEKIGF-AGTN	DGVDEQAPYLDKERLKVGRVEITTDSGINAGNHKITGLTNGIANT	KQLKDAKPTLNAGDGISINSNNGDLVDSSGNITPPTYNISVKTTKLNSNGTSGNNKFSVS 	LVTAKDLADYLNKVNETAD :     :  :  DKKVATVKDVATAIN	FNTLKLK-GENGVNITTPKLTVG 	SDTNGNRLVIEQVPSADGNSTKNI-IKGLSPTLPSIASPSGKNI   :        :   :   :         STADGLNFAKETADASGSKNVYLKGIATTLTEPSAGAKSSH	ASIDDVLNAGFNLKNNGKDKDFVSTXDTVDFIDGNATTATVTYDEANQTSKVAYDVNVDE    :  :  : ::  ::  :  :  :  :  ASIEDVLRAGWNIQGNGNNVDYVATYDTVNFTDDSTGTTTVTVTQKADGKGADVKIGA	KTIELTGDNGKQLGVKTIKLTETSTNGNATTESTDDDH    :                  KTSVIKDHNGKLFTG-KDLKDANNGATVSEDDGKDF		DKADDTNAITVGKDGTSGKV- 	-DIKTDKDGTVTFGINTQSGLKAGDSTTLN-NNGLSIKNTASNBQIQVGADGVKF 	AMVNNGVVGAGIDGTTRITRDEIGFTGTNGS- 	QSGBIAKNSHDAVTGGKIY :      ::    KSALKTYKDTQNTADETQDKEFHAAVKNANEVEFVGK	HSESYDTSKTSDVI 	TFAGENGITTKVNKGVVRVGIDQTKGLT
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380	353	407	467	519	573 611	623	683	737	778	835	895 938	942	975	1006	1059	1113	1153	1184
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qq	1331 TAQGTNANERGKVVVKGSNGATATETDKKKVATVGDVAKAINDAATFVKVENDDSATIDD 1390	0
Ογ	1212TPKLTVGNNNG 1222	2
qq	DKLSL	0
οy	1223 KGIVINSQNGQNTITGLSNTLANVTNDKGSVRTTEQGNIIKDEDKTR 1269	σ
qa	1451 KVNITSDTKGLNFAKDSKTGDDANIHLNGIASTLTDTLLNSGAT-TNLGGNGITDNEKKR 1509	6
Qy	0 AASIVDVLSAGFNLQGNGEAVDFVSTYDTVNFANGNTTTAKVTYD-DTSKT 131	6
QQ	3 AASVKDVLNAGWNVRGVKPASANNQVENIDFVATYDTVDFVSGDKDTTSVTVESKDNGKR 156	σ
οy	O SKVVYDVNVDDTTIEVKDKKLGVKTTLTSTGTGAN-KFALSNQATG 136	2
qa	GKLFTGKELKDA	m
Οy	1366 DALVKASDIVAHLNTLSGDIQTAKGASQANNSAGYVDADGNKVIYDSTDNKYY 1418	80
qа	1614 NGLVTAKAVIDAVNKAGWRVKTT-GANGQNDDFATVASGTNVTFADGNGTTAEVT 1667	7
Qy	1419 QAKNDGTVDKTKEVAKDKLVAQAQTPDGTLAQMNVKSVINKEQVNDANK 1467	7
qq	1668 -KANDGSITVKYNVKVADGLKLDGDKIVADTTVLTVADGKVTAPNNGDGK 1716	9
Qy	1468 KQGINEDNAFVKGLEKAASDNKTKNAAVTVGDLNAVAQTPLTFAGDTGTTAKKLGETLTI 1527	7
qq	1717 KEVDASGLADALNKLSWTA-TAGKEGTGEVDPANSAGQEVKAGDKVTF 1763	e
Οy	1528 KGGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGTKIDEKGIS 1578	80
qq	1764 KAGDNLKIKQSGKDFTYSLKKELKDLTSVEFKDANGGTGSESTKITKDGLT 1814	4
ΟŊ	1579 FVDANGQADTDAAN 1619	
qα	1815 ITPANGAGAAGANTANTISVTKDGISAGNKAVTNVVSGLKKFGDGHTLANGTVADFEKHY 1874	4
δλ	1620 VQQLNEVRNLLGLGNDNSDGNQVNIADIKKDPNSGSSSN 1658	89
QΩ	1875 DNAYKDLTNLDEKGADNNPTVADNTAATVGDLRGLGWVISADKTTGEPNQEYNAQVRNAN 1934	4
οy	1659 RTVIKAGTVLGG1687	7
QQ	1935 EVKFKSGNGINVSGKTLNGTRVITFELAKGEVVKSNEFTVKNADGSETNLVKVGDMYYSK 1994	4
ογ	WVKTQKDGSKKALLATYNAAGQTNYVTNNE	9
đ	1995 EDIDPATSKPMTGKTEKKVENGKVVSANGSKTEVTLTNKGSCYVTGNQVAD 2046	9
Qy	1737 RINEQGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEA 1785	2
qq	2047 AIAKSGFELGLADAAEAEKAFAESAKDKQLSKDKAETVNAHDKV 2090	0
QY	1786 AVAIGRQTQAGNQSIAIGDNAQATGDQSIAIGTGNVVAGKHSGAIGDPSTVK 1837	7
qq	TTTFVKT	4
Qy	1838 ADNSYSVGNNNQFTDATQTDVFGVGNNITVTESNSVALGSNSALSAGTHAGTQAKKSDGT 1897	7
qq	2145 ADGKWYELNADGTASNKEVTLGNVDANGKKVVKVTENG 2182	2
Qy	1898 AGTTTTAGATGTVKGFAGQTAVGAVSVGASGAERRIONVAAGEVSATS 1945	2
đ	2183 ADKWYYTNADGAADKTKGEVSNDKVSTDEKHVVRLDPNNQSNGKGVVIDNVANGEISATS 2242	7
ΟŊ	1946 TDAVNGSQLYKATQSIANATNELDHRIHQNENKANAGISSAMAMASMPQAYIPGRSM 2002	7
qq	2243 TDAINGSQLYAVAKGVTNLAGQVNNLEGKVNKVGKRADAGTASALAASQLPQATMPGKSM 2302	7
δλ	2003 VTGGIATHNGQGAVAVGLSKLSDNGQWVFKINGSADTQGHVGAAVGAGFHF 2053	
qq	2303 VAIAGSSYOGONGLAIGVSRISDNGKVIIRLSGTTNSOGKTGVAAGVGYOW 2353	

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97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 ESVDL---VSAYNNVEFITGDKNTLDVVLTAKENXKTTEVKFTPKTSVIKE----KDGKL 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 ---KYRRTRAQGHASTAVGAMSYAQGHFSNAFGTYATAEAAYSLAVGLAAQATKQSSIAV 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSNAKANAFAATAIGGNTVVNLGRGVALGFGSQILDRDNNTDA-----SAYVPLG----- 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 KQXTDEXTNASSFTYSLKKDLTDLTSVATEKLSFGANGDKVDLTSDANGLKLAKTGNGNV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 QTNKINNTLKGDALATGEASIAFGSLSKAQGSQAIAIGSVKPDPNNGSNGNVGSHAKGN- 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 EDEELDPVVRTAPVLSFHSDKEGTGEKEVTENSNWGIYFDNKGVLKAGAITLKAGDNLKX 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 8.6%; Score 890; DB 1; Length 1912; Best Local Similarity 23.8%; Pred. No. 3.5e-45; Matches 502; Conservative 227; Mismatches 680; Indels 702; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 -----TLNGSAYAQQI------TTKIEIG------T77
Sequence 4, Application US/08409995
; Sequence 4, Application US/08409995
; Patent No. 5646259
; GENERAL INFORMATION:
    APPLICANT: Barenkamp, Stephen I.
    APPLICANT: Gene III, Joseph W.
    TITLE OF INVENTION: Haemophilus Adhesion Proteins
    TITLE OF INVENTION: Haemophilus Adhesion Proteins
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
    STREET: Four Embarcadero Center, Suite 3400
    CITY: San Francisco
    STATE: CA
    COUNTRY: USA
                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: PATENTIAL PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
CURSEPTION:
CURSEPTION:
CURSEPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: S11va, Robin M.
REGISTRATION NUBER: 38,304
REFERENCE/DOCKET NUMBER: A-61053/RFT
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECEX: (415) 398-3249
TELEC: 910 277299
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1912 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: unknown
US-08-409-995-4
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	331 -ANGQNGDFATVASGTNVTEESGDGTTASVIADINGNALIVALDANYOOLKLVEE 358 301KTLADQYKATRQGDSTDIFSICNSNNNNSSIRRKIINVGAGSRDTDAVNVAQLKLVEE 358 385 DKKIVADTTALTVTGGKVAEIAKEDDKKKLVNAGDLVTA 423 359 LANRKITFKGDGDNNSNSVERGLGNTLTIKGDAQTNALTEANIGVVTDGNGLKV 412 1                       1   1   1   1
	KLAKELIGLISVSATNKITVSNINNNAELOSGGLIFSPITGIKTDKTYYSIDGLKFIND
	SNSIATRGTTRITTRITTE TO THE SNSIATRO SNSIATRGT
	579 APYLDKERLKVGRVEITTDSGINAGNHKITGLTNGIANT
	29
	9 SLVTAKDLADYLNKVNETADSALPSFKVQNGDNSNNAIT 9 SLVTAKDLADYLNKVNETADSALPSFKVQNGDNSNNAIT 1
	RLVIBQVPSADGNSTKNI-IKGLSPTLPSIASPSGRNIALGNTIEEKDKSNAASIDDV
	841 LNAGFNLKNNGKDKDFVSTYDTVDFIDGNATTATVTYDEANQTSKVAYDVNVDEKTIELT 900
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                                                                    1336 ANERGKVVVKGSNGATATETDKKKVATVGDVAKAINDAATFVKVENDDSATIDDSPTDDG 1395
                                                                                                                                                                                                                         1619 KAVIDAVNKAGWRVKTT-GANGQNDDFATV-ASGTNVTF------ADGNGT---TAE 1664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1276 VAEAKVGDGLEKDTDGKIKLKVDNTDGNNLLTVDATKGASVAKGEFNAVTTDATTAQGTN 1335
                                                                                                                     -- TPKLTVGNNNGKGIVIN 1228
                                                                                                                                                    1396 ANDALKAXDTLTLKAGKNLKVKRDGKNITFALANDLSVKSATVSDKLSLGTNGNKVNITS 1455
                                                                                                                                                                                                SQNGQN------TITGLSNTLANVINDKGSVRTTEQGNIIKDEDKTRAASIVD 1275
                                                                                                                                                                                                                                                                            1276 VLSAGFNLQG------NGEAVDFVSTYDTVNFANGNTTTAKVTYD--DTSKTSKVYYD 1325
                                                                                                                                                                                                                                                                                                                                                         1326 VNVDDTTIEVKDKKLGVKTTTLTSTG----TGAN-KFALSNQAT-----GDALVKA 1371
                                                                                                                                                                                                                                                                                                                                                                                              -----KIGAKTSVIKDHNGKLFTGKELKDANNNGVTVTETDGKDEGNGLVTA 1618
                                                                                                                                                                                                                                                                                                                                                                                                                                       1372 SDIVAHLNTLSGDIQTAKGASQANNSAGYVDADGNKVIYDSTDNKYYQAKNDGTVDKTKE 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VAKDKLVAQAQTPDGTL-AQMNVKSVINKEQVNDANKKQG---INEDNAFVKGLEKAASD 1487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1665 VTK-----ANDGSITVKYNVK-----VADGLKLDGDKIVADTTVLTVADGKVTAP 1709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1488 N-----KTKNAAVTVGDLNAVAQTPLTFAGDTGT------TAKKLGETLTIKGGQT 1532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1533 DTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSV----NAG----GTKIDEKGISFVDAN 1583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GQA-----KANTPVLSANGLDLGGKVISNVGKGTKDTDAANVQQLNEVRNLLGLGNDNAD 1638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: St. Geme III, Joseph W.
APPLICANT: Barenkamp, Stephen J.
TITLE OF INVENTION: HAEMOPHILUS ADHESION PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,467 FILING DATE: 2-JUL-1996 CLASSIFICATION: 424 PRIOR APPLICATION DATA:
                                       ---ITTKVNKGVVRVGIDQTKGLT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIALE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08685467
Patent No. 6060059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNQVNIADIKK 1649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | :|| :|
G---TVADFEK 1871
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-685-467-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           385 DKKIVADTTALTVTGGK--VAEIAKEDD----KKKLVNAG-------DLVTA 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 FTGKENNDTNKVTSNTATDNTDEGNG-----LVTAKAVID-AVNKAGWRVKTTT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 8.6%; Score 890; DB 3; Length 1912; Best Local Similarity 23.8%; Pred. No. 3.5e-45; Matches 502; Conservative 227; Mismatches 680; Indels 702;
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                                                                                                                                                       A-61053-2/RFT/RMS
US 08/409,995
                                                                                  NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 781-1989
TELEFAX: (415) 398-3249
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1912 amino acids
                          FILING DATE: 24-MAR-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              1: 1912 amino acids amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-685-467-4
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48;
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                                                                                                                                                                                                                                                                                                                                                        1619 KAVIDAVNKAGWRVKTT-GANGQNDDFATV-ASGTNVTF------ADGNGT---TAE 1664
                                                1432 VAKDKLVAQAQTPDGTL-AQMNVKSVINKEQVNDANKKQG---INEDNAFVKGLEKAASD 1487
                                                                             N-----KIKNAAVTVGDLNAVAQTPLIFAGDIGI------TAKKLGEILIIKGGQT 1532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               953 HTTKGTANTA---LQTFTVKKVDENDKADDTNAITVGKDGTSGKVNT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Barenkamp, Stephen I.
APPLICANT: St. Geme III, Joseph W.
IIILE OF INVENTION: Haemophilus Adhesion Proteins
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: CA
CUMPRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUW TYEE: FIDEPPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATENTIN RC-IDSS/MS-DOS
SOFTWARE: PATENTIN RC-IDSS/MS-DOS
SOFTWARE: PATENTIN RC-IDSS/MS-DOS
CURRENT APPLICATION NUMBER: US/08/409,995
FILING DATE: 24-MAR-1995
CLASSIFICATION:
NAME: S11va, RODIM M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61053/RFT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION
TELECOMMUNICATION OF 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1098 mmino acids
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US-08-409-995-2
; Sequence 2, Application US/08409995
; Patent No. 5646259
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Flehr, Hob
STREET: Four Embarcac
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                            1639 GNQVNIADIKK 1649
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1864 G---TVADFEK 1871
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1051 132 1111 152 1169 170	1225 220 1283 266 1335 326 1394 1394 384 1445 437	1555 530 1607 590 1667 1727 693	1781 738 1831 794	1885 848 1901 908 1926 968
997LKLKGKNGLDIKTDKDGTVTFGINTQSGLKAGDSTTLNNNGLSIKNTASNEQIQV	170   PYSSYDTSKTSDVITFAGENGITTKVNKGVVRVGIDQTKGLTTPKLTVCNNNGKGI	1503 VAQTPLTFAGDTGTTARKLGETLTIRGGQTDTNKLTDNNIGVVAGTDGFTVKL  1	TINDPAEAIDRINGGGIRFFHVNDGOPEPVVGRNGIDSSASGKHSVAIG-FOAKA	1832 DPSTVRADNSYSYGNNNQFTDATQTDVEGVGNNITVTESNSYALGSNSAISAGT 1885  795AKSGFELGLADEADAKRAEDDKTKALSAGTTEIVNAHDKVRFANGLNTKVSAAT 848  1886 HAGTQAK
64 64 64 64 64 64 64 64 64 64 64 64 64 6		6 6 6 6 6 6 6 6	OY Db Oy Db	60 60 60 60 60 60

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1984 SSAMAMASMPQAYIPGRSMVTGGIATHNGQGAVAVGLSKLSDNGQWVFKINGSADTQGHV 2043
                                                                                                         997 ---LKLKGKNGLDIKTDKDGTVTFGINTQSGLKAGDSTTLNNNG--LSIKNTASNEQIQV 1051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lery Match 6.7%; Score 690; DB 3; Length 1098; est Local Similarity 24.7%; Pred. No. 1.6e-33; atches 314; Conservative 151; Mismatches 439; Indels 366; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 KGLLNLNEKNASDKLLVEDNT------AATVGNLRKLGWVLSSKNGTRNEKSQ- 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------KGGVQVTS 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             953 HTTKGTANTA---LQTFTVKKVDENDKADDTNAITVGKDGTSGKVNT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,467
FILING DATE: 22-JUL-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,995
FILING DATE: 24-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61053-2/RFT/RMS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----DEVLFEG----
                                                                                                                                                                                                                                                                                                                                                          equence 2, Application US/08685467 tent No. 6060059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 781-1989
TELERAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1098 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)'
18-685-467-2
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                                                                                                                                                                                                           1089 GVAAGVGYQW 1098
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8-685-467-2
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2044 GAAVGAGFHF 2053

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SGAERRIQNVAAGEVSATSTDAVNGSQLY---KATQSIANATNELDHRIHONENKANAGI 1983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1832 DPSTVKADNSYSVGNNNQ-----FTDATQTDVFGVGNNITVTESNSVALGSNSAISAGT 1885
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                                                         1170 PYSSYDTSKTSDVITFAG--ENGITT--KVNKGVVRVGIDQTKGLTTPKLTVGNNNGKGI
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                                                                                                                                                   GENERAL INFURENTALON:
APPLICANT: PERAK, TAN RICHARD ANSELM
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SUFFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/ANU98/01031
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1999-12-12
PRIOR FILING DATE: 1999-12-12
PRIOR FILING DATE: 1999-12-12
PRIOR FILING DATE: 1997-12-12
                                                                                               Sequence 32, Application US/09377155
Patent No. 6197312
GENERAL INFORMATION:
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SEQ ID NO 32
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                  849 VESTDANGDKVTTTFVKTDVELPLTQIYNTDANGKKITKVVKDGQTKWYELNADGTADMT 908
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Patent No. 6200578
GENERAL INFORMATION:
APPLICANT: St. Geme, Joseph
APPLICANT: Barenkamp, Stephen J.
TILLE OF INVENTION: HAEMOPHILUS ADHESION PROTEINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPOUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS .
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,942
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STATE: California
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                                                                                                                                                                                                                                                                              A-61053-1/RFT/RMS/DAV
                                                                 APPLICATION NUMBER: US 08/409,995
FILING DATE: 24 WAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/4031
FILING DATE: 22 WAR-1996
ATTOMINE/AGENT INFORMATION:
NAME: VARCE, DOLLY A.
                                                                                                                                                                                                                  NAME: Vance, Dolly A.
REGISTRATION NUMBER: 39,054
REFERENCE/DOCKET NUMBER: A-61(
TELECOMMUNICATION: TELECOMMUNICATION:
TELEFAX: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 1098 amino acids
29-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-913-942-2
                     CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
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ATGDT -- VTFTPK ----
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                                                                                                                                                                                                                               D-----GEAAVAIGRQTQA-----GNQSIAIGDNAQATGDQSIAIGTGNVVAGKHSGAIG 1831
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1728 TNNPAEAIDRINEQGIRFFHVNDG----NQEPVVQGRNGIDSSASGKHSVAIG--FQAKA 1781
                                                                                                                LGGKGNNDTEKLATGGVQVGVDKDGNANGDLSNVWVKTQKDGSKKALLATYNAAGQTNYV 1727
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                                                                                                                                 -----VNGRREITFELAKGEVVKSNEFTVKETNGKETSL-----VKVGDKYYSKE 738
                                                                                                                                                                                                                                               909 KEVILGNVDSDGKKVVKDNDGKWYHAKADGTADKTKGEVSNDKVSTDEKHVVSLDPNDQS
                                                         VGKGTKDTDAANVQQLNEVRNLLGLGNDNADGNQVNIADIKKDPNSGSSSNRTVIKAGTV
                                                                           APPLICANT: St. Geme, Joseph
APPLICANT: St. Geme, Joseph
APPLICANT: St. Geme, Joseph
APPLICANT: Barenkamp, Stephen J.
APPLICANT: Barenkamp, Stephen J.
ATTLE OF INVEXTION: HARMOPHILUS ADHESION PROTEINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Flehr Hohbach Test Albritton & Herbert LLP
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STRATE: California
COUNTRY: Unitedia
COUNTRY: Unitedia
ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/913,942
FILING DATE: 29-DEC-1997
CLASSIFICATION: 514
PLOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-913-942-15; Sequence 15, Application US/08913942; Patent No. 6200578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1481 LEKAASDNKTKNAAVTVGDLNAVAQTPLFFAGDTGTTAKKLGETLTIKGGQTDTNKLTDN 1540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
5.6%; Score 583.5; DB 4;
Best Local Similarity 23.9%; Fred. No. 2.1e-27;
Matches 226; Conservative 115; Mismatches 223;
                                                                                                                                         39,054
ER: A-61053-1/RFT/RMS/DAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291 KDDGSADMNQKV------ENGELA-----
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/4031
FILING DATE: 22-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Vance, Dolly A.
REGISTRATION NUMBER: 39,054
REFERENCE/DOCKET NUMBER: A-61053-1/i
TELECOMMNICATION INFORMATION:
                                                                                                                                                                                                      TELEPHONE: (415) 781-1989
TELERX: (415) 781-1989
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
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1	Oy	· 55LVIGATLNCSAYAQQITTKIEIGQINKINNTLKG
470 KVTLKAGDNLKVKQEGTNFTYALKDELTGVKSVEFKDTANGANGASTKITKDGL 523	qa	60 ASIPQSVLASGLQGMSVVHGTATMQVDGNKTTIRNSVNAIINWKQFNIDQNEMEQFLQES 119
1890 QAKKSDGTAGTTTAGATGTVKGFAGQTAVGAVSVGASGAERRIONVAAGEVSATSTDAV 1949 	oy da	95 EASIAFGSLSKAQGSQAIAIGSVKPDPNNGSNGNVGSHAKGNESIAIGGDVLAEGDASIA 154
1950 NGSQLYKATQSIANATNELDHRIHQNENKANAGISSAMAMASMPQAYIPGRSMVTGG 2006 	Qy	155 IGSDDLYLPKNLDLKNEFHKLIHGHEILKKIQTSTDGKIKY 195
2007 IATHNGQGAVAVGLSKLSDNGQWVFKINGSADTQGHVGAAVGAGFHF 2053 :::     :  :    : :::	QY	196 RRTRAQGHASTAVGAMSYAQGHFSNAFGTXATAEAAYSLAVGLAAQATKQSSIAVGSNAK 255   : :
RESULT 11 US-08-617-697-10	Oy	256 ANAFAATAIGGNTYVVNLGRGVALGFGSQILDRDNNTDASAYVPLGKTLADQYKA 309 1
n US/08617697 p, Stephen J	Qy	310 TRQGDSTDIFSIGNSNNNNSSIRRKIINVGAGSRDTDAVNVAQLKLVEELANRKITFK 367 :: :: ::   ::   ::   ::   ::   304 - KEGEAEIGGVISAQNQAKGCKLMITGDKVTLKTGAVIDLSGK 346
	Qy	368 GDGDNNSNSVERGLGNTLTIKGDAQTNALTEANIGVVTDGNGLKVKLAKELTGLTSVSAT 427
ADDKESSEE: SNOEMBAEF and Martare, Ltd. STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza STREET: Bldg. 1 CITY: Arlington	Qy	428 NKITVSNTNNNNAEL-QSGGLTFSPITGTKTDKTVYSIDGLKFTNDSNSIATKGTT- 482  1
VIFGIL : U.S. 2202-02 READABI	Qy	483RITKKKIGFAGTNDGVDESKPYLDNEKLKVGNSTLNSGSLTVNNTTGNKQI 533
MEDIUM ITE: FIORPY GISH COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOGTWARRE: Patentin Release #1.0, Version #1.30	QY	534 QVGANGIKFATVANNVANTSATVGTARITEEKIGFAGTNDGVDEQAPYLDKERLKVGRVE 593     :   ::
COURGEN AFFICATION NUMBER: US/08/617,697 FILING DATE: 01-APR-1996 CLASSIFICATION: 424	QY	594 ITTDSGINAGNHKITGLFNGIANTDAVTIKQLKDAKPTLNAGDGISINSNNGD 646 
PATION APPLICATION DATA: PATION NUMBER: US 08/302,832 FILING DATE: 05-0CT-1994 PRIOR APPLICATION DATA:	oy op	647 -LVDSSGNITTPTYNISVKTTKLNSNGTSGNNKFSVSNAHDNNSLVTA 693 ::      : :       : :
215	Qy Pb	694 KDLADYLNKVNETADSALPSFKVQNGDNSNNAITVGKDFNGK-TFNTLKLKGENGVNITT 752   1   1   1   1   1   1   1   1   1
REGISTRATION NUMBER: 22,651 REFERENCE/DOCKET NUMBER: 1038-557 TELECOMMUNICATION INFORMATION:	Qy	753 NRATGTVTFGIDOSNGLTTPKLTVGSDTNGNRLVIEQVPSA 793 :
TELEGAT: (103) 413-10813 INPORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 1600 amino acids	QY D	794 DGNSTKNIIKGLSPTLPSIASPSGRNIALGNTIEEKDKSNAASIDDVLNA 843 
3 % ·	δδ	844 -GFNLKNNGKDKDFVSTYDTVDFIDGNATTATVTYDEANQTSKVAYDVNVDEK- 895 
Query Match 5.3%; Score 546.5; DB 2; Length 1600; Best Local Similarity 21.7%; Pred. No. 1.1e-24; Matches 418; Conservative 250; Mismatches 744; Indels 515; Gaps 95;	OY Db	896 TIELTGDNGKKQLGVKTIKLTETSTNGNATTFSTDDDHALVKASDIAGNLNTLAEEIH 953 :
VIENKATGTEMAVAEYAKSHSTGGGSCATGQVGSVRTLSFARIAALAV 54 :  :	Oy QQ	954 TTKGTANTALQTFTVKKVDENDKADDTNAITVGKDGTSGKVNTLKLKGKNGLDIKTD 1010   1   1   1   1   1   1   1   1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVNDANKKQGINEDNAFVKGLEKAASDNKTKNAAVTVGDLNAVAQTPLTFAGDTGTTAKK 1520
                                                                                                                                                                                                                                                                                                                                                                                  TTTAGST-----ISATTGNANITTKTGDINGKVESSSGSVTLVATGATLA---VGN 1298
                                                                                                                                                                                                        1096 TLNSEVKTSNGSSNAGNDNSTGLTISAKDVTVNNNVTSHKTINISAAAGNVTTKEGTTIN 1155
                                                                                                                                                                                                                                        SQNGQNTITGLSNTL-ANVTNDKGSVRTTEQGNLIKDEDK--TRAASIVDVLSAGFNLQG 1285
                                                                                                                                                                                                                                                                                                 1286 NGBAVDFVSTYDTVNF-ANGNT-TTAKVTYDDTSKTSKVVYDVNVDDTTIEVKDKKLGVK 1343
                                                                                                                                                                                                                                                                                                                    1299 ISGNIVIITADS------GKLTSTV------GSTINGT-----NSVTTSS 1331
                                                                                                                                       1044 -DLNISGFNKAEITAKNGS----DLTIGNASGGNADAKK--VTFDKVKDSKIST-DGHNV 1095
                                                                                                                                                                                --NGKGIVIN 1228
1011 KDGTVTFGINTQSGLKAGDSTTLNNNGLSIKNTASNEQIQVGADGVKFAMVNNGVYGAGI 1070
                                                         DGTTRITRDEIGFTGTNGSLDKSKPHLSKDGINAGGKKITNIQSGEIAKNSHDAVTGGKI 1130
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                                                                                                                     1131 YDLKTELENKISSTAKTAQNSLHEFSVADEQGNNFTVSNPYSSYDTSKTSDVITFAGEN-
                                                                                  Sequence 9, Application US/08617697
Sequence 9, Application US/08617697
Patent No. 5977336
GENERAL INFORMATION:
APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: Of No. 5977336-Typeable Haemophilus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: 8149...
                              955 ASGTOKTLINGNITNEKGD-----LNIKNIKADAEIQIGGN---
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STATE: Virginia
COUNTRY: U.S.A.
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Best Local Similarity 21.4%; Pred. No. 8.6e-23;
Matches 413; Conservative 257; Mismatches 734; Indels 530;
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2IP: 22202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,697
FILING DATE: 01-APR-1996
CLASSIFCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 05-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/02166
FILING DATE: 16-MAR-1993
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 1038-557
TELECOMMUNICATION INFORMATION:
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TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1599 anino acids
TYPE: amino acid
STRANDEDNESS: single
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US-08-617-697-9
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FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NATA:
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REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 103
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TELEPHONE: (703) 415-0810
TELEPAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: GB 92
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
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ADDRESSEE: Shoemaker
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STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202-0286
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:| :| :| :| :| :| 443 NVTIEAPSASRVELGADRNSH--SAEVIKVTLKKNNTSLTTLTNTT-----ISNLLKS 493
                                                                                                                                                                                                                                                                                   -----SNGTSGNNKFSVS----NAHDNNSLVTAKDLADYLNKVNETADSALPSFK 715
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                                                     ATVANNVANTSATVGTARITEEKIGFAGTNDGVDEQAPYLDKERLKVGRVEITTDSG--- 599
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                                                                                         494 AHVVNITARRKLTVNSSISIERGSHLILHSEGQGGQGVQIDK------DITSEGGNLT
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1574 EKGISFVDANGQAKANTPVLSANGLDL-----GGKVISNV----GKG---TKDTDAAN 1619
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   ---LTIGNS 1358
                                                        1514 TGTTAKKLGETLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGTKID 1573
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TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5928651-Typeable Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
   --IEGTISGN-TVNVTASTGD--
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, 'CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,470
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SYSTEM: PC-DOS/MS-DOS
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1324 NSVTTSSQSGD--
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                                                                                           ILKKIQTSTDGKIKY--RRTRAQGHASTAVGAMSYAQGHFSNAFGTYATAEAAYSLAVGL 238
                                                                                                                                                          ASAYVPLGKILADQYKATRQGDSTDIFSIGN--SNNNNSSIRRKIINVGAGSRDTDAVNV 350
                                                                  GOVFLINPNGITIGKDAIINTNGFTASTLDISNENIKARNFTLEOTKDKALAEIVNHG-- 129
                                                                                                                   ---LITVGKDGSVNLIGGKVKNEGVISVNGGSISLLAGQ------KITISD 171
                                              --LIHGHE 180
                        Gaps
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                       674; Indels 478;
 Length 1529;
4.9%; Score 512; DB 2;
21.8%; Pred. No. 1.2e-22;
tive 229; Mismatches 674;
                                                143 GDVLAEGDASIAIGSDDL----YLPKNLDLKNEFHK----
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826 IVGNL-SIAED-STFKGEASDNLNITGTFT-----
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                   Best Local Sim:
Matches 386;
      Query Match
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1332 IAGNINAANVTLNTTGTLTTTGDSKINATSGTLTINAKDAKLDGAASGDRTVVNATNASG 1391
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VGADGVKFAMVNNGVVGAGIDGTTRITRDEIGFTGTNGSLDKSKPHLSKDGINAGGKKIT 1110
                                                                                          NIQSGEIAKNSHDAVTGGKIYDLKTELENKISSTAKTAONSLHEFSVADEOGNNFTVSNP 1170
                                                                                                                                   EAENANLTIQTKELKLAG----DLNISGFNKAEITAKNGS----DLTIGNASGGNADAKK- 1007
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STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: alidg. 1
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/08719641

Sequence 10, Application US/08719641

Sequence 10, Application US/08719641

GENERAL INFORMATION:
APPLICANT: Barenkamp, Stephen J
APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: of No. 6218141-Typeable Haemophilus
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
ADDRESSEE: Shoemaker and Mattare, Ltd.
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1051 VGADGVKFAMVNNGVVGAGIDGTTRITRDEIGFTGTNGSLDKSKPHLSKDGINAGGKKIT 1110
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     SVAF-EREGDKARNATDAQITAQGTITVNKDDKQFRFNNVSINGTGKGLKFI---ANQNN 552
                                                                                                                                                           NSNNAITVGKDTNGKTFNTLKLKGENGVNITTNRATGTVTFGIDQSNGLTTPKLTVGSDT 780
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                                                     ------SLVTAKDLADYLN-----KVNETADSALPSFK----VQNGD
                                                                                  553 FTHKFDGELNISGIVTINQTTKKDV-KYWNASKDSYWNVSSLTLNTVQKFTFIKFVDSGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 AAQATKQSSIAVGSNAKANAFAATAIGGN-----TVVNLGRGVALGFGSQILDRDNNTD 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 IINPTITYSIAAPENEAINLGDIFAKGGNINVRAATIRNKGK.---LSADSVSKDKSGNIV 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 4.9%; Score 512; DB 4; Length 1529;
Best Local Similarity 21.8%; Pred. No. 1.2e-22;
Matches 386; Conservative 229; Mismatches 674; Indels 478; Gaps
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                             FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/302,832

FILING DATE: 16-SEP-1994

FILING DATE: 16-SEP-1994

FILING DATE: 16-MAR-1993

PRIOR APPLICATION NUMBER: US PCT/US93/02166

FILING DATE: 16-MAR-1993

ATTORNEY/AGENT INFORMATION:
NAMME: BECKSTERSSET, JETTY W

REGISTRATION NUMBER: 22,651

REFERENCE/DOCKET NUMBER: 1038-625

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                             APPLICATION NUMBER: US/08/719,641 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (703) 415-0810
TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1529 amino acids
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                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
mnDOTOGY: linear
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US-08-719-641-10
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                                                                                                                                                                                                                                                                                 VSATNKITVSNTNNNNAELOSGGLTFSPITGTKTDKTVYSIDGLKFTNDSNSIATKGTTR 483
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                                                                                                                                                                                                                                                                                                                                                                            574 GVDEQAPYLDKERLKVGRVEITTDSGINAGN-------HKITGLTNGIANTDAVTI 622
                                                                   -VVNL-GRGVALGFGSQILDRDNNTDASAYVPLGKTLADQYKATRQGDSTDIFSI-GNSN 325
                                                                                              326 NNNSSIRRKIINVGAGSRDTDAVNVAQLKLVEELANRKITFKGDGDNNSNSV----ERG 380
                                                                                                                                                                -----FTFEQTKDKA-----LAEIVNHGLITVGKDGSVN-----LIGGKVKNE 221
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SYAQGHFSNAFGTYATAEAAYSLAVGLAAQATKQSSTAVGSNAKANAFAATAIGGNT---
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                TVIKAGTVL---GGKGNNDTEKLATGGVQ-VGVDKDGNANGDLSNVWVKTQKDGSKKALL 1715
                                             1447 EVIEAKRVLEKVKDLSDEERETLAKLGVSAVREVEPNNA-----ITVNTQNEFTTRPSS 1500
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                                                                                                                                                                                                                                                                      APPLICANT: BARENKAMP, STEPHEN J
APPLICANT: ST GEME III, JOSEPH W
ATTLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
TITLE OF INVENTION: OF NON-TYPEABLE HAEMOPHILUS
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                               ALUNESSEE: Shoemaker and Mattare, Ltd
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Alington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----NIKARN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTAIN 22202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: DATE PLOPPY DISK
COMPUTER: DATE PLOPPY DISK
COMPUTER: DATE PROBAMS-DOS
SOFTWARE: PATENTIN RELABLE PATENTIN RELABLE PATENTIN RELABLE PATENT RELABLE TO SOFTWARE: US/08/038,682
FILING DATE: 16 MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.5%; Score 469; DB 1; 21.3%; Pred. No. 4.4e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
4.5%; Scorre 469; DB
BEST LOCAL Similarity 21.3%; Pred: No. 4.4e
BEST LOCAL Similarity 21.3%; Mismatches
399; Conservative 244; Mismatches
                                                                                            1716 ATYNAAGQTNYVTNNPAEAIDRINEQG 1742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1038-293
                                                                                                                      1501 QVTISEGKACFSSGNGARVCTNVADDG 1527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEPAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENTH: 1477 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | : : ! | KDAIINTNGFTASTLDISNE-----
                                                                                                                                                                                                                   Sequence 4, Application US/08038682
Patent No. 5549897
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: BERGSTRESSER; JERFY W
RECISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-08-038-682-4
                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Shoemaker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                          -08-038-682-4
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Matches
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-------NGSIAGSINAA--NVTLN---TTGTLTTVA------GSDIKATSGTLV 1313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1169 NPYSSYDTSKTSDVITFAGENGITTKVNKGVVRVGIDQTKGLTTPKLTVGNNNGKGIVIN 1228
                       1067 N---SNDGNSGAEAKTVTFNNVKDSKISADGHNVTLNS------KVKTSSSNG-GRESN 1115
                                                                                                                                                    1288 EAVDFVSTYDTVNFANGNTTTAKVTYDDTSKTSKVVYDVNVDDTTIEVKDKKLGVKTTTL 1347
                                                                                                                                                                          1348 TSTGTGANKFALSNQATGDALVKASDIVAHLNTLSGDIQTAKGAS-QANNSAGYVDADGN 1406
                                                                                                                                                                                                                                                         1407 KVIYDSTDNKYYQAKNDGTVDKTKEVAKDKLVAQAQTPDGTLAQMNVKSVINKEQVNDAN 1466
                                                                                                                                                                                                                                                                                                                                1467 KKQGINEDNAFVKGLEKAASDNKTKNAAVTVGDLNAVAQTPLTFAGDTGTTAKKLGETLT 1526
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1527 IKGGQTDTNKLIDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGT-KIDEKGISFVDANGQ 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1586 AKANTPVLSANGLDLGGKVISNVGKGT-----KDTD-----AANVQQLNEVRNLLGLG 1633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : |||: :|| |: |
1357 LN-----TVNGLN----IISKDGRNTVRLRGKEIEVKXIQPGVASVEEVIEAKRVLEKV 1406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1634 NDNADGNQVNIADIKKDPNSGSSSNRTVIKAGTVLGGKGNNDTEKLATGGVQVGVDKDGN 1693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1229 SQNGQNTITGLSNTLANVTNDKGSVRTTEQGNIIKDEDKTRAASIVDVLSAGFNLQG-NG 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1460 SSGNGARVCTNVADDG 1475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1694 ANGDLSNVWVKTQKDG 1709
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Search completed: September 13, 2001, 12:38:28 Job time: 48224 sec

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4.5
Compugen Ltd.
 version 4
- 2000 (
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sw model OM protein - protein search, using September 13, 2001, 12:39:59 Run on:

; Search time 76.31 Seconds (without alignments) 2049.356 Million cell updates/sec

US-09-361-619-9 10356

1 MNHIYKVIFNKATGTFMAVA.....NGSADTQGHVGAAVGAGFHF 2053 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched: Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000

219241

Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:\* pir2:\* pir3:\* PIR\_68:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	surface protein XF	probable adhesin Z	surface protein XF	probable RTX famil	190K surface antiq	cell surface antiq	hemagglutinin/hemo	probable invasin Z	hypothetical prote	-54	hypothetical prote	filamentous hemadd	hemagglutinin/hemo	ABC-type transport	hypothetical prote	toxin-like outer m	hypothetical prote	tical	mucin, submaxillar	high-molecular-wei	hypothetical prote	extracellular matr	outer membrane pro	high-molecular-wei	hemolysin A precur	outer membrane pro	toxin-like outer m	toxin-like outer m	lactocepin (EC 3.4
SUMMARIES	ΩI	D82671	A86036	A82615	B85547	A41477	B71704	F81045	E85822	T31105	D64962	S76109	T31102	н81193	C48399	C83339	A64556	F83068	T34434	T03099	B43855	A83412	T31110	D71630	A43855	A35140	.JC1340	Н	┛	206997
	BB							7					7	N	~	~	7	7	~	~	7	7	~	7	7	CI	7	7	7	7
	Length	2059	1588	1190	5188	2249	2340	2514	2660	4919	2383	3029	4152	2703	2020	5627	2893	2154	2232	13288	1477	2468	2055	1643	1536	1577	1651	2902	3194	1902
æ	Query Match	11.5	9.4	8.9		5.9	•	5.3	٠		5.1	5.1	•	4.9	4.8	4.7	4.7	4.5	4.5	4.5	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.3	4.3	4.2
	Score	1191.5	971.5	704.5	623.5	608	591.5	553	542.5	4	526.5	526	513	512.5	499.5	487	484.5	464.5	462	461.5	460	460	459	456.5	455	453.5	452.5	449	446	439.5
	Result No.	1	7	m	4	'n	Ø	7	œ	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59

crystalline surfac	cell wall-associat	lactocepin (EC 3.4	probable hemagglut	lactocepin (EC 3.4	probable PPE prote	plasma membrane-as	fat protein - Syne	RTX toxin RtxA VC1	toxin-like outer m	hemagglutinin-like	outer membrane pro	surface-associated	hypothetical prote	hypothetical prote	cellulose-binding
JN0896	S32920	A32634	E83641	B45764	A70524	T17372	S75200	C82199	H71879	E82750	T30852	S61441	T32271	F82885	A44140
7	7	7	7	~	7	7	7	7	7	7	7	7	7	7	7
1645	2334	1962	3535	1902	2204	1403	1965	4558	2399	3282	1029	2508	1459	4688	1848
4.2	4.2	4.2	4.2	4.1	4.1	4.1	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0
436.5	432.5	431.5	430	426.5	422.5	420.5	419	417	416	416	414	413.5	413	411	410.5
30	31	35	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT

A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr. J.D.; Unqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A; Authors: da Silva, A.C. da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.C. A; Reference number: A59328
A; Contents: annotation
C; Genetics: A; Genet

Gaps 101; 79 TNKINNTLKGDALATGEASIAFGS---LSKAQGSQAIAIGSVKPDPNNGSNGNVGSHAKG 135 136 NESIAIGGDVLAEGDASIAIGSDDLYLPKNLDLKNEFHKLIHGHEILKKIQTSTDGKIKY 195 76 VTGYARFFGPSG--TAAEQQGASRNL------TLGGSLY----VNSGQVGV 114 19 VAEYAKSHSTGGGSCATGQVGSVRTLSFARIAALAVLVIGATLNGSAYAQQITTKIEIGQ 78 657; Length 2059; 11.5%; Score 1191.5; DB 2; Length 23.4%; Pred. No. 6.9e-38; Live 362; Mismatches 771; Indels Query Match
Best Local Similarity 23.4%; Pr
Matches 548; Conservative 362;

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196 RRTRAQGHASTAVGAMSYAQGHFSNAFGTYATAEAAYSLAVGLAAQATKQSSIAVGSNAK 255

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Db 1090	Oy 1186	Db 1135	Qy 1244	Db 1176 0v 1304		Qy 1354	Db 1275	Qy 1414	Db 1326	Oy 1468	Db 1383	pp 1428		Db 1487	QY 1593	Db 1547	0y 1643	.0p1 qa	Qy 169	Db 166	Qy 174	Db 171	Qy 180	771 da	Qy 184	Db 183	Qy 187	Db 189	Qy 193	Db 19	Qy 19	Db 20	RESULT A86036
1		VPLGKTLADOYKATKUGU : :  		STDIFSIGNSNNNNSSIRRKIINVGAGSRDTDAVNVAQLKLVEELANKKITFRGUGUNNS [   :	254VSIGEN SSINEN 132		TNNNNAELOSGGLTFSPITGTKTDKTVYSIDGLKFTNDSNSIATKGTTRITKKKIGFAGT			VSE	TVGTARITEEKIGFAGTNDGVDEQAPYLDKERLKVGRVEITTDSGINMAN	SLGQSVVISGESSIAGITSOCKER	003 - ARTICLINGTINGTON TO THE STAND OF THE S											875VIYDEANQTSKVAYD-VNVDEKTIELTGDNGKKQLGVKTIK 914	NEGAVKKSLGQSVVI	DHALVKASDIAGNLNTLAEEIH					104	1069 GIDGTTRITRDEIGFTGTNGSLDKSKPHLSKDGINAGGKKTNIQSGBARNSHDAV 1123  1.   1   1   1   1   1   1   1   1   1	TGGKIYDLKTELENKISSTAKTAQNS

Db Qy Db

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GSNSAISAGTHAGTQAKKSDGTAGTTTTAGATGTVKGFAGQTAVGAVSVGASGAERRIQN 1935 936 VAAGEVSATSTDAVNGSOLYKATOSIANATNELDHRIHONENKANAGISSAMAMASMPOA 1995 NNNOFTDAT----NSVAL 1875 1845. GDNAQATGDQSIAIGTG-----NVVAGKHSG------AIGDPSTVKADNSYSVG 1845. DAKEAMDAVNLROLDAVAQKSNLQTDDMRHEINNIEDVFKITKGDSASSVKGMGVNAMAI 1894 91 DGNANG----DLSNVWVKTQKDGSKKALLATYNAAGGTNYVTNNPA---EAIDRINEQGI 1743 62 SLGAMGLFIANGPSVTASGFNAGDK---VISHVAVGMADTDAVNVSQLKQAVQSVTVKAT 1718 RFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGRQTQA-GNQSIAI 1802 75 GRNAIASADGSVALGDGAKDGGRGAESYTGKYSGVQNNTVGTVSVGDAKGETRSISNVA 1834 93 ----LSANGLDLGGKVISNVGKGTKDTDAANVQQLNEVRNLLGLG----NDNADGNQV-- 1642 43 -NIADIKK-DPN---SGSSSNRTVI-----KAGTVLGGKGNNDTEKLATGGVQVGVDK 1690 07 GGTVDLKNTDGNLAISKSGDSNDVVFNLSKDFKVDEVTAG----NTVVNTDGVKVGSDV 1661 : | | | 1546 37 KVSSNVLLDSNELVITSHSSTSSVKTLANGESVVNRTVVNGDGVNIDDVVVVNDLGLSIV 1546 996 YIPGRSMVTGGIATHNGOGAVAVGLSKLSDNGOWVFKINGSADTYGGHVGAAVGAGFHF 2053 [1:1] | 1:1:1] | 1:1| | 1:1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| | 1:1| KG-----GQTDTNKLTDNNIGVVAGTDGFTV--KLAKDLTNLNSVNAGGTKIDEKGI 1577 8 KOGINEDNAFVKGLEKAASDNKTKNAAVTVGDLNAVAOTPLTFAGDTGTTAKKLGETLTI 1527 3 FGNVVINNG---GKISGVTAGTEETDAVNFSQLKSI------STAVDQGWTLTA 1427 ANKFALSNQATGDALVKASDIVAHLNTLSGDIQTAKGASOANNSAGYVDADGNKVIYDST 1413 GLTIANGPAVTASGIDAGSKVISHV------AAGAVSETSTDAVNGSOLNAVQVQAS 1325 4 DNKYYQAKNDGTVDKTKEVAKDKLVAQAQTPDGTLAQMNVKSVINKE-----QVNDANK 1467 --GNTTTAKVTYDDTSKTSKVVYDVNVD------DTTIEVKDKKLGVKTTTLTSTGTG 1353 AGENGITTKVNKGVVRVGIDQTKGLTTPKL--TVGNNNGKGIVINSQNGQNTITGLSNTL 1243 ---GESSTAGTY 1134 SGGN-LKSVVDEAAGRIHLQLA---DSPKFGNVVINNGGK-----ISGVT---ANYTNDKGSVRTTEOGNIIKDEDKTRAASIVDVLSAGFNLQGNGEAVDFVSTYDTVNFAN NGSQLNAVQVQASQPVTFTG-----NEGAVKRSLGQSVVIS----35 46 9/ 44 13

Qy         726 ITVGKDTNGKTF	27 1098 29 1098 29 1158 29 1158 20 1158 20 1218 20 1394 20 1394 20 1394 20 1394 20 1394 20 1394 20 1394 20 1394 20 1394 20 1394 20 1394 20 1394 20 1394 20 156 20
QY         1705         TQKDGSKKALLATVNAAGQTNYVTNNPAEAIDRINEQGIRFEHVNDGNQEPVVQGRNGID         1764           Db         1351        TGSTKYFKTNTDGVD         1366           QY         1765         SSASGKHSVALGFQAKADGEAAVALGRQTGRQTGRQTGBGALGTGGNAGG         1824           1765         SSASGKHSVALGFQAKADGEAAVALGRQTGQTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	RESULT 3  AB2615  Surface protein XF1981 [Imported] - Xylella fastidiosa (strain 9a5c)  Surface protein XF1981 [Imported] - Xylella fastidiosa (strain 9a5c)  C;Sacesian: AS512  AND AND AND Superior Exevision 20-Aug-2000 ttext_change 20-Aug-2000  C;Sacesian: AS513  AND AND AND AND AND AND AND AND AND AND

280 FGSQILDRDNNTDASAYVPLGKTLAD-QYKATRQGDSTDIFSIGNSN-NNNS	1/61 ISGQVTGAAAGDTVTVTLGGATYTATVQANLSWSVDVPASALQELGNGELTISA 330 SIRRKIINVGAGSRD-TDAVNVAQLKLVEELANRKITFKGDGDNNSNSVERG  : :	1815 SVTNSVGNTGNGTREITIDANLEGELR-VDTVAGDDVVNIIEHGQALVIIGS 381LGNTLFIKGDAQTNALTEANIGVYDGNGL  ::       :    :	1865 SSGLAAGSNVTLTINGQTYVAAVLADGTWSVGVPAVDVSAWPAGSVTIAASGSTSAGNPV 411 KVKLAKELTGL-TSVSATNKITVSNTNNNNAELQSGGLTFSPITGTKTDKTVXSIDGL	DD 1925 SVTHEVTVDLSAVAVSINAITADDVINAEKGAALTLSGSTSGVEAGGTVTVTFGG 1980  QY 468 KFINDSNSIATKGTTRITKKKIGFAGTNDCVDESKPYLDNEKLKVGNSTLN 518	QY 519 SGSLTVNNTTGNKQIQVGANGIKFATVANNVANTSATVGTARITEEKIGFAGTNDGV- 575	576 DEQAPYLDKERLKVGRVEITTDSGINAGNHKITGLTNGIANTDAVTIK	QY 624 QLKDAKPTLNAGDGISINSNN-GDLVDSSGNITTPTYNISVKTTKLNSNG 672	QY 673 TSGNNKFSVSNAHDNNSLVTAKDLADYLNKVNBTADSALPSFKVQNGDNSNNA 725	Qy 726 -ITVGKDTNGKTENTLKLKGENGVNITTNRATGTVTFGIDQSNGLTTPKLTVGSDTN 781 : : :           : :	QY 782 GNRLVIEQVPSADGNSTKNIIKGLSPTLPSIASPSGRNIALGNTIEEKDKSNAASID 838	QY 839 DVLNAGFNLKNNGKDKDFVSTYDTVDF-IDGNATTATVTYDEANQTSKVAYDVN 891	OY 892 VDEKTIELTGDNGKKQLGVKTIKLFETSTNGNATTFSTDDDHALVKASDIAGNLNTLAEE 951 1	QY 952 IHTTKGTANTALQTFTVKKVDENDKADDTNAITVGKDGTSGKVNTLKLKGKNGLDIKTDK 1011  1	OY 1012 DGTVTFGINTQSGLKAGDSTTLNNNGLSIKNTASNEQIOVGADGVKFAMVNNGVVGAGID 1071 11	OY 1072 GTTRITRDEIGFTGTNGSLDKSKPHLSKDGINAGGKKI 1109 .	QY 1110 TNIQSGEIAKNSHDAVT-GGKIYDLKTELENKISSTA 1145		Qy 1198 GVVRVGIDQTKGLTTPKLTVGNNNGKGIVINSQNGQNTITGLSNTLANVTNDKG 1251
:   :     :   :   :   :   :   :   :	OY 1793 TOA-GNOSIAIGDNAQATGDQSIAIGTGNVVAGKHSGAIGDPS 1834	QY 1835 TVKADNSYSVGNNNQFTDATQTDVFGVGNNITVTESNSVALGSN 1878    STATES   QY 1879 SAISAGTHAGTQAKKSDGTA-GTTTTAGATGTVKGFAGGTAVGA 1921	1922 VSVGASGAERRIQNVAAGEVSATSTDAVNGSQLYKATQSIANATNELDHRIHQNENKANA	1982 GISSAMAMASMP(   ::  :    119 GVAAAIATANLPC	Qy 2042 HVGAAVGAGFHF 2053	RESULT 4 B85547 Probable RTX family exoprotein [imported] - Escherichia coli (strain 0157:H7)	C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001 C; Accession: B85547 R; Perna, N.T.; Plunkett III. (3; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew illor I. Grotheok F. I. Davie N. W. Fortheok F. F. Davie N. W. Fortheok F. F. Davie N. W. Fortheok F. F. Davie N. W. F. Fortheok F. F. Davie N. W. F. F. F. Davie N. W. F. F. Davie N. W. F. F. Davie N. W. F. F. F. Davie N. W. F. F. Davie N		A/Status: preliminary A:Molecule type: DNA A:Residues: 1-5188 <sto> A:Residues: 1-5188 <sto> A:Cross-references: GR-AROURI74. NID:G12513368. DIDN:AAG54838 1. GSDDB.GN00145. HWGD:706</sto></sto>	A; Experimental source: strain 0157:H7, substrain EDL933 C; Genetics: A; Gene: 20615	Query Match 6.0%; Score 623.5; DB 2; Length 5188; Best Local Similarity 22.6%; Pred. No. 1e-15; Matches 526; Conservative 287; Mismatches 846; Indels 673; Gaps 126;	VIGATLNGSAYAQOITTKIEIGOTNKINNTLKGD-       ::     ::     ::     :     :     :       :	90	141 IGGDVLAEGDASIAIGSDDLYLPKNLDLKNEFHKLIH	178 GHEILKKIQTSTDGKIKYRRTRAQG-HASTAVGAMSYAQGHFSNAFGTYATA 1647 VDIINAAEKGADLAITGTSNOPAGTOITVTNGNYTTTADASGNWSVTVPASRSALG	229 EAAYSLAVGLAAQATKQSSIAVGSNAKANAFAATAIGNTVVNLGR-GVLG   1   1   1   1   1   1   1   1   1		

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C;Species: Rickettsia rickettsii
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 08-Oct-1999
C;Accession: A41477
R;Anderson, B.E.; McDonald, G.A.; Jones, D.C.; Regnery, R.L.
Infect. Immun. 58, 2760-2769, 1990
A;Title: A protective protein antigen of Rickettsia rickettsii has tandemly repeated,
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                                                                                                                                                                                                                                                                                                                                                         SSG---FAAGTALTVVINNOTYAATVLANGSWSVGVPAT-----DVSN-W----PAGTLN 3108
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                                                                                                                  ATGDALVKASDIVAHLNTLSGD---IQTAKGASQANNSAGYVDADGNKVIYDSTDNKYYQ 1419
                                                                                                                                                            AKNDGTVDKTKEVAKDKLVAQAQTPDGTLAQMNVKSVINKEQVNDANKKQGINEDNAFVK 1479
                                                                                                                                                                                                       GLEKAASDNKTKNAAVTVGDLNAVAQTPLTFAGDTGTTAKKLGETLTIKGGQTDTNKLTD 1539
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                                                                                                                                      ASRIVIVSLSAPVISINTIAGDDVINATEKGSDLA--LSGTSDQPAGTAITVTLNGQNYS 2881
SVRTTEQGNIIKDEDKTRAASIVDVLSAGFNLQGNGEAVDFVSTYDTVNFANGNTTTAKV 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SV--ISGLADGTVTISATITDSAGNSSTQTHNVQVNTAAVSLSVSTISGDNLI----NAA
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                                                                                                                                                                                                                           GNSSTASHNVQVNTALPGITINPVATDDIINASEAGSAQTISGQVTGAAAGSTVTVEL--
                                                                                                                                                                                                                                                                     -----GGKTYTATVQADL----SWNVSVPAADWQAL----GNGELTVNASVTNA----
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                                                                           -----NKFALSNO
                                                                                            -----TTLDASGNWSVGVPAADVTALGSGAQTITASVSDRAGNSDD
                                           1980 NAGISSAMAMASMPQAYIPGRSMVTGGIAT--HNGQGAVAVGLSKLSDNGQW 2029
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                                                                           1312 TYDDTSKTSKVVYDVNVDDTTIEVKDK-KLGVKTTTLTSTGTGA--
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A;Reference number: A41477; MUID:90354033
A;Accession: A41477
A;Molecule type: DNA
A;Residues: 1-2249 cAND>
A;Residues: 1-2249 cAND>
A;Cross-references: GB:M31227; NID:9152465; PIDN:AAA26380.1; PID:9152466
A;Cross-references: GB:M31227; NID:9152465; PIDN:AAA26380.1; PID:9152466
A;Note: the authors translated the codon GAT for residue 430 as Gly, and CAA for resl
C;Keywords: surface antigen; tandem repeat
F;1-20/Domain: signal sequence (uncleaved) #status predicted <SIGU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NSVERGL - - - GNTLTIKGDAQTNALTEANIG - - - VVTDGNGLKVKLAKELTGLTSVSAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                             -----AKGNESIAIGGDVLAEGDASIAI------GSDDLYLPKNLDLKNEFHKLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273 GRGVALGFGSQILDRDNN-TDASAYVPL---GKTLADQYKATRQGDSTDIFSI-----
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                                                                                                                                                                                                                                                                                                                                                INNTLKGDALATGEASIAFGSLSKAQGSQAIAIGSVKPDPNNGSNGNVGSH-----
                                                                                                                                                                                                                                                                                                       704;
                                                                                                                                                                                                                                                      Length 2249;
                                                                                                                                                                                                                                                 Query Match 5.9%; Score 608; DB 2; Length 224 Best Local Similarity 22.5%; Pred. No. 1.3e.15; Matches 491; Conservative 224; Mismatches 765; Indels
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Oy Db	818	RNIALGNTIEEKDKSNAASIDDVLNAGFNLKNNGKDKDFVSTYDTVDFIDGNATTATV 87      :     :   :   :   :   TATLGGAVIKATTTKLTNAASVLTLTNANAVLTGAVDNTTGGDNVGVLNLNGALSQV 87	2, L
Qy Dp	876 872	TYDEANQTSKVAYDVNVDEKTIELTGDNGKKQLGVKTIKLTETSTNGNATTFSTD 930	10
Qy Db	931	DDHALVKASDIAGNLNTLAEEIHTTKGTANTALQTFTVKKVDEN 97.	<b>4 4</b> 1
Oy Dp	975	DKADDTNAITV-GKDGTSGKVNTLKLKGKNGLDIKTDKDGTVTFGINTQSGLKAGDSTTL 103:	1033 1019
Qy Db	1034	NNNGLSIKNTASNEQIQVGADGVKFAMVNNGVVGAGIDGTTRITRDEIGFTGTNG	1088 1069
O.Y	1089	SLDKSKPHLSKDGINAGGKKITNIQSGEIAKNSHDAVTGGKIYDLKTELENKISSTAKTA ::	1148
Oy Dp	1149	ONSLHEFSVADEQGNNFTVSNPYSSYDTSKTSDVITFAGENGITTKVNKGVVRVGI	1204
o o	1205	DQTKGLTTPKLTVGN-NNGKGIVINSQNGQNTITG-LSNTLANVTNDKGSVRTTEQGNII	1262 1189
Qy Dp	1263	KDEDKTRAASIVDVLSAGFNLQGNGEAVDFVSTYDTVNFANGNT	1306 1239
Oy Db	1307	EVKDKKLGVKTTTLTSTGTGA 	1354
Qy Dp	1355 1296	NKFALSNQATGDALVKASDIVAHLNTLSGDIQTAKGASQANNSAGTVDAD	1404 1340
Oy Db	1405	GNKUIYDSTDNKYYQAKNDGTVDKTKEVAK	1439
Oy Db	1440	OAQTPDGTLAQMNVKSVINKEQVNDANKKQGINEDNAFVKGLEKAASDNKTKNAAVTV	1497 1447
Qy Dp	1498	GDLNAV-AQTPLTFAGDTGTTAKKLGETLTIKG-GQTDTNKLTDNNIGVVAGTDGFT   :	1552 1491
δ ć	1553	NGLDLGGKVISNVGKGT  :	1612
Q. V	1613	KDTDAANVQQLNEVRNLLGLGNDNADGNQVNIADIKKDPNSGSSSNRT	1560
QQ	1506	ATTANVVLENDAVQLTQTGNIGGFLDFNAKNGMVTLNNNVNVAGAVQNTGTNNGT	1561
0y 0b	1661 1562	VIKAGTVLGGKGNNDTEKLATGGYQVGVDKDGNAN-GDLSNVWYKTQKDGSKRALLA	1716 1611
لام مع	1717	TYNAAGQTNYVTNNPAEAIDRINEQGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIG	1776
CT.	7101	HFNLTGSINKTGGQALKLNFMNGGSVSGVV	1641

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Q O	1642 -	GTAANSVGDITTAGATSFASSVNAKGTATLGGTTSFANTFTNTGAVTLAK 1691
δy	1830	IGDPSTVKADNSYSVGNNNQFTDATQTDVFCVGNNITVTESNSVALGSNSAISAGTHAGT 1889
qq	1692 -	GSITSFAKNVTATSF-VANSATINFSNSLAFNSN1TGG 1728
Qy	1890	QAKKSDGTAGTTTTAGATGTVKGFAGQTAVGAVSVGASGAERRIQNVAAGEVS 1942
Op	1729 -	GTTLTLGANQVTYTGT-GSFTDTLTLNTTFDGAAKSGGNILIKSGSTLDLS 1778
Qy	1943 A	ATSTDAVNGSQLYKATQSIANATN 1966
q	1779 G	GVSTLALVVTATN 1791
RESU B717	LT 6	
Cell C;Sp	surfac ecies:	ce antigen (sca3) RP451 - Rickettsia prowazekii Rickettsia prowazekii
C; Da	te: 21-	Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000 1: B71704
R; An Natu	derssor re 396,	dersson, J.O.; Sicheritz-Po
A;Ti A;Re	tle: The	ne genome sequence of Rickettsia prowazekii and the origin of mitochondria. 2 number: A71630; MUID:99039499
A; AC	atus: F	1: B/1/04 preliminary; nucleic acid sequence not shown; translation not shown
A; Re	sidues: oss-ref perimen	A; Messidues: 1-2340 <and> A; Residues: 1-2340 <and> A; Cross-references: GB:AJ235271; GB:AJ235269; NID:g3868717; PIDN:CAA14908.1; PID:g386 A; Experimental source: strain Madrid E</and></and>
A; Ge	ne: sca	33; RP451
On Be	ery Mat st Loca	Ouery Match 5.7%; Score 591.5; DB 2; Length 2340; Best Local Similarity 21.5%; Pred. No. 5.9e-15;
Ma	tches	307
Qy	35 T	TGQVGSVRTLSFARIAALAVLVIGATLNGSAYAQQITTKIEIGQTNKINNTLKGDAL 91
qq	123 T	TSIITGVGTKTFSNIDFAGKNATLQINKDLNITTKIDNTVAG 164
Qy	92 4	ATGEASIAFGSLSKAQGSQAIAIGSVKPDPNNGSNGNVGSHAKGNESIAIGGDVL 146
qq	165 -	ITFEGSGIISNHIGYTN
Οy	147 4	AEGDASIAIGSDDLYLPKNLDLKNEFHKLIHGHEILKKIQTSTDGKIKYRRTRAQGHA 204
qq	193	GNGEAKIYAPEANNITINAKNINLTHNNSILTLCDGNI 230
Qy	205 8	STAVGAMSYAQGHFSNAFGTYATAEAAYSLAVGLAAQATKQSSIA-VGSNAKANAFAATA 263
QQ	231	TLKGNINNTTEIDGGGILNLAYDLGSSSIITGDIGNIGSLDTINVLLGSA 281
Οy	264 1	IGGNTVVNLGRGVALGFGSQILDRDNNTDASAYVPLGKTLADQYKATRQGDSTDIFSIGN 323
qq	282 I	TFNSTILK-ATNINLKHNISTLNLDDN
Qy	324 8	SNNNNSSIRKIINVGAGSRDTDAVNVAQLKLVEELANRKITFKGDGDNNSN 375
qq	314 1	IKGNNNKDILNFKVHGTNLDNEMIIPAPQKTHGTLNFKGNATLNGNINNLNI 365
Qy	376	-SVERGLGNTLTIKGDAQTNALTEANIGVYDGKULAKELTGLTSV 424
qq	366 I	KFSGGHCKTLNLQGNTKVDNLVFAD-SVLDSGTISVNGLLDTDCVTFNNSNVNGGTLII 424
δy	425 9	SATINKITUSNTNINNAELQ-SGGLTFS-PITGTKTDKTVYSIDGLKFTNDS 473
qq	425 N	NAKNTISAKLLNATKAKIQINANLTMNHPSAGDISDIRIADNTIYTIDAKNGNVNLLNNN 484

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RIONVAAGEVSATSTDAVNGSQL----YKATQSIANATNELDHRIHQNENKANAGISSA 1986 -----THYLSQDIIIKPELHWFINYQCKNKLPNIDARLD-------GIDEP 2287 AGTHAGT-----QAKKSDGTAGTTTTAGATGTVKGFAG--QTAVGAVSVGASGAER 1931 NNPAEAIDRINEGGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVA 1788 DLGGKVIS----NVGKGTKDT-DAANV--QOLNEVRNLLGLGNDNADGNQVNIADIKK-- 1649 | ||| |-----ELTGNGTV 1541 ---HRTTITPMFGMRYATFKNNGYKENNTTFQNLSIKKNYYDKFETILGLNSV-----IGRQTQAGNQSIAIGDNAQATGDQSIAIGTGNVVAG----KHSGAIGDPSTVKADNSYSVG 2139 GLYNWLTNNFEVEALGVYGRNKIKNYEKRITTITDQIAIGKFINTFYSYELLGGYNYLIS -----TQTDVFGVGNNITVTESNSVALGSNSAIS 1693 -NANG-----DLSNVWVK-----TQKD-GSKKALLA---TYNAAGQTNYYT DPN------SGSSS---NRTVIKAGTVLGGKGNNDTEKLATGGVQVGVDKDG--GVKTTTLISTGTGANKFALSNQATGDALV-----KASDIVAHLNTLSGD-IQTAKGASQ AN-NSAGYVDAD-GNKVIYDSTDNKY--YQAKNDGTVDKTKEVAKDKLVAQAQTPDGTLA ANFKDAVVIDAHIDNGGILKFNDNAWLTOEIKNANII----EIASDKFM-----LL QMNVKS------VINKEQVNDANKKQGINEDNAFVKGLEKAASDNKTKNAAVTVG 1709 OKNIKAATLIADNANLVLLDNVEVNTNLNVRDIVLDLA---NYELKYTGNVTHNGLLTI-1499 DLNAVAQTPLTFAGDIGTTAKKLGETLIIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKD LINLNS-----VNAGGTKIDEKGISFVDANGQAKANTPVLSANGL------1542 TINSPHUYSSITTANNAQGNVKLNIEGGITYDLGSKIKSLANVQISEDTTIRGDVYSKYL --EAVDFVSTYDTVNFANGN---TTTAKVTYDDTSKTSKVVYDVNVDDTTI--EVKDKKL 1491 LGAASOVTNITIAGNNIHTLEVIDEDTGNDGIIGDAN-NRLKSI : | | : |||:| | LTIREKPAKITYN--LGGGISTKN 2310 MAMASMPQAYIPGRSMVTGGIATHN 2011 1846 ----NNNOFTDA-----2288 2199 1932 1987 1883 1977 1729 2037 1789 2083 1599 1864 1650 1765 1559 1341 1602 1662 1450 1394 1288 g g õ g g δy QQ ò g δ ò q õ qq ò g ò g ò ος Op ò q ò В g ò g ŏ δ

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OY   712PSFKYQNGDNSNNAITYGKDTNGKTFNTLKLKGENGVNITTNRATGTVTFGIDQS 766	Qy   875 -VTYDEANQTEKVAYDVNVDEKTIELTGDNGKKQLGVKTIKLTETSTNGNAT   925	OY 981NAITV-GKDGTSGKVNTLKLKGKNGLDIKTDKDGTVTFGINTQSG 1024   : :    : :       : :          : :      Db 955 PAKIISGNDLTIDGKEVFNTDSQIIAGGN-LIVQTEKDGLHNEQTFGEKKVFSENG 1009   Qy 1025 LKAGDSTTL	QY         1035         NNGLSIKNTASNEQIQVGADGCVKFAMVNNGVYGAGIDGTTRITRDEIGFTGTNGSLDK         1092           :	QY         1150 NSLHEFSVADEGGNNFTVSNPYSSYDTSK-TSDVITFAGENGITTKVNKGVVRVGIDOTK 1208	QY         1245 NVTNDKGSVRTTEQGNIIKDEDKTRAASIVDVLSAGFNLQGNGEAVDFVSTYDTVN 1300           .	Qy         1361 NQATGDALVKASDIVAHLNTLSGDIQTAKGASQANNSAG	1458 NKEQVNDANKKQGINEDNAFVKGLEKAASDNYTKNAAVTVGDLNAVAQTPL	1538 TDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGTKIDEKGISFVDANGQAKANTP 1538 TDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGTKIDEKGISFVDANGQAKANTP 1577 TGSTVGSLKGDFTTVAGKHYEOIGGSTVSSPEGNNTTYAGSIDIOAAHNKLNSYTTOTY
Science 287, 1809-1815, 2000 AyAuthors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve AyAuthors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A; Reference number: A81000; MUID:20178755 A; Status: preliminary A; Status: preliminary A; Residues: 1-2514 <tet> A; Residues: 1-2514 <tet> A; Residues: 1-2514 <tet> A; Cross-references: GB:AE002526; GB:AE002098; NID:g7227015; PIDN:AAF42109.1; PID:g722702 A; Experimental source: serogroup B, strain MC58 C; Genetics: A; Genetics:</tet></tet></tet>	Query Match  5.3%; Score 553; DB 2; Length 2514;  Best Local Similarity 20.0%; Pred. No. 1.9e-13;  Matches 503; Conservative 332; Mismatches 895; Indels 782; Gaps 121;  4 IYKVIFNKATGTFMAVNEYARSHSTGGGSCATGQVGS-VRTLSFARIAALAVLVIGATL 61  1.	SLSKAQGSQAI :     : : DKAAPKTQQATIL GGDVLAEG	DASIAIGSDDLYLPKNLDLKNEFHKLIHGHEILKKIQTSTDGKIKYRRTRAQGHASTAVG :  :    :	SKIDAPVWGQDVRVVAGGNTVVNLGRGVALGFGSQILDRDNNT-DASAYVPLGKGK	AVNVAQLKLVEELANRKITFKCDGDNNSNSVERCLGNTLTIKGDAQTNALTEANIGVTD  AVNVAQLKLVEELANRKITFKCDGDNNSNSVERCLGNTLTIKGDAQTNALTEANIGVVTD	LKFTNDSNSIATKGTTRITKKKIGFAGTNDGVDESKPYLDNEKLKVGNSTLN	490 SYNASFHSSTTTPTTATG-TGTATVSISNITAPTFAD-GTIRTHGALDNS 537  579 APYLDKERLKVGRVEITTDSGI-NAGNHKITGLTNGIANTDAVTIKQLKDA 628  538 GSIIANGQTDVSAQQGLNNAGQIDIHQLNAKGSAFDNHNGTIISDAVHIQ 587  629 KPTLNAGDGISINSNNGDLVDSSGNITTPTYNISVKTTKL	DNGNITT-RQQLE VSNAHDNNS

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0y 1592	RESULT 8  B65822  D70bable invasin 23135 [imported] - Escherichia coli (strain 0157:H7)  C;Species: Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli R; Perra, N.T.; Plunkett III, G; Burland, V; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew R; Perra, N.T.; Plunkett III, G; Burland, V; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew R; Perra, N.T.; Plunkett III, G; Burland, V; Mau, B.; Glasner, J.D.; Rose, N.T.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001 A; Perra 1000

Qy Dp	1003	NGLDIKTDKDGTVTFGINTQSGLKAGDSTTLNNNGLSIKNTASNEQIQVGADGVKFA 1059 
o v	1060	NVNNGVVGAGIDGTTRI
9 6 7	1080	
ý f	1126	TGGKIYDLKTELENKISSTAKTAQNSLHEFSVADEQGNNFTVSNPYSSYDTSK
G &	1179	TSDVITFAGENGITTKVNKGVVRVGIDQTK-GLTTPKLTVGNNNGK
2 G	1399	
Qy	1226	VINSQNGQNTITGTENTLANVTENTLANVTHDKG 1251 ::   :
δý	1252	SVRTTEQGNIKDE
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ò	1317	
· 6	1629	
QY	1339	TIGHT TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TREE TO THE TREE TREE TREE TREE TREE TREE TREE
qq	1689	NGVPQQEVTLSVSPSEGVTPSNNAIYTTNHDGNFYASFTAXKAGVYQVTATLENXDSMQQ 1748
λ 2	1358	ALSNQATGDALVKASDIVAHLNTLSGDIQFAKGASQANNSAG 1399 ::     : :   : :     : :           : :   :
οy	1400	YVDADGNKVIYDSTDNKYYQAKNDGTVDKTKEVAKDKLVA 1439
QQ	1809	
λõ	1440	QAQTPDGTLAQMNVKSVINKEQVNDANKKQGINEDNAFVKGLEKAASDNKTKNAAVT 1496
3 8	1497	VGDI.NAVAOPPI.PEAG.PEGETTAKKI.GETI.TIKA-GOMDINKI.TININIGVVAGEDGETUKI.
7 A	1921	ITDINGKAEVTLSGTKSGTYPVTVSVNNYGVSDTKQVTLIADAGTAKL 196
δ d	1556	
3 ;	1604	A SELSOY ESE VYST I EGGALMIASOY LUDMIGNEY EGGLANYNE ROLISY I ESSI SY EL DURGERAE UT CAMPARTARARA AMINOSI MENDAMI I OT CAIRMIA ROLINGA RAFOY DIMICOCOLUMBET
g c	2028	VISNVANSTRUDAMANVILNEYRNILLEGENDRADGNIVANILLINDENSESSENKIVI 1062 ::::         ::         ::
οy	1663	
qq	2086	RAHVNDQFGNPILNESVTFSAEPPEHMTISONIVSTDTHGIAEVTWTPERNGSYMVKA 2143
γο	1694	ANGDLSNVWVKTQKDGSKKALLATYNAAGQTNVTNNPAEAIDRINEQ 1741
2 0	1742	GIRF

hypothetical protein 2 - Haemophilus ducreyi
C;Species: Haemophilus ducreyi
C;Species: Haemophilus ducreyi
C;Species: Haemophilus ducreyi
C;Accession: T31105
R;Ward, C.K.; Lumbley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, E.J.
A;Title: Haemophilus ducreyi secretes a filamentous hemagglutinin-like protein.
A;Reference number: 220984; MUID:99030326
A;Accession: T31105
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A;Accession: T311 Gaps 122; A;Cross-references: EMBL:AF057696; NID:g3329021; PID:g3929023; PIDN:AAC79761.1 C;Genetics: 1789 IGRQTQAGNQSIAIGDNAQATGDQSIAIGTGNVVAGKHSGAIGDPSTVKADNSYSVGNNN 1848 1849 QFTDATQTDVFGVGN---NITV---TESNSVALGSNSAISAGTHAGTQAKKSDGTAGTTT 1902 1903 TAGATGTVKGFAGQTAVGAVSVG---ASGAERRIQNVAAGEVSATSTDAVNGSQLYKATQ 1959 2329 RGAITGSVTVSAVTTAGGMQTVDITLVAGPADASQSVLKNNRSSLKGDFTDSAELHLVL- 2387 2388 ------HDISGNPIKVSEGLEFVQSGTNAPYVQVSAIDYSKNFSGEYKATVTGGE 2437 185 63 LGLHNHSPLKVFK-GKNLSVVLLSLMPAMQVWADSSNAIVDH-----SHGAKQTAVDER 115 116 DPKNGKEKVVVINIAKPDEQGISDNHFSKFNIPNSAVFNNSI-----KEGNSQL-VG- 166 231 STSEVVEPHIKQLNVQRGKVIIGKDGVATNGLSHFDVVAKNIEQOGKVSIEGDSKPAKLA 290 44 LSFARIAALAVLVIGATLNGSAYAQQITTKIEIGQTNKINNTLKGDALATGEASIAFGSL 103 104 SKAQGSQ-AIAIGSVKPD-----PNNGSNGNVGSHAKGNESIAIGGDVLAEGDASIAIGS 157 158 DDLYLPKNLDLKNEFHKLIHGHEILKKIQTSTDGKIKYRRTRAQGHASTAVGAMSYAQGH 217 --IFSIGNSN------NNNSSIRKII-----NVGAGSRDTDAVNVAQLKLVEELAN 361 2 NHIYKVIFNKATGTFMAVAEYAKSHSTGGGS-------CATGQVGSVRT 43 3 NKRYKLIFSKVKNCLVPVAENIKSASGNSGSSSNSKIAEDQEEEPDSLACSLSPLSSSIH 62 2281 STLKATVED--GSGNLIEGLTVYFALKSGSATLTSLTAVT------DONGIATTSV 218 FSNAFGTYATAEAAYSLAVGLAAQATKQSSIAVGSNAKANAFAATAIGGNTVVNLGRGVA -----VTGDQESKISGGLEVFGEKADLFIINPN-----GVTLNGVKTINTDRFVA -----LGFGSQILDRDN--NTDASAYVPLGKTLADQYKATRQGDSTD----2006 GIAT-----SADTQGAVAVGLSKLSDN-GQWVFKING-----SADTQGHVGA 2045 2438 GIATLIPVLNGVHQAGLSTTIQFTRAEDKIMSGTVLVNGANLPTTFPSQGFTGA 2492 Query Match 5.2%; Score 540.5; DB 2; Length 4919; Best Local Similarity 19.9%; Pred. No. 1.4e-12; Matches 503; Conservative 331; Mismatches 913; Indels 785; 1960 SIANATNELDHRIHQNENKANAGISSAMAMASMPQAYIPG---------LLGENKNLGSQAAKTIFNQ------167 278 q g δ qq q ò g QQ Op Ωÿ qq g Db δy ò qq ŏ ŏ à õ ŏ . ò

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Qy	1446 GTLAQMNVKSV	GTLAQMNVKSVINKEQVNDANKKOGINEDNAFVKGLEKAASDNNTKNAA 1494
QQ	1570 VYLAKQTIEEV	AGYAVGLE
QY	1495 VT	٠,
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Qy	1518	AKKLGET 152.
qq	1683 ASELKGNTGQ	174
ογ	1525	SVN
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Qy	1567	AANVQQLNEV 162
qq	1801	185
٥y	1627	9 6
qq	1853	191
οy	1682 GGVQVG	NANGDLSNVWYKTOKDGSKKALLATYNAAGOTNYVTNNPAEAIDR 173
Dp	1912	
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QΥ	1785	184
QQ	2027	1I. 2
ò	1845	TA 190
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οy	1905	GATCTVKGFAGOTAVGAVSVGASGAERRIQNVAAGEVSATSTDAVNGSQL-YKATQSI 1961
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qa	2183	- L'HL - DVKGDTNVVSKQDSYSRKERGVNYSVSAGVGVSTAGGARPNGSVGL
Qy	2019	2WV 2030
qq	2241	KIV 2252

Db 708 KPGVTTDWKETADGVXKATYTAYTKGSGLTAKLLMQNWNEDLHTAGFIIDANPQSAK 764 Qy 631TLNA-GDGISINSNNGDLVDSSGNITTPTXNISVKTTKLNSNGTSGNNK 678	679FSVSNAHDNNSLVTAKDLADYLNKVNETADSALPSFKVQNGDNSNNAITVG	Db 881 NDSVTMTATVRDAKGNLLNDVMVTFNVNSAEAKLSQTEVNSHDGIATATLTSLKNGDY 938 QY 785 LVIEQVPS-ADGNSTKNIKGLSPTLPSIASPSGRNIALGNTIEE	QY 830 DKSNAASIDDVLNAGFNLKNNGKDKDFVSTYDTVDFIDGNATT 872   1   1   1   1   1   1   1   1   1	QY 873 ATVTYDEANQTSKVAYDVN-VDEKTIELT-GDNGKKQLGVKTIKLT 916  DD 1058 MTFVADKDRAVVVLQTSKAEIIGNGVDETTLTATVKDPSNHPVAGITVNFTMPQDVAANF 1117	917	QY 966 FTVKKVDENDKADDTNAITVG-KDGTSGKVNTLKLKGKNGLDIKTDKDGTVTFGI 1019	QY 1020 NTQSGLKAGDSTTLNNNGLSIKNTASNEQIQVGADGVKFAMVNNGVVGAGIDGTTRI 1076	QY 1077 TRDEIGFTGTNGSLDKSKPHLSKDGINAGGKKITNIQSGEIAKNSHDAVTGGKIYDLKTE 1136	1137 LENKISSTAKTAQNSLHEFSVADEQGN-NFTVSNPYSSYDTSKTSDVITFAGENGITT	1194KYNKGVVRVGIDQTKGLTTPKLTVGNNNGKGIVINSQNGQNTITGLSN	QY 1242 TLANVTNDKGSVRTT-EQGNIIKDEDKTRAASIVDVLSAGFNLQGNGEAVDFVSTYDTVN 1300  DD 1425 PSEGVTPSNNAIYTTNHDGNFYASFTATKAGVYQLTATLENGDSMQQTVTY-VPN 1478	QY 1301 FANGNTTTAKVTYDDTSKTSKVVZDVNVDDTTIEVKDKKLGVKTTLLTSTGTGANKFALS 1360	QY 1361 NQATGDALVKASDIVAHLNTLSGDIQTAKGASQANNSAGYVDADGNKVIYDSTDNKYYQA 1420  DS 1517 NTEVTFTLPEDVKANFTLSDGGKVITDAEG 1546	OY 1421 KNDGTVDKTKEVA	QY 1458 NKEQVNDANKKQGINEDNAFVKGLEKAASDNKTKNAAVTVGDLNAVAQTPLTFAGDTGTT 1517  1	QY 1518 AKKLGETLTIKG-GQTDTNKLTDNNIGVVAGTDGETVKLAKDLTNL 1562
RESULT 10 D64962 probable membrane protein b1978 - Escherichia coli C;Species: Escherichia coll C;Date: 12-Sep-1997 #sequence revision 17-Sep-1997 #text change 02-Feb-2001	erna, N.T.; Burlan La coli K-12.	ccession: D84962 tatus: nucleic acid sequence not shown; translation not shown Olecule type: DNA esidues: 1-2383 <blat> essidues: 1-2383 <blat> coss:references: GB.AE000289; GB:U00096; NID:91788285; PIDN:AAC75042.1; PID:91788288;</blat></blat>	Keywords: nucleotide binding; P-loop; transmembrane protein 54-70/Domain: transmembrane #status predicted <tmm> 1564-1571/Region: nucleotide-binding motif A (P-loop)</tmm>	Ouery Match 5.1%; Score 526.5; DB 2; Length 2383; Best Local Similarity 22.0%; Pred. No. 1.8e-12; Matches 523; Conservative 302; Mismatches 933; Indels 615; Gaps 125;	AVLVIGATLNGSAYAQOITTKIEIGQTNKINNTLKGDALAI 	95 EASIAFGSLSKAQGSQAIAIGSVKPDPNNGSNGNVGSHAKGNESIAIGG 143	144DVLAE-GDASIAIGSDDLYLPKNLDLKNEFHKLIHGHEILKK 184 	FEDDLSKY KRAGIGA - EWRDY IKLSSNAYIRITMM	BAAYSLAVGLAAQATKOSSIAVGSNAKANAFAATAIGGNTVVNLGRGVALGFGSQI :	285 LDRDNNTDASAYVPLG-KTLADQYKATRQGDSTDIFSIGNSNNNN 328	329 SSIRKIINVGAGSRDTDAVNVAQLKLVEELANRKITFKGDGDNNS-NSVERGLGN 383	384 TLTIKG-DAQTNALTEANIGVVTDGNGLKVKL-AKELTGLFSVSATNKITVSNTNNNN 439				KVGRVEITTDSGINAGNHKITGLTNGIANTDAVTIKQLKDAKP

SATI GKPI PTVT		450 SPITGTKTDK 1195 DTTAPTVIN 510 LKVGNSTLNS :	614 1328 668 668 1378 726 726 7418 782 782 782 782 7839	Db 1547
LESANGLDLGGK       :   :   :   :   :   :   :   :   :	OY 1710 SKKALLATYNAAGGTNYVTNNPABAIDRINEOGIREFHVNDGMEN 1730	2074 1925 2074 1982 2123 2020	SULT 11. 6109 pothetic pothetic Variety Variety Variety Narcessi Kaneko, K., Ok N., R., Ok N., R., Ok N., R., Ok Title: Title: Status S	Ouery Match  Quest Match  Action 10.4%; Score 526; DB 2; Length 3029;  Best Local Similarity 20.4%; Pred. No. 2.6e-12;  Best Local Similarity 20.4%; Pred. No. 2.6e-12;  Best Local Similarity 20.4%; Pred. No. 2.6e-12;  Action 2.6e-12;  Qy 60 TLNGSATAQOITTRIEIGQTMKINNTLKG

λ	1066	
ą	1649	GEWILDYTGTLLADGDYELSVTATNPTGNSATATQTIVVDTTAPTVTINAIP
<u>X</u>	1105	
ą	1709	EAGSPVAVSGTTTGVEDGQVVTVTIDGN
Ϋ́	1151	STHE
ą	1768	;
<u>&gt;</u>	1196	NKG-VVRVGIDQTKGLTTPK
ą	1823	EDGQVVTVTIDGNTYTATVTGNAMTFNIPVADIANFEATEEVVATVSD 1870
<u>≯</u>	1249	
ą	1871	LAGNPATPATRIITVDTVAPAVTIDSISDDTGAQANDFITNDDTLVF-NGTAEA 1923
Σ.	1307	-TTAKVIYDDTSKTSKVVYDVNDDTTIEVKDKKLGVKTTTLLSTGTGANKFALSNQ 1362
ā	1924	DSTVVVSLDGIEIGTVTANGAGEWT
<u>&gt;</u>	1363	ATGDALVKASDIVAHLNTLSGDIQTAKGASQANNSAGYVDADGNKVIYDSTDNKYYQA 1420
Ð	1977	ATQTIVVDTTAPTVTINA
<u>&gt;</u> .	1421	KNDGTVDKTKEVAKDKLVAQAQTPDGTLAQMNV 1453
ą	2037	TVTGNAWTFNIPVADIANFEATEEVVATVSDLAGNPATPATRNITVDTTAPTVTINAIAV 2096
Σ.	1454	KSVINKEQVN
ð	2097	DDIINAVEAGSPVAVSGTTTGVEDGQVVTVTIDGNTYTATVTGNAWTFNIPVADIANFEA 2156
<u>≯</u>	1490	TKNAAVTVGDLNAVAQTPLTFAGDTGTTAKKLGETLTIKGGQTDTNK
ą	2157	
<u> </u>	1545	VAGTDGFTVKLAKDLTNLNSVNAGGTKIDEKGISFVDANGQ1585
ð	2213	FNGTAEADSTVVVSLDGIEIGTVTANGAGEWTLDYTGTLLADGDYELSVTATNPTGNSAT 2272
λ	1586	AKANTPVLSA10LDGGKV-ISNVGKGTKD
ą	2273	ATQTIVVDTTAPTVTINAIAVDDIINAVEAGSPVAVSGTTTGVEDGQVVTVTIDGNTYTA 2332
Ϋ́	1615	TDAANVQQLNEVRNLLGLGNDNADGNQVNIADIKKDPNSGSSSNRTV 1661
ð	2333	TVTGNAWTFNIPVADIANFEATEEVVATVSDLAGNPATPATRNITV 2378
λ	1662	I
ð	2379	DITAPTVIINAIAVDDIINAVEAGSPVAVSGTTTGVEDGQVVTVIIDGNTYTA 2431
Ϋ́	1694	
q	2432	TVTGNAWTFNIPVADIANFEATEEVVATVSDLAGNPATPATRNITVDTVAFAVT 2485
۲	1735	
ą	2486	IDSISDDIGAQANDFITNDDILVFNGTAEADSTVVVSLDGIEIGTVTANGAGEWTLDYIG 2545
λ	1778	
ð	2546	TLLADGDYELSVTATNPTGNSATATO
Δ	1824	
ð	2606	GTTTGVEDGQVVTVTIDGNTYTATVTGNAWTFNIPVADIANFEATEEVVATVSDLAGNPA 2665

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filementous hemagglutinin 1 - Haemophilus ducreyl Gispecies: Haemophilus ducreyl Gispecies: Haemophilus ducreyl Cispecies: Haemophilus ducreyl dispecies: Haemophilus ducreyl dispecies: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999 Giaccession: T3102
R.Ward, C.K.; Lumbley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, E.J.
J. Bacteriol. 180, 6013-6022, 1998
A.Title: Haemophilus ducreyl secretes a filamentous hemagglutinin-like protein. A.Reference number: 220984; MUID:99030326
A.Reference number: 220984; MUID:99030326
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 14152 GWAR>
A.Residues: EMBL.AF057695; NID:93929017; PID:93929018; PIDN:AAC79757.1
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-- NSVALGSNSAISAGTHAGTQAKKSDGTAGTTTT 1903
                              2666 TPATRNITVDTTAPTVTINAIAVDDIINAVEAGSPVAVS-GTTTGVE----DGQVVTVTI 2720
                                                                                                     1904 AG--ATGTVKGFAGQTAVGAVSVGASGAERRIQNVAAGEVSATSTDAVNGSQLYKATQSI 1961
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 ---CSLSPLSSSIHLGLHNHSPLKVFKGKSLSVVLLSLMPATPLLAQONYAEALNGKVYV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 HKLIHGHEILKKIQTSTDGKIKYRRTRAQGHASTAVGAMSYAQGHFSNAFGTYATAEAAY 232
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2772 TVDTVAPAVNELD 2784
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1887 AGTQAKKSDGTAGTTTTAGATGTVKGFAGQTAVGAVSVGASGAERRIQNVAAGEVSATST 1946
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                                                                                                                                                                                                                                                                                                                                              -----TTAKKLGET-----LTIKG--GQTDTNKLTDNNIGVVAGTDGFTVKLAKDLT 1560
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                                                                                                                 | : | | : | | : | | : | | SEGHIYLETDKDKNVDLTASELKGNTGQIKAKDLNLNDIYETSYKYKYEKLFGKNGGEIG 1595
                                                                  D--KTKEVAKDKLVAQAQTPDGTLAQMNVKSVINKEQVND-------ANKKQGI 1471
---KVDDVRNTGTI 1480
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                                                                                                                                                                                                      NEDNAFV-----KGLEKAASDNKTKNAAVTVGDLNA--VAQTPLTF-----AGDTG
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       1433 AQEVLVPQVYLAKQTIEEVEKORGVGTGQIRAGIIDV----
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hemagglutinin/hemolysin-related protein NMB0493 [imported] - Neisseria meningitidis (hemagglutinin/hemolysin-related protein NMB0493 [imported] - Neisseria meningitidis (c. Species: Nisseria meningitidis (c. Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001 (c. Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001 (c. Date: 31-Mar-2001 M.) #sertelin, H.; Sanders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, R.; Pettelin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Mastgnanl, V.; Pizza, M. ri, H.; Olin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Mastgnanl, V.; Pizza, M. Science 287, 1809-1815, 200 (j. Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoll, R.; A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A; Reference number: A81000; MUID:2017575 A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-2703 <TET>
A;Cross-references: GB:AE002405; GB:AE002098; NID:g7225708; PIDN:AAF40927.1; PID:g722
A;Cross-references: GB:AE002405; GB:AE002098; NID:g7225708; PIDN:AAF40927.1; PID:g722
A;Cross-references: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB0493

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13		2 14	147 154	07 91	264 245	319 288	377	437	496 418	മ	595 521	642 580	685 640	724	782	839 801	875 849
Match 4.9%; Score 512.5; DB 2; Length 2703; Accal Similarity 20.0%; Pred. No. 7.2e-12; Indels 887; Gaps 531; Conservative 345; Mismatches 893; Indels 887; Gaps	MNH-IYKVJENKATGTEMAVAEYAKSHGGGSCATGQVGSVRTLS 45    :     :    :	FARIAALAVLVIGATLNGSAYAQQITTKIEIGQTNKINNTLKGDALA 92 	TGEASIAFGSLSKAQGSQAIAIGSVKPDPNNGSNGNVGSHAKGNESIAIGGDVLA 147   1   1   1   1   1   1   1   1   1	EGDASIAIGSDDLYLPKNLDLKNEFHKLIHGHEILKKIQTSTDGKIKYRRTRAQGHASTA 207   :     :     :     :     :     :       :	VGAMSYAQGHFSNAFGTYATAEAAYSLAVGLAAQATKQSSIAVGSNAKANAFAATAI 264	GGNTVVNLGRGVALGFGSQILDRDNNTDASAYVPLGKTLADQYKATRQGDSTDIF 3 ::	SIGNSNNNNSSIRRKIINVGAGSRDTDAVNVAQLKLVEELANRKITFKGDGDNNSNSV 3:   :   :                     ::     ::	ERGLGNTLTIKGDAQTNALTEANIGVYTDGNGLKVKLAKELTGLTSVSATNKITVSNTNN 4	-FAGTND  : RLKNQNN	GVDESKPYLDNEKLKVGNSTLNSGSLTVNNTTGNKQLQV 53:	GANGIKFATVANNVANTSATVGTARITEEKIGFAGTNDGVDEQAPYLDKERLKVGRVEIT 59:	TDSGINAGNHKITGLTNGIANTDAVTIKQLKDAKPTLNAGDGISINS- 6	NNGDLVDSSGNITTPTYNISVKTTKLNSNGTSGNNKFSVSNAH	DNNSLVTAKDLADYLNKVNETADSALPSFKVQNGDNSNN 7	AITVGKDTNGKTFNTLKLKGENGVNITTNRATGTVTFGIDQSNGLTTPKLTVGSDTNG 7	NRLVIEQVPSADGNSTKNIIKGLSPTLPSIASPSGRNIALGNTIEEKDKSNAASIDD-8	VVERDLTAGKQLNLSIKGRLKNTHTLQAGHTLKLNAGKDFVSTYDTVDFIDGNATTATV 87
Query Matc Best Local Matches 5	пп	46 59	93	148 155	208	265	320	378	438 365	497	536	596	643 581	686	725	783	840
Qué Bes Mat	ZY Ob	2y Ob	oy Ob	Qy Dp	oy Ob	op Op	oy Ob	oy Ob	oy Dp	Oy Db	oy Op	oy Db	Oy Dp	oy Bb	S G	Oy Db	cy Op

δy	876	TYDEANQTSKVAYDVNVDEKTIELTGDNCKKQLGVKTIKLTETSTNGNATTFST 929
QQ	850	GTGKI
οy	930	ALQT
QQ	903	LNREETTEGSTRAGAIAARKRLDIGAKEIHNQEGALLSSEGIFAVGNRLDEQHHA 957
οy	983	ITVGKDGTSGKVNTLKLKGKNGLDIKTD1010
qq	958	GMADTE-VNGSAGLEVQ
οy	1011	1027
qq	1009	VLGQNTYYQAGKDGLFDNSQGQKDQTTATFHLKNGSRIEANQWHVRDYHIETYKERIIEN 1068
Oy .	1028	GDSTILNNNGLSIKNTASNEQIQVGADGVKFAMVNNGVVGAG 1069
Op	1069	RPAHITVGGDLTASGQNWLNKDSRIVVGGRIITDDLNQKEITNQSTTGKGRTDAV 1123
Qy	1070	IDGTTRITRDE1GFTGINGSLDKSKPHLS 1098
qq	1124	GTQWDSVTKKGWYSGRKRQRRTERNHTPYHDTQLFTHDFDTPVSVIQQNAASPSFQPAAS 1183
Qy	1099	KDGINAGGKKITNIQSGEIAKNSHDAVTGGKIYDLKTELENK1140
QQ	1184	AIKLIDGVSTAAVNGQRIHTGNVVSLNNATVTLPNSSLYTTHPDNKGWLVETDPQFAD 1241
Qy	1141	ISSTAKTAQNSLHEFSVADEQGNNFTVSNPYSSYDTSKTSDVI 1183
QQ	1242	YRRWLGSDYMLQQLQLDTNHLHKRLGDGYYEQKLVNEQIHQLTGYRRLDGYRSDEE 1297
Qy	1184	TFAGENGITTKVNKGVPRVGIDQTKGLTTPKLT 1216
qq	1298	QFKALMDNGLTAAKTFGLTPGIALSAEQVARLTSDIVWMENQTVTLSDGSTQTVLVPKVY 1357
δy	1217	VGNNNGKGIVINSONGQNTITGLSNTLANVTNDKGSVRTTEGG 1259
QQ	1358	ALARKGDLNTSGGLISAEQVLLKLQNGNLT
δλ	1260	NIIKDEDKTRAASIVDVLSAGFNLQGNGEAVDF
QQ	1418	
Qy	1312	TYDDTSKTSKVVYDVNVDDTTIEVKDKKLGVKTTTLTSTGTGANKF 1357
qq	.1470	
ΟŸ	1358	ALSNQATGDALVKASDIVAHLNTLSGDIQTAKGA-SQANNSAGYVDADGNKVI 1409
Dp	1524	돲
Óλ	1410	;
qq	1584	LAAGRDVIISEGRQITELDTSVSGKSKGILSSTKTHDRYRFSHDEAVGSNIGGGKMIVAA 1643
δλ	1442	QTPDGTLAQMNVKSVINKEQVNDANKKQGINEDNAFVKGLE 1482
qq	1644	GQDINVRGSNLISDKGIVLKAGHDIDISTAHNRYTGNEYHESKKSGVMGTGGLGFTIGNR 1703
ΟŸ	1483	KAASDNKTKNAAVTVGDLNAVAQTPLTFAGDTGTTAKKLGETLTIKGGQTDTN 1535
QQ	1704	Ä
δλ	1536	KLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGTKIDEKGISFVDANG
qq	1751	
δλ	1596	NGLDLGGKVISNVGKGTKDTDAANVQQLNEVRNLLGLGNDNADGNQVN 1643
q	1791	AQNFIQAAQNVGKSKNKRVNAMAAANAAWQSYQATQQMQQFAPSSSAGQGQNNNQSPSIS 1850
ò	1644	IADIKKDPNSGSSSNRTVIK-AGTVLGGKGNNDTEKLATG-GVOVGVDKDGNANG 1696

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1056 VKF---AMVNNGVVGAGIDGTTRITRD-EIGFTGTNGSLDKSKPHLSKDGINAGGKKITNI 1112
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                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     832 --SNAASIDDVLNA-GENLKNNGKDKDFVSTYDTVDFIDGNATTATVTYDEANQTSKVAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NITTNRAT----GTVTFGIDQSNGL------TTPKL,TVGSDTNGNRLVIEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----NLWQI-----DEANNTVALEGVSADGATKWQYNHNGELVITGD---NATVNNNGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            403 VYTDGNGLKVKLAKELTGLTSVSATNKITVSNTNNNNAELQSGGLTFSPITGTKTDKTVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232 TTVDG------KDSTG-TEIN------GNNGKVIQDGDLDVSG------
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                                                                                                                                                                                       2020;
                                                                                                                                                                                                                                                                                                                                                                  147 ILDKTEKT-----LTIRDSVFTYTENAÖGT--ISLQDSNGRKATI---
                                                                                                                                                                                          Length
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hes 663;
                                                                                                                                                                                             DB 2;
A; Experimental source: strain K-12, substrain MG1655 C; Genetics:
A; Gene: ydbA_2
A; Start codon: GTG
                                                                                                                                                                                                                                                 405; Conservative 224; Mismatches
                                                                                                                                                                                          4.8%; Score 499.5; 20.8%; Pred. No. 1.5
                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                       Query Match
Best Local S:
Matches 405;
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A, Experimental source: strain K-12
A, Note: sequence inconsistent with the nucleotide translation
A, Note: sequence extracted from NGB backbone (NCBIN:88089, NCBIP:88090)
B, Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
A,; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A, Fittle: The complete genome sequence of Escherichia coli K-12.
A, Reference number: A64720; MUID:97426617
A, Accession: D64891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: nucleic acid sequence not shown; translation not shown A;Status: nucleic type: DNA A;Molecule type: DNA A;Residues: 'M', 915-2020 (BLA2> A;Residues: 'M', 915-2020 (BLA2> A;Cross-references: GB:AE000237; GB:U00096; NID:91787665; PIDN:AAC74487.1; PID:91787672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1839, 'LDLPHYFOTSVIT' <BLA1>
A; Residues: 1839, 'LDLPHYFOTSVIT' <BL00096; NID:g1787665; PIDN:AAC74483.1; PID:g1787668; A; Cross-references: GB:AE000237; GB:U00096; NID:g1787665; PIDN:AAC74483.1; PID:g1787668; A; Experimental source: strain K-12, substrain MG1655
A; Accession: H64891
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C,Species: Escherichia coli
C,Species: Bscherichia coli
C,Species: 19-Nov-1993 #sequence_revision 16-Oct-1998 #text_change 08-Oct-1999
C,Accession: C48399; D64891; H64891
E;Moszer, I.; Glaser, P.; Danchin, A.
Biochimie 73, 1361-1374, 1991
A,Title: Multiple IS insertion sequences near the replication terminus in EsA;Reference number: A48399; MulD:92190338
A,Reference number: C48399.
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LGNTQSYERYQ---EARTLLEAELGNTDSEA----EKAAFRASLGQVNAYLAENQSRYDT 2300
                                      :: | : | : | : | : | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 1008 | 10
                                                                                                                       DL---SNVWVKTQK-DGSK--KALLATYNAAGQTNYVTNNPAEAIDRINEQGIRFFHVND 1750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D-GIVIDKQGRPIDRISPAAGYGSDGDSKNSTIRSGVNTHNIHITDEAGQLA--RIGRIA
                                                                                                                                                                                                                                                 1751 GN-----QEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGRQTQAGN-----Q
                                                                                                                                                                                                                                                                                                        GNIGKGKEQGGSTTHRHTHVGSTTGKTTIRSGGDTTLKGVQLIGKGIQADTRNLHIESVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TDATQTDVFG------VGNNI----TVT-----ESNSVALGSNSAISAGT
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| ALTADNHIRLQSAKQDGSEQSKNKSSGWN-AGVAVKIGN---
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A; Residues: 464-2020 <MOS>
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OTKGLTTP 1213 GKDPAPSP 893 TEQCNIIK 1263	SDIVAHLNTL 1381 ::	TYGDL- 1500   :   :   :   I ::     ::   NIGVVA 1546     ::	ANGLDLG 1601   : : -NNVDVS 1225 DIKKDPN 1652	OKDGSK 1711 : : :SSEGNN 1319 :IDSSAS 1768 ::: :NISN 1364		GTWGREAG 1915   :        EBNNGTINIFAN 1502  ANATNELDHR 1971      
GENGITTKVNKGVVRVGIDQTKGLTTP		KKQGINEDNAFVKGLEKAASDNKTKNAAVTVGDL-	AKANTPVLS     :: VIKNAGVMT ADGNQVNIA	GVDKDGNANGDLSNVW-VK 	GNGITVTESNSVALGSN  SHOW THE STATE OF THE	GTWGTTTTGTWGFAG  NNGTINLGTAGTTTTT
SSYDTSKTSDVITFA-	VVYDVNUDDTIEVKDKKLGVKTTTLTSTGTGANKFALSNQATGDALVKASDIVAHLNTL : :	PDGTLAQMNVKSVINKEQVNDANKKQCINEDNAFVKGLEKAASDNKTKNAAVTVGDL-	IINN DAAN	SGSSSNRTVIKAGTVLGGKGNNDTEKLATGGVQVGVDKDGNANGDLSNVW-VKTQKDGSK	SSHNGAVNAW	VNNGT RIQNV AMASM :: YTL
VADEOGNNETVSNPY		OTPDGTLAQMN     VYEHGT		SGSSSNRTVIKAG    : : SGSVTGRMM KALLATYNAAGOT :   : TCMLEVNNSAFN GKHSVAIGFOAKA		
1157 862 1214 894 1264	1322 1002 1382 1045	1442 1084 1501 1124	1547 1182 1602 1226	1653 1269 1712 1320 1769	1365 1365 1395	1885 1443 1916 1503 1555 2028 1596
0	8 5 B 5	9 9 9 9	90 oy	6 a 6 a 6	6 6 6 6	

RESULT 15 C83339 hypothetical protein PA2462 [imported] - Pseudomonas aeruginosa (strain PAO1)

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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accesion: C8339
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A;Reference number: A82950; MUID:20437337
A;Accession: C83339
A;Accession: C83339
A;Accession: C83339
A;Accession: C83339
A;Coloule type: DNA
A;Residues: 1-5627
A;Coss.references: GB:AE004673; GB:AE004091; NID:99948501; PIDN:AAG05850.1; GSPDB:GN
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA2462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps 111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1927 ---SASLDNSQGGIVSA----KGAAE-----IRTGSLNNSQKG-----GI 1959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2151 KGDLQVTVGTLEQQGGELASQGTLTLDADSLDNRNGGLVSADGGVTAEARQIDNRGGEIS 2210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2070 DSLTLRIAQALDNSLQGVLSASGGL------DVAALVFDNHSGIVASKGDT 2114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --LKNEFHKLIHGHEILKKIQTSTD-----GKIKYRRTRAQGHASTAVGAMSYAQGHF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNAFGTYATAEAAYSLAVGLAAQATKQSSIAVGSNAKANAFAATAIGGNTVVNLGRGVAL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279 GFGSQILDRDNNTDASAYVPLGKTLADQYKATRQGDSTDIFSIGNSNNNSSIRRKIINV 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 387 IKGDAQTN------ALTEANIGVVTDGNGLKVKLAKELTGLTSVSATNK----- 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 538 NGIKFATVA--NNVANTSATVGTARITEEKI-----GFAGTNDGVDEQAPYLDK---ERL 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KVGRVEITTDSGINAGNHKITGLTNGIANTDAVTIKQ-LKDAKPTLNAGDGISINSNNGD 646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 ESIAI-----GGDVLAEGDASI------AIGSDDLYL--PKNLD------ 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   483 RITKKKIGFAGTNDGVDESKPYLDNEKLKVGNSTLNSGSLTVNNTTGNKQI-----QVGA 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NKVNETADSALPSFKVQNGDNSNNAITVGKDTNGKTFNTLKLKGENGVNITTNRATGTVT 760
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Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;
A protective protein antigen of Rickettsia rickettsii has tandemly repeated, near-identical sequences.";
Infect. Immun. 58.2760-2769(1990).
-!-FUNCTION: ELICITE PROTECTIVE IMMUNITY.
-!-FUNCTION: ELICITE PROTECTIVE IMMUNITY.
-!-FUNCTION: CLYCOSYLATED (POSSIBLE).
-!- FUN GLYCOSYLATED (POSSIBLE).
-!- DISEASE: PROBABLY PLARS AN IMPORTANT ROLE IN THE PATHOGENESIS OF AND IMMUNITY TO ROCKY MOUNTAIN SPOTTED FEVER.
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13 X APPROXIMATE TANDEM REPEATS.
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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190 KDA ANTIGEN PRECURSOR (CELL SURFACE ANTIGEN)
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PIR; A41477; A41477.
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3 I (INCOMPLETE). A9D6646C089DF087 CRC64;

(TYPE II

5.9%; Score 608; DB 1; Length 2249; Similarity 22.5%; Pred. No. 1.1e-14; 1; Conservative 224; Mismatches 765; Indels 704; Gaps	INNTLKGDALATGEASIAFGSLSKAQGSQAIAIGSVKPDPNNGSNGNVGSH 134 	AKGNESIAIGGDVLAEGDASIAIGSDDLYLPKNLDLKNEFHKLI 176	FGT	HGHEILKRIGTSTOOLDALTAN TANGEN TO THE TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TOTAL TO THE TOTAL TOTAL TOTAL TOTAL TO THE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TO THE TOTAL TOTA	YATABAAYSLAVGLAAQATKQSSIAVGSNAKANAFAATAIGGNTVVNL 272	IALGGANAALIIQSAAPSKITLAGNIDGGGILTYKIDA-AINOITGNINALAINOITGNINAAINOITGNINAAINOITGNINAAINOITA	GRGVALGEGOLLLENDIN LOADING TO THE STREET OF THE GROUP CONTROLLENDING CONTROLLEND CONTROLLENDING CONTROLLEND CONTROLLENDING CONTROLLENDING CONTROLLENDING CONTROLLENDING CON		ָרָ לְּ	NSVERGLGNTLTIKGDAQTNALTEANIGVVTDGWGLKVKLAKELIGLIGLIGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	NA-NNGIVIETGUGITATONIOTIATONIOTIATURE NA NA NA NA NA NA NA NA NA NA NA NA NA	NKITYSNINNNNEELZOOTIE   :       :	-TTRITKKKIGFAGTUDGVDESKPYLDNEKLKVGNSTLNSGSLTVNNTTGNKQIQV-G 536	ANAVLTG AIDNTTGGDNVGVLN	ANGIKFATVANNVANTSATVGTARITEEKIGFACTNDGVDEQ 5/8	LNG-ALSQVIGNIGNINDLALITY CAROLITY CAROL		TDAVTIKQLKDAKPTLNAGDGISINSNNGDLVDSSGNITTPTYN 660	_		8	AGTATLGGAVINALLIA	LTVGSDTNGNRLVIEQVPSADGNSTKNIIKGLSPTLPSIASPSG 81/		RNIALGNTIEEKDKSNAASIDDVLNAGENLKNNGKDFVSTYDTVDFILGNATIATV 0/2  RNIALGNTIEEKDKSNAASIDDVLNAGENLKNNGKDKDFVSTYDTVDFILDVLNIALV 0/2	FATLGGAVIANTII NAIMENOVALLIIN NAIMENOVALLII NAIMENOVALII	TYPEANQTRYVAIDYNVERTIELIGENOSMALS	DDHALVKASDIAGNLNTLAEEIHTTKGTANTALQTFTVKKVDEN 974
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2 70	DOTKGLTTPKLTVGN-NNGKGIVINSONGONTITG-LSNTLANVTNDKGSVRTTEOGNII 126
QQ	gdigntnalatvnvgagitlqaggsl
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2 2	NKFALSNOATGDALVKASDIVAHLNT
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Qy dy	1440 QAQTPDGTLAQMNYKSVINNEQV
8 8	GDLNAV-AQTELTEAGDTGTTAKKLGETLTIKG-GQTDTNKLTDNNIGVVAGTDGFT 155:
QQ	149
οy	1553 VKLAKDLTNLNSVNAGGTKIDEKGISFVDANGQAKANTPVLSANGLDLGGKVISNVGKGT 1612
qq	
δλ	1613 KDTDAANVQQLNEVRNLLGLGNDNADGNQVNIADIRKDPNSGSSSNAK 1000
qq	1506 ATTANVVLENDAVQLTQTGNIGGFLDFNAKNGMYTLNNNNNNAGAVQ- NIGGT NIG
οy	1661 VIKAGTVLGGKGNNDTEKLATGGVQVGVDKDGNAN-GDLSNVWYNIUMUSARNTEL 
g	1562
ΟŊ	1717 TYNAAGGTNYVTNNPAEAIDRINEGGIKEFHVNUGEVVGGKNGLEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
q	1612 HFNLTGSINKTGGQALALMERMAGGSVSGV
Οy	1777 FQAKADGEAAVAIGRQTQAGNUSIALGUNAQA1 GOOTIN
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δλ	1830 IGDPSTVKADNSYSVGNNNOFTDATQTUVFGVGNNILT LESSONSTATIONS
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CONFLICT
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 ----GTTLTLGANQVTYTGT-GSFTDTLTLNTTFDGAAKSGGNILLIKSGSTLDLS 1778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alba H., Baba T., Fullita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Rashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Morih K., Mori T., Wotomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Santo N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takedo J., Takeuohi Y., Wada C., Yamamoto Y., Horluchi T., Takeuoki Y., Wada C., Yamamoto Y., Horluchi T., Takeuoki Y., Wada C., Yamamoto Y., Horluchi T., A., A. 570-kb DAN sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAID-KIZ / MG1657.
STRAID-KIZ / MG1657.
Pubmed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Geregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOSZET I., Glaser P., Danchin A.;
"Multiple IS insertion sequences near the replication terminus in Escherichia coli K-12.";
"Is sinsertion sequences near the replication terminus in Escherichia coli K-12.";
-!- SIMILARITY: TO S.TYPHIMURIUM ORF NEAR CYSG (AC P25928).
-!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CODING FOR THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT BETWEEN AMINO ACIDS 839 AND 840.
                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                            YDBA_ECOLI STANDARD; PRT; 2003 AA. P3666 F70677; P76859; P76859; P76856 F70607; P76858; P76857; P76859; P76850; P76859; P76859; P76851, 28, Created) 01-0CT-2000 (Rel. 40, Last sequence update) 01-0CT-2000 (Rel. 40, Last annotation update) VHYPOTHETICAL 205.9 KDA PROTEIN IN PAAY-ACPD INTERGENIC REGION. YDBA OR B1401/F91405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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.; D90778; BAA15009.1; ALT_SEQ.
.; D90778; BAA18801; ALT_SEQ.
.; D90779; BAA1881.1; ALT_SEQ.
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sene; EG11307; ydbA.
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                                1943 ATSTDAVNGSQLYKATQSIANATN 1966
                                                              1779 GVSTLAL------VVTATN 1791
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MEDLINE=92190338; PubMed=1665988;
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CONFLICT 489 48
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949 AEEIHTTKGTANTALQTFTVKKVDENDKADDTNAITVGK------DGTSGKVNTLKLKG 1001
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ----NLWQI----DEANNTVALEGVSADGATKWQYNHNGELVITGD---NATVNNNGK
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                                                                                                                                                                                      663; Indels
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BB3A12C8B53220EE CRC64;
                                                                                                                      Score 496; DB 1;
Pred. No. 8.9e-11;
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495 I ->
205949 MW;
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495 49
2003 AA;
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Best Local 9
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QLVNNGTINLGTAGTTDTGMIGMQLDANATADAVIENNGTINIFANDSFAFSV-LGTVGH 1498
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                                                                                                                                                                                                                                                                                                   VAQTPLTFAGDTGTTAKKLGETLTLKGGQTDTNKLTDN··NIGVVAGTDGFTVKLAKDLT 1560
                                    GIVINSQNGQNTI----TGLSNTLANVTNDKGSVR-TTEQGNIIKDEDKTRAASIVDVL 1277
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                                                                                                                                          1336 KDKKLGVKTTTLTSTGTGANKFALSNQATGDALVKASDIVAHLNTLSGDIQTAKGASQAN
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SAGENLQGNGEAVDEVSTYDTVNFANGNTTTAKVTYD - - DTSKTSKVVYDVNVDDTTIEV
                                                                                                             SGIIDLYGRG-SVGMLAIADSTABNQGKITLDSWAVDANDTTAMRDIASNSAIDFGT---
                                                                                                                                                                                               1396 NSAGYVDADGNKVIYDSTDNKYYQAKNDGTVDKTKEVAKDKLVAQAQTPDGTLAQMNVKS
                                                                                                                                                                                                             VINKEQVNDANKKQGINEDNAFVKGLEKAASDNKTKNAAVTVGDL-----
                                                            891 GIITCKVTEQHSVFNKYSTGTSNSFI-FNNDVSSITGLVAQSN----
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IDENTIFICATION OF CLEAVAGE SITE.
MEDLINE-92104668; PubMed-1729180;
Hackstadt T., Messer R., Cleplak W. Jr., Peacock M.G.;
Hackstadt T., Messer R., Cleplak W. Jr., Peacock M.G.;
Hackstadt T., Messer R., Cleplak W. Jr., Peacock M.G.;
Hackstadt T., Messer R., Cleplak W. Jr., Peacock M.G.;

"Evidence for proteolytic cleavage of the 120-kilodalton outer
membrane protein of rickettsiae: identification of an avirulent mutant
deficient in processing.":
Infect. Immun. 60:159-165(1992).
Infect. Immun. 60:159-165(1992).
Infect. Immun. 60:159-165(1992).
INFOCTOR: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
VIRULENCE FACTOR AND/OR IMMUNGEN DURING INFECTION.
ITHE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.
ILAYER WITH HEXAGONAL SYMMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carl M., Dobson M.E., Ching W.M., Dasch G.A.; "Characterization of the gene encoding the protective paracrystalline-surface-layer protein of Rickettsia prowazekii: presence of a truncated identical homolog in Rickettsia typhi."; Proc. Natl. Acad. Sci. U.S.A. 87:8237-8241(1990).
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
OUTER MEMBRANE PROTEIN B PRECURSOR (168 KDA SURFACE-LAYER PROTEIN)
(SURFACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SCAS) (ROMP B)
(CONTAINS: 120 KDA SUBFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTIGEN)
(120 KDA OUTER MEMBRANE PROTEIN OMPB); 32 KDA BETA PEPTIDE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ching W.M., Carl M., Dasch G.A.; "Mapping of monoclonal antibody binding sites on CNBr fragments the S-layer protein antigens of Rickettsia typhi and Rickettsia prowazekii.";
                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moron C.G., Yu X.J., Walker D.H.; "Sequence analysis of ompB of Rickettsia prowazekil."; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
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EMBL; AF161079; AAD42234.1; --
EMBL; AJ235273; CAA15140.1; --
AAL19Gn; S-layer; Cell Wall. 120 KD.
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MEDLINE-99039499; PubMed-9823893;
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SEQUENCE FROM N.A.
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1643 32 KDA BETA PEPTIDE.  257 V -> A (IN STRAIN BREINL). 1010 Y -> D (IN STRAIN BREINL). 1450 A -> S (IN STRAIN BREINL). 179 AA -> VC (IN REF. 1). 201 TYGEAPLTICA -> INSRSSYHLVS (IN REF. 1). 212 T -> I (IN REF. 1). 313 Q -> L (IN REF. 1). 1104 D -> G (IN REF. 2). 1123 T -> S (IN REF. 2). 1124 T -> S (IN REF. 2). 1125 AA; 169854 WW; 735FDF392E6346CC CRC64;	4.4%; Score 456.5; DB 1; Length 1643; ilarity 22.4%; Pred. No. 1.8e-09; Conservative 227; Mismatches 628; Indels 517; Gaps 100;	LNSGSLTVNNTTGNKQIQVGANGIKFATVANNVANTSATVGTARITEEKIGFAGT 571 :::  :  :	NDGVDEQAPYLDKERLKVGRVEITTDSGINAGNHKITGLINGIANTDAVII 622 	KQLKDAKPTLNAGDGISINSNNGDLVDSSGNITTPTYNISVKTTKLNSNGTS 674	GNNKFSVSNAHDNNSLVTAKDLADYLNKVNETADSALPSFKVQNGDNSNNAITVGKDTNG 734  :	LKGENGVNITTNRATGTVTFGIDQSNGLTTPKLTVG 777 	SDTNGNRLVIEQVPSADGNSTK-NIIKGLSPTLPSIASPSGRNIALGNTIEEK 829 :	DKSNAASIDDVLNAGFNLKNNGKDKDFVSTYDTVDFIDGNATTATVTYDEANQ 882 	TSKVAYDVNVDEKTIELTGDNGKQLGVKTIKLTETSTNGNATTFSTDDDHALVKASDI- 941 	AGNLNTLABEIHTTKGTANTA-LQTFTVKKVDENDKADDTNAITVGKDGTS 991 	GKVNTLKLKGKNGLDIKTDKDGTVTFGINTQSGLKAGDSTTLNNNGLSIKNTASNEQIQV 1051   :: : :	GADGVKFAMVNNGVVGAGIDGTTRITRDEIGFTGTNGSLDKSKPHLSKDG 1101  ::   :   :   :   :   :   :   :   :   :	INAGGKRITNIQSGEIAKNSHDAVFGGKIYDLKTELENKISSTAKT 1147 	AQNSLH-EFSVADEQGNNFTVSNPYSSYDTSKTSDVITFAGENGITTKVNKGVVRVGIDQ 1206 	TKGLTTPKLTVGNNNGKGIVINSQNGQNTITGLSNTLANVTNDKGSVRTTEQGNIIKDED 1266 
1329 257 1010 1450 178 191 313 1104 1123	Sir Sir	LNSGSLTVNNT :::  :  : ISAGLVTASTA	NDGVDEQAPYLI           NIPVAP	KQL :  LGFITNIAQQA	GNNKFSVSNAH	KTFNTLKLKGENG 	SDTNG :     GNTINFNGIDG	DKSNAASIDDV :   GAANAVIGTD-	TSKVAYDVNVD :  ::    GGQVTFEHIVD	AGNLNTLAEET	GKVNTLKLKGK   :: : : G-IHIAELRLG	GADGVKFAMVNI  ::  ALMNI	INAGGKKITNI     : ANIIGANY	AQNSLH-EFSV :   : NNQTLTINGSI	TKGLTTPKLTV   :   TYLITKTINA
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1692
1267 KTRAASIVDVLSA--GFNLQGNGEAVDFVSTYD----TVNFANGNTTTAKVTY--DDTSK 1318
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                                                                                                                                                                                   1379 NTLSGDIQTAKGASQANNSAGY-----VDADGNKVIYDSTDNKYYQAKNDGTVDKTK 1430
                                                                                                                                                                                                                                                                          1431 EVAKDKLVAQAQT-----PDGT-LAQMNVKSVINKEQVNDANKKQGINEDNAFVKGLE 1482
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30-MAY-2000 (Rel. 39, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
OUTER MEMBRANE PROTEIN B PRECURSOR (168 KDA SURFACE-LAYER PROTEIN)
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                              1804 DNAQATGDQ-SIAIGTGNVVAGKHSGAIGDPS----TVKADNSYSVG----NNNQFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKDKSNAASIDDVLNAGFNLKNNGKDK--DFVSTYDT--VDFIDGNATTATVTYDEANQT 883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167
                                                                                                                                                                                                                                                                                                          FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR (BY SIMILARITY). SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
(SURFACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SCAS) (ROMP B) (CONTAINS: 120 KDA SURFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTIGEN) (120 KDA OUTER MEMBRANE PROTEIN OMPB); 32 KDA BETA PEPTIDE].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K------LNSNGTSGNNKFSVSNAHDNNSLVTAKDLADYLNKVN---ETADSALPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1656;
                                                                                                                                                                                                                              Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 KDA SURFACE-EXPOSED PROTEIN.
32 KDA BETA PEPTIDE.
POLY-GLY.
168097 MW; 3132A69C9DD5999F CRC64;
                                                                              Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=35790;
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Matches 397; Conservative 204; Mismatches
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1656 AA;
                                                                        Rickettsia japonica
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                                                                                                    VNTLKLKGKNGLDIKTDKDGTVTFGINTQSGLKAGDSTTLNNNGLSIKNTASNEQIQVGA 1053
                                                                                                                                                                DGVKFAMVNNGVVGAG---IDGTTRITRDEIGFTGTNGSLDKSKPHLSKDG---INAGGK 1107
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                                                                                                                                                                                                                                                                                                          598 VDASS-LTNAQTLTISGTIGINGANNTTL----GQFNIGSSKTTLNGGNVAINBLVIGNN 652
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--AASIVAITQNSNFG----TTDFGNLAAQVT
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                                                                      411 VPDTMTLTGNFTGDANNPGNTAGVITFAANGTLASASADANVAV--TNNITAIE--ASG-
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                                                                                                                                                                                                                                                                                   1498
  -- YLGTPEMV-GSEAGAI--PAAVAAGD 1365
                                                                                                                                                                                                                                    QLYKATQSIAN--ATNELDHRIHQNENK-----ANAGISSAMAMASMPQAYIPGRSMV 2003
                                            --- DN-SYSVGNNNQFTDATQTDVFGVGNNITVTESNSVALGSNSAISAGTHAGTQAKKS 1894
                                                                                             -----AGYKAKTT 1400
                                                                                                                                           DGTAGTTTTAGATGTVKGFAGQTAVGAVSVGASGAERRIQNVAAGEVSATSTDAVNG--S 1952
                                                                                                                                                                                                                                                                                                                               TGGIAT----HNGQGAVAV----GLSKLSDNGQWVFKING-------SADTQGHV 2043
                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: OUTER MEMBRANE.
MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPMA REQUIRES HPMB FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                                                                                                                                                    GIVIGLDTLAN-----KTD-VNGFSF
                                                                                                                                                                                                                                                               | | | | : | | : | : | : | | : | 1446 SIYGAQQFVENFFAQGSAIFSLNQVKNKSQRYFFDANGNMSKQIAAGNYD------NMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEMOLYSIN.
W; 175975E0C924B2D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAY BE RESPONSIBLE FOR PORE FORMATION.
SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1577 AA
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STRAIN=ISOLATE 477-12;
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                                                                                          EAVDNVAYGIWARPFYTDAHQSKKGGL ---
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1320 TNAQLDVAKDIQAQLGNRLGALR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       494 TNDGVDESKPYLDNEKLKVGNSTLNSGSLTVNNTTGNKQIQVGANGIKFATVANNVANTS
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                                                                           627;
                                                                     Indels
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                                                                     643;
      Pred. No. 2.2e-09;
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al Similarity 21.0%; Pred. No. 2.2e-399; Conservative 229; Mismatches
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:: -: -:

Length 1577;

DB 1;

Score 453.5;

4.48;

Query Match

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DSVTGNVGGSLNIASQKES---DRHVTVGVNVGYNHTNDPKSSQVNK----TAKAGGSL 1399
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
00TER MEMBRANE PROTEIN B PRECURSOR (168 KDA SURFACE-LAYER PROTEIN)
(SURFACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SCA5) (ROMP B)
(CONTAINS: 120 KDA SURFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTIGEN)
(120 KDA OUTER MEMBRANE PROTEIN OMPB); 32 KDA BETA PEPTIDE).
                           1301 FANGNITIAKVIYDDISKISK----VVYDVNVDDITIEVKDKKL---GVKTILISIGIG 1353
                                                                                    ------GDIQTAKGASQA---N 1395
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                                                                                                                                                                                                                               996 HETKGGGQIGVSTKTGSD-ITVALKGEGOTTDNALMETKAKGSQFTSNGDISINVGENAH
                                                                                                        ----AQMNVKSVINKEQVNDANKKQGINEDNAFVKGLEKAASDNKTKNAAVTVGD---
                                              1396 NSAGYVDADGNKVIYDSTDNKYYQAKNDGTVDKTKEVAKDKLVAQAQTPDGTL-----
TKNRGS-QTEVAGDLTITANK-----DLLHEGASHHVEGRYQESGENIQHLAVNDS--
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
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                                                                                          1354 ANKFALSNQATGDALVKASDIVAHLNTLS-----
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Q53047;
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OUTER MEMBRANE P
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Gillmore R.D. Jr., Joste N., McDonald G.A.;
"Cloning, expression and sequence analysis of the gene encoding the "Cloning, expression and sequence analysis of the gene encoding the 120 kp surface-exposed protein of Rickettsia rickettsii.";
Mal. Microbiol. 3:1579-1586(1989).
Mal. Microbiol. 3:1579-1586(1989).
-1. FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTRAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL STRUCTROR. AND/OR IMMUNOGEN DURING INRECTION.
-1. SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY LAYER WITH HEXAGONAL SYMMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAGLVTASTATIVASFAGSAMGAAIQQNRTT------NGAATTVDGAGF---
                                                                                                                                                            Gilmore R.D. Jr., Cleplak W. Jr., Policastro P.F., Hackstadt T.; The 120 kilodalton outer membrane protein (rOmp B) of Rickettsia rickettsii is encoded by an unusually long open reading frame: evidence for protein processing from a large precursor."; Mol. Microbiol. 5:2361-2370(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1654;
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32 KDA BETA PEPTIDE.
POLY-THR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.3%; Score 443.5; DB 1;
1larity 22.0%; Pred. No. 5.2e-09;
Conservative 189; Mismatches 567;
Rickettsleae; Rickettsla
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-90136087; PubMed-2515418;
                                                                                                                                                         MEDLINE=92167802; PubMed=1724278;
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1654 AA; 1
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Matches 383; Conserv
                                                                                              SEQUENCE FROM N.A.
             Rickettsiaceae;
                                       NCBI_TaxID=783;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). 1894 SDGTAGTTTTAGATGTVKGFAGQTAVGAVSVGASGAERRIQNVAAG-EVSATSTDA---- 1948 1338 YLGTPETAEMAG------PEAGAISAAVAAGDEAIDNVAYGIWAKPFYTDAHQSK 1386 1949 VNGSQLYKA-----TQSIAN----ATNELDHRIHONENKANA-GISSAMA 1988 MASMPQAYIPGRSMVTGGIATHNGQGAVAVGLSKLSDNGQWVFKINGSADTQGHVGAAVG 2048 1447 GA------QQLVKNFFA----QGSAIFSLNQVKNKSQRYF-----FDANGNMSKQIA 1488 MEDLINE 89312288; PubMed=2501630; Kiwaki M., Ikemura H., Shimizu-Kadota M., Hirashima A.; Kiwaki M., Ikemura H., Shimizu-Kadota M., Hirashima A.; Kiwaki M., Ikemura H., Shimizu-Kadota M., Hirashima A.; Molaracterization of a cell wall-associated proteinase gene from Streptococcus lactis NCDO763."; Mol. Microbiol. 3:359-369(1989).

-! FUNCTION: PROPERSE WHICH BREAKS DOWN MILK PROTEINS DURING THE GROWTH OF THE BACTERIA ON MILK.
-!- CATALYTIC ACTIVITY: ENDOPPETIDASE ACTIVITY WITH VERY BROAD SPECIFICITY, ALTHORGH SOME SUBSITE PREFERENCE HAVE BEEN NOTED, E.G. LARGE HYDROPHOBIC RESIDUES IN THE PLAND 4 POSITIONS, AND PRO IN THE P2 POSITION. BEST KNOWN FOR ITS ACTION ON CASEINS, ALTHOUGH IT HAS BEEN SHOWN TO HYDROLYSE HEMOGLOBIN AND OXIDIZED 01-APR-1990 (Rel. 14, Last sequence update) 15-UDL-1998 (Rel. 35, Last annotation update) PIL-TYPE PROTEINASE PRECUESOR (E. 3. 4.21.96) (LACTOCEPIN) (CELL WALL-ASSOCIATED SERINE PROTEINASE) (LP151). Plasmid pLP763. Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae; INSULIN B-CHAIN.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. CELL WALL.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
SUBTILASE FAMILY. Lactococcus lactis (subsp. lactis) (Streptococcus lactis). PRT; 1902 AA. InterPro; IPR001209; -.
InterPro; IPR01899; -.
Pfam; PF00746; Gram\_pos\_anchor; 1.
Pfam; PF00082; Peptidase\_S8; 3.
PRINTS; PR00723; SUBTILISIN.
PROSITE; PS00136; SUBTILASE\_ASP; 1. 01-APR-1990 (Rel. 14, Created) EMBL; X14130; CAA32350.1; -. PIR; S06997; S06997. HSSP; P00782; 2SBT. STANDARD; SEQUENCE FROM N.A. STRAIN-NCDO 763; MEROPS; S08.019; NCBI\_TaxID=1360; 2049 AGFH 2052 1489 AGHY 1492 P2P\_LACLA P15293; RESULT 7 P2P\_LACLA 1989 1.1 q ŏ g ŏ g δŻ Dp δ g 

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                                                                                       MEMBRANE ANCHOR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                202
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                                                                                                                                                                                                                                                                                                                                                               192 -KIKYRRTRAQGHASTAVGAMSYAQG-HFSNAFGTYATAEAAYSLAVGLAAQA-----
                                                                                                                                                                                                                                                  31 AKAAISOQTKGSSLA-----NTVTAATAKQAAIDITAATTN-QAIATQLAAKGIDYNK
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                               Plasmid;
                                                                                                                                                                                                            649;
                                                                                                                                                                                        Length 1902;
                                                                                                                                                                                        4.2%; Score 439.5; DB 1; Length 1 ilarity 21.0%; Pred. No. 8.5e-09; Conservative 241; Mismatches 847; Indels
SUBTILASE_HIS; 1.
SUBTILASE_SER; 1.
GRAM_POS_ANCHORING; 1.
protease; Cell wall; Zymogen; Signal;
                                                                                                                                                              4B8D8B844D88CDF7 CRC64;
                                                            POTENTIAL.
PII-TYPE PROTEINASE.
EXTRACELLULAR (POTENTIAL).
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     PROSITE; PS00137; SPROSITE; PS00138; SPROSITE; PS00343; GHydrolase; Serine F
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                                    Hydrolase; Sei
Transmembrane.
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Matches 462;
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1514 TGTTAKKLGETLTIKGGQIDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGG---T 1570 -----GETVQYSAD------GKTYQ 1541 KIDEKGISFVDANGQAKANTPVLSANGLDLGGKVISNVGKGTKDTDAANVQQL-NEVRNL 1629 FVSTYDTVNFANGNTTTAKVTYDDTSKTSKVVYDVNVDDTTIEVKDKKLGVK----TTT 1346 QGVTFGANEF---NATSAKF-YDPKTGIATITGKVKHPTTTLQVDGKQIPIKDDLTFSFT 1365 1264 VDVPVNYGDNTIKVTATDEDGNTTIEGKTITSSYDP------DMLK------NSVTFD 1309 TTADGYTKIETPLSDEQAQA-----LGNG-----DNSAELYLTDNASNATDQDAS 1102 1092 KSKPHLSKDG--INAGG--KKITNIQSGEIAKNSHDAVT-GGKIYDLKTELENKISSTAK 1146 -----LTAPTFTDLKFNNGSDQTSEATIKVTGTVSADTKTVNVGDTVAALDAQHHFS 1263 -----SNTLANVTNDKGSVRTTEQGNIIKDEDKTRAASIVDVLSAGFNLQGNGEAVD 1291 DSKAPTVRHVALSAKTENGKTQYYLTAEAKDDLSGLDATKSVKTAINEVTNLDATFTDAG 1057 TLNNNGLSIKNTASNEQIQVGADGVKFAMVNNGVVGAGIDGTTRITRDEIGFTGTNGSLD 1091 KLKGENGVNITTNRATGTVTFGIDQSNGLTTPKLTVGSDTNGNRLVIEQVPSADGNSTKN 800 829 887 1347 LTSTGTGANKFAL----SNQATGDALVKASDIVAHLNTLSGDIQTAKGASQANNSAGY VDADGNKVIYDSTDN-KYYQAKNDGT-----VDKTKEVAKDKLVAQAQTPDGTLAQMNV 1454 KSVINKEQVNDANKKQGINEDNAFVKGLEKAASDNKTKNAAVTVGDLNAVAQTPLTFAGD TAQNSLHEFSVA-DEQGNNFTVSNPYSSYDTSKTSDVITFAGENGI----TTKVNKGVVR 1202 VGIDQTKGLTPKLT-VGNNNGK------GIV---INSQNGQNTITGL-----774 AIKAGS----NITVPAGKTAQIEFTLSLPKSFDQQQFVEGFLNFKGSDGSRLNLPYMGFF Y-----DV-----NVDEKTIELTGDNGKKQLGVKTIKLTETSTNGNATTFSTD FSSDKNALYNDISMKYYLLRNISNVQVDILDGQGNK-----VTTLSSSTNRKKTYYNAH DTNAITVGKDGTSGKVNTLKLKGKNGLDIKTDKDG-----TVTFGINTOSGLKA--GDST DDHAL---VKASDIAGNLNTLAEEIHTTKGTANTALQTFTVKKVDE-NDKAD-----524 PFIAGSQALLKQALNNKNNPFYAYYKQLKGTALTDFLKTVEMNTAQPINDINYNNVI-VS NAHDNNSLVTAKDLADYLNKVNET -- ADSALPSFKVQNGDNSNNAITVGKDTNGKTFNTL PRRQGAGLVDVKAAIDALEKNPSTVVAENGYPAVELKDFTSTD-----KTF---IIKGLSPTLPSIASPSGRNIALGNTIE-EKDKSNAASIDDVLN-----AGFNLK-------NNGKDKDFVS-----TYDTVDFIDGNATTAT-----VTYDEANQT---SKVA -STTEPAKTVTLTANSAAT-----1475 1542 1401 1292 1310 1212 1240 1032 688 866 1058 931 888 801 583 741 q οy ö g Qγ qq à g ŏ g qq

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-!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
-!- FUNCTION: THE 3Z KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.
-!- SUBCELLUTAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
S-LAYER WITH HEXAGONAL SYMMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
0UTER MEMBRANE PROTEIN B PRECURSOR (168 KDA SURFACE-LAVER PROTEIN)
SURFACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SCA5) (ROMP B)
[CONTAINS: 120 KDA SURFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTIGEN)
(120 KDA OUTER MEMBRANE PROTEIN OMPB); 32 KDA BETA PEPTIDE].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94040787; PubMed=8224886; Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.; Cloning and Sequence analysis of the gene encoding the crystalline surface layer protein of Rickettsia typhi."; Gene 133:129-133(1993).
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LGLGNDNADGNQVNIADIKKDPNSGSSSNRTVIKAGTVLGGKGNNDTEKLATG--GVQVG
                                 -----TQKAQTALDQTNAS
                                                                           VDKDGNANGDLSNVWVKTQKDGSKKALLATYNAAGQTNYVTNNPAEAIDRINEQGIRFFH
                                                                                                                                                                                     ---GNQ-----TDSSTGK----TFTAALDDLVA-----QAQAGTQT---DDQLQ
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                                                                                                                                                                                                                                                                                                                                     1760 TSGQASADASDKLAHLQALQSLKTKVAAAVEAAKTVGKGDGTTGTSDKGGGQGTPAPTPG
                                                                                                                                                  VNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGRQTQAGNQSIAIGDNAQ
                                                                                                                                                                                                                           ATGDQSIAIGTGNVVAGKHSGAIGDPSTVKADNSYSVGNNNQFTDATQTDVFGVGNNITV
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                                                                                                          VDSLTGANRDLQT-----AINQLAAKLPADKKTSLL--NQLQSVKAALETDL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hackstadt T., Messer R., Cieplak W., Peacock M.G.; "Evidence for proteolytic cleavage of the 120-kilodalton outer membrane protein of rickettsiae: identification of an avirulent mutant deficient in processing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rickettsia typhi.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettslaceae; Rickettsieae; Rickettsia.
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MEDLINE=92114896; PubMed=1370573;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the S-layer protein antigens of prowazekii.";
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                                                                                                                                                                                                                                                                                                                                                                                    83;
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                                                                                                                                                                                                                                                                                                                                                  Length 1645;
                                                                                                                                                               Antigen; S-layer; Transmembrane; Cell wall.
CHAIN 1353 120 KDA SURFACE-EXPOSED PROTEIN.
CHAIN 1354 1645 32 KDA BETA PEPTIDE.
TRANSMEM 1415 1429 MEMBRANE ANCHOR (POTENTIAL).
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V -> I (IN REF. 2).
G -> A (IN REF. 2).
G -> S (IN REF. 2).
MW; OCB5641C7EB185EE CRC64;
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21.8%; Pred. No. 9.2e-09;
ive 185; Mismatches 566
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1996 -----YIPGRSMYTGGIATHNGQGA-VAVGLSKLSDNGQWVFKINGSADTQGHVGAAVG 2048
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1273 IVDVLSAGFNLQG--NGEAVDFVSTYDTVNFANGNTTTAKVTYDDTSKTSKVVYDVNVDD 1330
                                                          TTIE--VKDKKLGVKTTTLTSTGT----GANKFALS--NQATGDALVKASDIVAHLNTLS 1382
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                                                                                                                       1383 GDIQTAKGASQANNSAGYVDADGNKVIYDSTDNKYYQAKNDGTVDKTKEVAKDKLVAQAQ
                                                                                                                                                 ND------IVAADPINTYLITKTIN----AANQGKI----IVAADPINTDTA
                              547 KILTLS-GANIIGANAGGAIHFQ-----ANGGTIQL-----TSTQNNILVDFDLDV
                                                                                         TTDQTGVVDASSLTNNQTLTINGSIGTIGANTKTLGRFNVGSSKTILNAGDVAINELVME
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01-0cT-1994 (Rel. 30, Created) 01-0cT-1994 (Rel. 30, Last Sequence update) 01-0r-1995 (Rel. 32, Last annotation update) 0ALL-ASSOCIATED PROTEIN PRECURSOR.

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                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 704263;

MEDLINE-9521908; PubMed-7704263;

MEDLINE-9521908; PubMed-7704263;

MEDLINE-9521908; PubMed-7704263;

A Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;

AY Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;

AY Cloning and sequencing of a 29 kb region of the Bacillus subtilis

AT Cloning and sequencing of a 29 kb region of the Bacillus Y.;

AT Cloning and sequencing of a 29 kb region of the Bacillus Y.;

AT Cloning and sequencing of a 29 kb region of the Bacillus Y.;

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2-2.
2-3.
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WALL-ASSOCIATED PROTEIN.
3 x 101 AA APPROXIMATE TANDEM REPEATS.
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                                                                                                                                                               "Molecular analysis of three major wall-associated proteins of Bacillus subtilis 168: evidence for processing of the product of gene encoding a 258 kba precursor two-domain ligand-binding
 Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                      MEDLINE=93302506; PubMed=8316082;
                                                                                                                                                                                                                                            Mol. Microbiol. 8:299-310(1993).
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EMBL; D31856; BAA06656.1; --
EMBL; D299815; BAA06656.1; --
EMBL; D89026; BAA11683.1; --
EMBL; Z99124; CAB15959.1; --
PIR; S32920; S32920.
Subtilist; BG10797; wapA.
Pfam; PF02018; CBD_6; 1.
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Db 975 KKADGTYQPPGVYLELTETADQFILKTKDQTNAYFNKKGGKLQK 1019  Qy 863 VDFIDGNATTATVTYDEANQTS	1045SNEQIQUGADGVKFAMYNNGVVGA-GIDGTTRITRDEIGFTGTNGSLDKSKP   1124	DD 1866GGTSFSYDERNLVSSLHIGDKNGGDILTESYEYD 1899 Qy 1651 PNSGSSSNRTVIKAGTVLGGKGNNDTEKLATGGVQVGVDKDGNANGDLSNVWVRT 1705
FT REPEAT 1732 1751 2-15. FT REPEAT 1753 1772 2-16. FT REPEAT 1753 1772 2-16. FT REPEAT 1820 1839 2-18. FT REPEAT 1840 1859 2-19. FT REPEAT 1840 1859 2-20. FT REPEAT 1861 1880 2-20. FT REPEAT 1906 2-21. FT REPEAT 1908 1927 2-22. FT REPEAT 1909 1927 2-22. FT REPEAT 1909 2-23. FT REPEAT 2002 2-25. FT REPEAT 2002 2-25. FT REPEAT 2003 2007 2-26. FT REPEAT 201 2000 2-20. FT REPEAT 201 2000 2-30. FT REPEAT 201 2000 2-30. FT REPEAT 201 2000 2-30.	QUELY WAICH  Best Local Similarity 20.3%; Pred, No.1.99-08;  MAICHES 466; CONSELVATIVE 20.3%; Pred, No.1.99-08;  BOTH LANGER CONSELVATIVE 277; MISMACHES 781; Indels 779; Gaps 118;  S18 LKRIGISTOCKIKKRYRRAGGHST-AVGA-MSYAGGHSNARGYATABAAYSIANGLA 239  S19 LKRIGHSTOCKIKKYRRRAGGHST-AVGA-MSYAGGHSNARGYATABAAYSIANGLA 239  S10 LKRIGHSTOCKIKKYRRRAGGHST-AVGA-MSYAGGHSNARGYATARAGSILDRBNNT 291  S10 LKRIGHSTOCKIKKYRRAGGHST-AVGA-MSYAGGHSNARGYATARAGSILDRBNNT 291  S10 LKRIGHSTOCKIKKYRRAGGHST-AVGA-MSYAGGHSNARKYBEANGG 424  S11 LKROWSSINANANAPARATAGGHVVNHG	Db 918 SIDGRGPGLGLSRTYNSLDSSDHLFGQGWYADAETSVISTDGGAMYIDEDATTHRFT 974 Qy 815

CC
DR HSSP, Q99405; AMPT. DR HSSP, Q99405; IMPT. DR InterPro; IPR00209; DR InterPro; IPR001899;
DR Pfam; PF00/146; Gram_Pos_ DR Pfam; PF00082; Peptidase DR PRINTS; PR00723; SUBTILI DR PROSITE; PS00136; SUBTILI DR PROSITE; PS00137; SUBTILI
KW Transmembrane FT SIGNAL FT PROPEP FT CHAIN 1
FT ACT_SITE FT ACT_SITE FT DOMAIN FT
SQ SEQUENCE 1902 AA, Query Match Best Local Similarity Matches 457; Conser
20 2
DD 31 ARAHASQQARQSSET
QY 119 PDPNNGSNGNV Db 143 QQTAGESYGYVVNGFSTK
Qy 142GGDVLAEGDASI
257
QY 243TKQSSIAVGSNAKANA :       : : Db 317 FTNSDTSATTGSSTLVS
301

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EXTRACELLULAR (POTENTIAL).

MEMBRARA MANCHOR (POTENTIAL).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CONSERVED IN GRAM-POSITIVE COCCI SURFACE
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FKVRVVDIPKLKQIAGVKTVTLAKVXYPTDAKANSMANVQAVWS 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVGAMSYAOG-HFSNAFGTYATAEAAYSLAVGLAAOA----- 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAFAATAIGGNTVVNLGRGVALGFGSQILDRDNNTDASAYVPLG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----NNTLKGDALATGEASIAFGSLSKAQGSQAIAIGSVK 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 663; Gaps
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                                                                                                                                                                                                                                                                                    ILASE_HIS; 1.
ILASE_SER; 1.
BOS_ANCHORING; 1.
Gage; Cell wall; Zymogen; Signal; Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.1%; Score 423.5; DB 1; Length 1902; 80.7%; Pred. No. 3.1e-08; ve 235; Mismatches 851; Indels 663;
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MW; 2901C7F19B2E5D0B CRC64;
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ILASE_HIS; 1.
ILASE_SER; 1.
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se_S8; 3.
LISIN.
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Oy Db	478	TKGTTRITKK-KIGFAGTNDGVDESKPYLDNEKLKVGNSTLNSGSLTVNNTTGNKQIQ 534	
Qy	535	VGANGIKFATVANNVANTSATVGTARITEEKI	
Qy	573 577	DGVDEQAPYLDKERLKVGRVEITTDSGINAGNHKITGLTNGIANTDAVTIKQLKDAKPTL 632   :	
Oy Dp	633	NAGDGISINSNNGDLVDSSGNITTPTYNISVKTTKLNSNGTSGNNKFSVSNAH 685 : :: :	
oy 4	989	74	
6 P	744	GCAGLUDVRAALDALEKNESTVVAENGYPAVELKDFTSTDKTFKL- 730 GENGVNITTNRATGTVTFGIDQSNGLTTPKLTVGSDTNGNRLVIEQVPSADGNSTKNIIK 803	
QQ	731		
Qy Db	804	GLSPTLPSIASPSGRNIALGNTIE-EKDKSNAASIDDVLNAGFNLK 848	
OY Dp	849	NNGKD  :   NDGKI	
ò d	894 408	EKTIELTGDNGKKQLGVKTIKLTETSTNGNATTFSTDDDHALVKASDIAGN-LNTLAE ::	
δγ	951	NTALQTETVKKVDE-NDKAD-	
g	931	STNLTKTYYNAHSQQYIYYNAPAWDGTYYDQRDGNIKTADDGSYTYRISGVPEGGDKRQV 990	
Oy Dp	979	DTNAITVGKDGTSGKVNTLKLKGKNGLDIKTDKDGTVTFGINTQSGLK 1026  :	
Qy Dp	1027	AGDSTTLNNNGLSIKNTASNEQIQVGADGVKFAMVNNGVVGAGIDGTTRITRDEIGFT 1084	
ρŷ	1085	GTNGSLDKSKPHLSKDGINAGGKKITNIQSGEIAKNSHDAVT-GGKIYDLKTELEN  :	
qq	1096		
Qy Dp	1140	KISSTAKTAQNSLHEFSVA-DEQGNNFTVSNPYSSYDTSKTSDVITFAGENGITTK 1194 :	
Qy	1195	VNKGVVRVGIDQTKGLTTPKLT-VGNNNGKGIVINSQNGQNTITGL 1239	<b>a</b> 10
Qy Ph	1240	DACHHESUNDVUVEDNITKUANTEDENTIKDEDKTRAASIVDVLSAGFNLQ 1284	
l &	1285	GNGEAVDFVSTYDTVNFANGNTTTAKVTYDDTSKVVYDVNVDDTTTEVKDKKLGVK	
οp	1304		_
Qy	1344		_
g	1359	DLTFSFTLDLGTLGQKPFGVVVGDTTQNKTFQEALTFILDAVAPTLSLESST 1410	
οy	1394	ANNSAGYVDADGNKVIYDSTDN-KYYQAKNDGTVDKTKEVAKDKLVAQAQTPDG 1446	

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01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
PILI-TYPE PROTEINAS, PRECUSOR (EC 3.4.21.96) (LACTOCEPIN) (CELL WALL-ASSOCIATED SERINE PROTEINASE). 1624 -NEVRNLLGLGNDNADGNQVNIADIKKDPNSGSSSNRTVIKAGTVLGGKGNNDTEKLATG 1682 1683 --GVQVGVDKDGNANGDLSNVWVKTQKDGSKKALLATYNAAGQTNYVTNNPAEAIDRINE 1740 1666 ------QAQAGTQT- 1708 1801 AIGDNAQATGDQSIAIGTGNVVAGKHSGAIGDPSTVKADNSYSVGNNNQFTDATQTDVFG 1860 1861 VGNNITVTESNSVALGSN-----SAISAGTHAGTQAKKSDGTAGTTTTAGATG 1908 1447 TLAQMNVKSVINKEQVNDANKKQGINEDNAFVKGLEKAASDNKTKNAAVTVGDLNAVAQT 1506 1507 PLTFAGDTGTTAKKLGETLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSVN 1566 1567 AGG---TKIDEKGISFVDANGQAKANTPVLSANGLDLGGKVISNVGKGTKDTDAANVQQL 1623 1590 KQELTNL-----TQKAQTA 1627 Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae; 1709 --DDQHQAT----LAKVLDAVLAKLAEG-----IKAATPAEVGNAK---DAATGKTWY 1508 P-----STIEPAKTVILTANSAAT-------GETVQYSAD-----1628 LDQTNASVDSLTGANRDLQT-----AINQLAAKLPADKKTSLL------1741 QGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGRQTQAGNQSI Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris). 1909 TVKGFAGQTAVGAVSVGASGAERRIQNVAAGEV-----SATSTD 1947 1813 TPAPAPG-----DIGKDKGDEGSQPSSGGNIPTNPATTTSTSTD 1851 PRT; 1902 AA. SEQUENCE FROM N.A., AND SEQUENCE OF 188-197 STRAIN=SK11; MEDLINE-89340435; PubMed=2760036; STANDARD; Lactococcus. NCBI\_TaxID=1359; P3P\_LACLC P15292; Plasmid RESULT 11 P3P\_LACLC Ω ò g qq g ò ΩD ò g οy q a δy δ δ ò ò

467 LKF	467	522 LTV	514 LI	575 VDE	562 VK	623 KQI	622	676 NNI	677 NN	734 GK	726 - K	794 DG	774	847 LK	823 LP	899 LT	. 851	953 HT	905 YI	666	944 00	1029 D	1000 K	1070	1060 A	1107 -	1120 I	1163 N	1174 N	1218 G	1221 K	1249 D	1281 C	1306 1	1321 #	1360
ò	qq	Οy	q	οy	qq	Qy	qa	Qy	qq	Οy	QQ	Qy	qq	Οy	Q	Qy	qq	οy	qq	δλ	qq	οy	QQ	Qy	qa	ΟŊ	qq	οy	qq	δy	qa	٥y	Op	QY	G	οy
	CC modified and this statement is not removed. Usage by and lot commerce. CC entitles requires a license agreement (See http://www.isb-sib.ch/announce/	T E	PIR; A32634; P	MEROPS; S08.019;		Pfam; Pro0/40; Peptidase_S8; 3.	DR PRINTS; PROUZS; SUBILIDIAN. DR PROSITE; PSOUGLAS, SUBILIASE_ASP; 1.	PROSITE; PSOCIATION SOUTHERNS TO PROSITE; PSOCIATION SOUTHERN SOUT	Hydrolase, Serine protease; Cell wall;	SIGNAL 1	CHAIN 188 1902	TRANSMEM 1975 MEMBRANE ANCHOR (POTENTIAL)	ACT_SITE 217 217	RELAY SYSTEM (BY VED IN GRAM-POSIT	SPOILENCE 1902 AA	מבעכונים	. Match 4.1%; Score 423.5; DB 1; Length 1902;	vative 230; Mismatches 817; Indels 735; Gap		87	11	Į.		MS.			RTRAQGHASTAVGAMSYAQGHFSNAFGTYATAEAAYSLAVGL		Z O	36	RRKIINVGAGSRDTDAVN 34		GNTLTIKGDAQTNALTEANIGVVTD 4	₹ .	VSATNKITVSNTNNNNAELQSGGLTFSPITGTKTDKTVYSIDG 4	Db 437 GTGLQLGPETIQLSS

	575 576 733	793 773 846 822	898 850 952	998 943 1028 999	1069 1059 1106	1162 1173 1217 1220	1248 1280 1305 1320 1359 1379
INSTLNSGS 521 :QAAGAAG 51: -GEAGTNDG 57/ :     57/ :   62/ :   62/ IANTDAVTI 62/ TINMSGTSM 62/	67 73 72	TELKIKGENGVNITTURATGTVTFGIDQSNGLTTPKLTVGSDTNGNRLVIEQVPSA 79  TILL	CHARLES STANDENDE TO STANDE TO STANDE STANDER TERM STANDER TO STANDER TO STANDER TO STANDER TO STANDER TO STANDER TO STANDER TO STANDER TO STANDER TO STANDER TO STANDER TO STANDER TO STANDER	DGTSGKVNTLK	VGAG 1069  VTNLDATFTDAGTT 1059  DGINAGG 1101  PGSTSFDLIVNGGG 1111	116 117 121 122	OHHESUDVPUNGDNTATT 12 GEAVDFVSTYDT-VNFANG-N 13 GEAVDFVSTYDT-VNFANG-N 13TTTLTSTGTGANKFN 13TTTLTSTGTGANKFN 13 DDLTFSFTLDLGTLGOKPFGVV 13 OANNSAGYVDADGNKVIYDSTD 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----SAISAGTHAGTQAKKSDGTAGTTTTAGATGTVKGFAGQTAVGAVSVG---A 1926
                                                                                                                                                                                    QAKANTPVLSANGLDLGGKVISNVGKGTKDTDAANVQQL-NEVRNLLGLGNDNADGNQVN
                                                                                                                                                                                                                                                                                     1644 IADIKKDPNSGSSSNRTVIKAGTVLGGKGNNDTEKLATG--GVQVGVDKDGNANGDLSNV
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                                                                                                                                                                                                                                                                                                                                                                    binding protein A.";
Proc. Natl. Acad. Sci. U.S.A. 89:3483-3487(1992).
-!- FUNCTION: BINDS TO CELLULOSE FIBERS AND COORDINATES CELLULASE
                                            NKYYQAKNDGTVDKTKEVAKDKLVAQAQTPDGTLAQMNVKSVINK-EQVNDANKKQG---
                                                                          -----LSINGSSVASQYEDININSGKPGHMA
                                                                                                                                                                 KGGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGG---TKIDEKGISFVDANG
                                                                                                                                                                                                                                                       TFKFKSTDLYGNESPAVDYVVTNI ----KADDPAQLQAAKQELTNL-------
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                                                                                                     INEDNAFVKG----LEKAASDNKTKNAAVTVGDLNAVAQTPLTFAGDTGTTAKKLGETLTI
                                                                                                                                                                                                                                                                                                                   IASAKTLSASGKYDDATT----TALAAA----TQKAQTALDQTNASVDSLTGANRDLQT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clostridium cellulovorans.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=92228810; PubMed=1565642; Shoseyov O., Takagi M., Goldstein M.A., Doi R.H.; "Primary sequence analysis of Clostridium cellulovorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1994 (Rel. 30, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CELLULOSE BINDING PROTEIN A PRECURSOR.
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CONTAINS ABOUT 10% OF CARBOHYDRATES.
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01-OCT-1994 (Rel. 30, Last seq
15-DEC-1998 (Rel. 37, Last ann
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                                                                          NAQYLS----
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P38058;
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 ILKKIQTS-----TDGKIKYRRTR--AQG-----HASTAVGAMSYAQGHFSNAFGTYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    284 ILDRDNNTDASAYVPLGKTLADQY----KATRQGDSTDIFSIGNSNNNNSSIRRKIINVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VNNTTGNKQIQVGANGIKFATVANNVANTSATVGTARITEEKIGFAGTNDGVDEQAPYLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               581 ISPVTATFDKKAPA------DVATTMTLNGYTFN----GITGLTTSDYSISGNV
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   and for
                                                                                                                                                              wall; Repeat; Signal; Glycoprotein.
POTEMPIAL.
CELLULOSE BINDING PROTEIN A.
CELLULOSE-BINDING (BY SIMILARITY).
MW; B5FA6CE6F771AFIA CRC64;
                                                                                                                                                                                                                                                                    Length 1848;
                                                                                                                                                                                                                                                                 Query Match
4.0%; Score 410.5; DB 1; Length :
Best Local Similarity 21.3%; Pred. No. 8.8e-08;
Matches 443; Conservative 252; Mismatches 786; Indels
   рy
    Usage
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modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
                                                                                              InterPro; IPR001956; -
InterPro; IPR001956; -
Pfam; PF00942; CBD_3; 1.
Pfam; PF00963; Cohesin; 9.
Cellulose degradation; Cell wa
SIGNAL 1 28 F
CHAIN 29 1848 C
                                                    EMBL; M73817; AAA23218.1; -.
PIR; A44140; A44140.
HSSP; Q06851; 1NBC.
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89 <b>4</b> 798	946	966	1031 960	1083	1130	1185	1244	1304		1399	1449	1488	1537	3 1584 2 1534	I 1644 - 1575	N 1700 P 1615	G 1759 - 1652
ലഗ		rsgkvnt :   VLAT	GDST   :  ATVGTAT	RITRDEIGF : : ! -VLNPSVNF	AVTGGKI   : VFADGTL	TSDVITE :  :L	GLSNTLA   :   IGSTIKLL	NVTNDKGSVRTTEQGNIIKDEDKTRAASIVDVLSAGFNLQGNGEAVDFVSTYDFVNFANG	FLDDTLGSQLISKOGYDDTSKTSKVVXDVNVDDTTIEVKDKKLGVKTTLTSTG NTTAKVTYDDTSKTSKVVXDVNVDDTTIEVKDKKLGVKTTLTSTG 	QATGDA-LVKASDIVAHLNTLSGDIQTAKGASQANNSAG 	YVDADGNKVIX-DSTDNKYYOAKNDGTOD-KTKEVAKDKLVAQAQTPDGTLA YVDADGNKVIX-DSTDNKYYOAKNDGTUD-KTKEVAKDKLVAQAQTPDGTLA YVNGSTIKTELDTLGSQLISK-DGVPATINFKIKAVPSTGTTPVAISGTPVFADGTLA	QMNVKSVINKEQVNDANKKQGINEDNAFVKGLEKAASDN :	KIKNAAVIVGDLNAVAQTPLIFAG-DTGTTAKKLGETLFIKGGQTDTNKL	LEEVASITANDI VENEDATE DOTTE DE TENENS PAGGET TO DE MENORME TONNIGVVAGTDEFTVKLAKDLTNLNSVNAGGTKIDEKGISFVDANG TONNIGVVAGTDEFTVKLAKDLTNLNSVNAGGTKIDEKGISFVDANG TONNIGVVAGT	QAKANTPYLSANGLDLGGKVISNYGKGTKDTDAANVQQLNEVRNLLGLGNDNADGNOVNI QAKANTPYLSANGLDLGGKVISNYGKGTKDTDAANVQQLNEVRNLLGLGNDNADGNOVNI	LGGKGNNDTEKLATGGVQVGVDKDGNANGDLSNL       :     :     :   :     :     :     :     :     :     :       :     :       :         :         :         :         :         :         :           :	VWVKTQKDSKKA-LLATYNAGOTNYVTNNPAEAIDRINEGGIRFFHVNDGNGEPVVQG
NOTSKVAN   ::	IAGNLN-:  :    VPGIATA	ITVGKDG: :     :QLISKDG	QPVKTVT.	SIDGTTRI :	SIAKNSHD : : PVAVSGTP	YSSYDTSK	QNGQNTIT   : : VNFSSVV	VDFVSTYI	KLGVKTT:     VKTVTAT	IQTAKGA:	VAQAQTP    :     VAISGIP	EDNAFVKG /SGIATVE	rikggord 	GTKIDEKG : : DSTVAPIA	LLGLGNDN	QVGVDKDC  : QI	RFFHVND   : : -FSAIKN
ATVTYDEA         ADGTLAE-	HALVKASD    : AVPVTLSN	NDKADDT-NAITVGKDGT:    :::    FLDDTLGSQLISKDGV	GSVTIEPS	NNGVVGAG   : TVGDI	TTNIQSGI : : VTSKVTTI	INFTVSNP            GETVAVP	GKGIVIN-SQNGQNTITGLSNTLA   :   :   IVLNPSVNFSSVVNGSTIKLL	NLQGNGEA	FTIEVKDK     VTIEPSQP	HLNTLSGE     GE	VAKDKL   VPSTGTTE	INI INI     VPVTLSN	-KLGETL	ALNSVNAG	QLNEVRN ::: 7TISK	EKLATGGV : : vvvavkei	DRINEQGI
IDGNATT	TESTDDD	VKKVDEND :  : IKLL	SLKA  :: SLQSKTVA	VKFAMV ::   : TLLEVASI	-INAGGKK      TINFKAKT	OGP     VGTATVKS	TVGNNNGF    : TVGD	DVLSAGFN	YDVNVDD   :  XETVAGS	KASDIVA	TVD-KTKE	KKQG     GKAGDTVA	TAK     TIKILFLI	SAAGRLT	DTDAANV(	GKGNNDTI    : DKGNSAK	NNPAEAI
LNAGENLKNNGKDEVSTYDTVDEIDGNATTATVTYDEANQTSKVAYDVNVD)	KTIELTGDNGKKOLGVKTIKLTETSTNGNATTFSTDDDHALVKASDIAGNLN 	-TLAEEIHTTKGTANTALQTFTVKKVDENDKADDT-NALTVGKDGTSGKVNT 	LKLKGKNGLDIKTDKDGTVTFGINTOSGLKA	TLNNNGLSIKNTASNEQIQVGADGVKFAMVNNGVVGAGIDGTTRITRDEIGF 	TG-TNGSLDKSKPHLSKDGINAGGKKITNIQSGEIAKNSHDAVTGGKI	YDLKTELENKISSTAKTAONSLHEFSVADEQGNNFTVSNPYSSYDTSKTSDVITF  YDLKTELENKISSTAKTAONSLHEFSVADEQGNNFTVSNPYSSYDTSKTSDVITF	AGENGITTKVNKGVVRVGIDQTKGLTTPKLTVGNNNGKGIVIN-SQNGQNTITGLSNTLA :	KTRAASIV	-YDDTSKTSKVVXDVNVDDTTIEVKDKKLGVKTTTLTSTG- 	TGANKFALSNQATGDA-LVKASDIVAHLNTLSGDIQTAK 	KNDG1         CBVFA	-KEQVNDANKKQG 	KTKNAAVTVGDLNAVAQTPLTFAG-DTGTTAK KI	GDI VENESTRE SOFTINGER SERVICE STATES OF THE	QAKANTPULSANGLDLGGKVISNVGKGTKDTDAANVQQLNEV  QAKANTPVLSANGLDLGGKVISNVGKGTKDTDAANVQQLNEV	VIKAGTVLGGKGNNDTEKLATGGVQV VILAGTVLGGKGNNDTEKLATGGVQV	AGQTNYVT     NGNT
GKDKDFV:      FKAKSVT:	KTIKLTE   : KTV	TAN : LNPSVNFS	DGTVT    /AVSGTPV	EQ	SKPHI:	KTAQNSLI   :   VTIEPSQI	RVGIDQTE :       QVGFDATI	NIIKDED	TPVFADG	OO PGIATAEVO	FDNKYYQA	AADIKAVR	VAQTPLTE	TDGI   	DLGGKVI	ADIKKDPNSGSSSNRTVIKAGTV	VWVKTOKDGSKKA-LLATYNAAGOTNYV'   :  :  :  :    VVATFEKTAAKQADVVVTMSLNGNT
4N	GKKQL	TTKG     ITVGDIVI	LDIKTDK-   TSTVTTP\	IKNTASN:	DK      TKLLFLD	NKISSTA   : : IMKTVAGS	KVNKGVV:	SVRTTEQG	SQLISKDG F TTPVAVSC	FALSN	KVIY-DST   :::     KILFLDD	ININI	TVGDLNA     :		VLSANGL	NSGSSSN	KDGSKKA-   : :  KTAAKQAL
LNAGFNLKN   :  : LGSQLISKD	KTIELTGDW      VTINAIGP-	-TLAEEIHTTKG 	LKLKGKNGLDIKTDK- :         INFKAKTVTSTVTTPV	TLNNNGLSIKNTASN : ::      VKSGETVAVPVTLSNVP	TG-TNGSLDK :       SSVVNGSTIKLL	YDLKTELE	AGENGITT :      SNVPGIAT	NVTNDKGS	FLDDTLGSQLISKDG NTTTAKVT    :    KTVTSKVTTPVAVSGTPV	TGANKFALSN- 	YVDADGN   :   :   VVNGSTI	QMNVKSVIN ::  :  EVOYKTVAGSV	KTKNAAV				
841 L 1 745 L	895 K	947 - 848 A	997 L 901	1032 T			y y		1166	1352	1400	1450	1489	1538	1585	1645	1576 1701 1616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.9%; Score 404; DB 1; Length 1608;
ilarity 20.1%; Pred. No. 1.3e-07;
Conservative 255; Mismatches 702; Indels 624; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1872
                                                                                                                        1873 VALGSNSAISAGTHAGTQAKKS-------------------------DGTAGT--TTTAGATGTVKG 1912
                                                                                                                                                        1746 ISFDSSVLTYVGTTAGTSIKNPAVNFSSQLNGNTITLLFFDNTIGNELITADGQFATI-- 1803
1760 RNGIDSSASGKHSVAIG---FOAKADGEAAVAIGROTOAGNQSIAIGDNAQATGDOSIAI 1816
                     SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.
STRAIN=SNB;
MEDLINE=88557037; Pubmed=3290200;
POOLE K., Schiebel E., Braun V.;
Molecular characterization of the hemolysin determinant of Serratia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i-FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTE BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA REQUIRES SHLB FUNCTION.
-i- SUBCELLULAR LOCATION: OUTER MEMBRANE.
-i- SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERCENTIAL 170:3177-3188(1988).
J. BECLETIOL, 170:3177-3188(1988).
-!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                                            1817 GTGNVVAGKHSGAIGDP----STVKADNSYSVGNNNQFTDATQTDVFGVGNNITVTESNS
                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 1608 HEMOLYSIN.
1608 AA; 165078 MW; D669B476FE7DAD51 CRC64;
                                                                                                                                                                                        1913 FAGQTAVGAVSAVGASGAERRIQNVA----AGEVSATSTDAVNGS 1952
                                                                                                                                                                                                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                         PRT; 1608 AA.
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Best Local Similarity 20.1%;
Matches 398; Conservative 255
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                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A28182; A28182
                                                                                                                                                                                                                                                                                                                                                                                        HEMOLYSIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                         Serratia marcescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serratia.
NCBI_TaxID=615;
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P15320;
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SEQUENCE
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GLSHNQYQDFNVNQPGAVLNNSREAGLSQLAGQLGANPNLGGREASVILNEVIGRNPSLL 122	GDQYKATRQGDSTDIFSIGNSNNNNSSIRKIINVGAGSRDTD 346	AVN-VAQLKLVEELANRKITFKGDGDNNSNSVERGLG-NTLTIKGDAQTN 394  ::	ALTEANIGVYTDGNGLKVKLAKELTGLTSVSATNKIT 431 ::   ::	VSNTNNNNAELQSGGLIFSPITGTKTDKTVYSIDGLKFTNDSNSIATKGTTRITKKKIGF 491 :	AGTNDGVDESKPYLDNEKLKVGNSTLNSGSLTVNNTTG 529	NKQIQVGANGIKFATVANNVANTSATVGTARITEEKIGFAGTNDGVDEQ 578 	APYLDKERLKVGRVEITTDSGINAGNHKITGLTNGIANTDAVTIKQLK-DAKPTL 632     :: ::         :    :	NAGDGISINSNNGDLVDSSGNITTPTYNISVKTTKLNSNGTSGNNKFSVSNAHDNNSLVT 692 	AKDLADYLNKVNETADSALPSFKVQNGDNSNNAITVGKD-TNGKTFNTLKLKGENG 747   :	VNITTHRATGTVTFGIDQSNGLTTPKLTVGSDTNGNRLVIEQVPSADGNSTKNIIKGLSP 807	TLPSIASPSGRNIALGNTIEEKDKSNAASIDDVLNAGFNLK-NNGKDKDFV-STYDTVDF 865  -	IDGNATTATVTYDEANQTSKVAYDVNVDEKTIELIGDNGKRQLGVKTIKLTETSTNGN 923 : :   :	ATTESTDDDHALVKASDIAGNLNTLAEEIHTTKGTANTALQTFTVKKVDENDKADDTNAI 983      :     :     :   EKTTRTENSASSLSG736	TVGKDGTSGKVNTLKLKGKNGLDIKTDKDGTVTFGINTQSGLKAGDSTTLNNNGL 1038 ::   ::  ::  ::  ::  ::	SIKNTASNEQIQVGADGVKFAMVNNGVVGAGIDGTTRITRDEIGFTGTNGSLDKSKPHLS 1098	KDGINAGGKKITNIQSGEIAKNSHDAVTGGKIYDLKTELENKISSTAK-TAQNSLHEFSV 1157 	ADEQGNNFTVSNPYSSYDTSKTSDVITFAGENGITTKVNKGV-VRVGIDQTKGLTTPKLT 1216     : :     :                   GGAYQENAAGVDHLAAADTASTTTTKTDVGVNIGANVDXS-AVTRP 892	VGNNNGKGIVINSQNGQNTITGLSNTLANVTNDKGSVRTTEQGNIIKDEDKTRAASIVDV 1276 
GLSHNC	неооет	AVN-VA ::  SLNGTL	QQMPTA	VSNTNN : SNKNGG	AGTNDG   VADNHA	NKQIQV : :  REQLQ-	APYL   : HLAGLV	NAGDGIS    :  KAGRNV-	AKDLAD   RDDKTS	VNITTN     : VTITGS	TLPSIA  :   TVDKID	IDGNAT:	ATTEST     EKTTRT	TVGKDG	SIKNTA	KDGINA  :  GSGVEA	ADEQGN GGAYQE	VGNNNG     VERAVG
63	304	347	395	432	492	530 396	579	633	693 534	748	808	866	924	984	1039	1099	1158 848	1217 893
QQ	Qy	Qy	Qy Db	Oy Db	Qy Db	Oy Dp	Oy Dp	Qy	QY Db	Oy Db	Oy Db	Oy Db	Qy Db	Qy Db	Oy Dp	Qy Db	Qy Db	Qy Dp

1036 1441 1128 1293 DAGGKVDPNIGKDIH--TLGAGLKVGVEQQDKTIHANIGITAGDVILNSGKDIRLAGARV 1350 1791 946 QAGSIDINAKGEVRDQGTQYQASKGAVNLTADSHRSEAAANRQDEQSRDTRGSAGVRVYT 1005 1557 KDLTNLNSVNAGGTKIDEKGISFVDANGQ---AKANTPVLSANGLDLG--GKV-ISNVGK 1610 1611 GTKDTDAANVQ-------QLNEVRN------LLGLGNDNADGNQVNIA 1645 1458 ATPAGEKPQGPLWDRGART-----VGGAVKDSITGPAGRQGHLKV--NADVVNNN-- 1505 1277 LSAGFNLOGNGEAVDFVSTYD----TVNFA--NGNTTTAKVTYDDTSKTSK-----VVYD 1325 1442 QTPDGTLAQMNVKSVINKEQVNDANKKQGINEDNA-FVKGLEKAASDNKTKNAAVTVGDL 1500 1501 NAVAQTPLIFAGDIGITAKKLGETLIIKG ---- GQTDINKLTDNNIGVVAGTDGFTVKLA 1556 1646 DI--KKDPNSGSSSNRTVIKAGTVLGGKGNNDTEKLATG---------GVQV 1686 1687 GVDK-DGNANGDLSNVWVKTQKD---GSKKALLLATYNAAGQTNYVTNNPAEAI-DRINEQ 1741 1792 QTQAGNQSIA-IGDNAQATGDQSIAIGTGNVVAGKHSGAIGDPSTVKADNSYSVGNNNQF 1850 1897 --TAGTTTTAGAT--GTVKGFAGQTAVGAVSVGASGAERRIQNVAAGEVSATSTDAVNG 1951 1851 TDATOTDVFGVGNNITVTESNSVAL--GSNSALSAGTHAGTQAKKSDG------1326 VNVDDTTIEVKDKKLGVKTTTLTSTGTGANKFALSNQATGDALVKASDIVAHLNTLSGDI 1006 TTGSDLTVDAK-----VTGSI 1386 QTAKGASQANNSAGYVDADGNK-VIYDST---DNKYYQAKNDGTVDKTKEVAKDKLVAQA 1742 GIRFFHVNDGN-QEPVVQGRNGIDSSASGKH-SVAIGFQAKADGEAAVAIGR-----SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=90355839; PubMed=2388559; Relman D.A., Domenighini M., Tuomanen E., Rappuoli R., Falkow S.; "Genetic characterization of Bordetella pertussis filamentous haemagglutinin: a protein processed from an unusually large Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae; Bordetella. (Rel. 12, Created) (Rel. 33, Last sequence update) (Rel. 33, Last annotation update) PRT; 3591 AA FILAMENTOUS HEMAGGLUTININ FHAB. STANDARD; Bordetella pertussis NCBI\_TaxID=520; 01-OCT-1989 01-FEB-1996 01-FEB-1996 FHAB\_BORPE P12255; RESULT 14 FHAB\_BORPE 1129 qq g g Ω Q ōλ g δ a δý q δ g g ò g ολ ŏ ò g Óγ Ω οy οy δ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        601 İĞRARSDSDVKVSAHGALSIDSMTALGAIGVQAGGSVSAKDMRSRGAVTVSGGGAVNLGD 660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IGVVTDGNGLKVKL--AKELTGLT-----SVSATN-----KITVSNTNN-NNAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.9%; Score 404; DB 1; Length 3591; Best Local Similarity 20.1%; Pred. No. 3.2e-07; Matches 487; Conservative 282; Mismatches 904; Indels 750;
                                                        MEDLINE-89202884; PubMed=2595956; Relman D.A., Domenighini M., Tuomanen E., Rappuoli R., Falkow Serlman D.A., Domenighini M., Tuomanen E., Rappuoli R., Falkow Serliamentous hemagglutinin of Bordetella pertussis: nucleotide sequence and crucial role in adhorence."; Proc. Natl. Acad. Sci. U.S.A. 86:2637-2641(1989).
                                                                                                                                                                                                                                                                                                                                                                             EMBL; M60351; AAA22974.1; -.
EMBL; M60351; AAA22975.1; ALT_INIT.
EMBL; M60351; AAA22976.1; ALT_INIT.
AAA1291, Hemagglutinin.
SEQUENCE 3591 AA: 367420 WW; EF7418B30D6E5138 CRC64;
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     Mol. Microbiol. 4:787-800(1990).
                                              SEQUENCE OF 1-3261 FROM N.A.
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RNDIALDVADFTNTGSLYAEHDATLTLAQGTQRDLVVDQDHILPVAEGTLRVKAKSL--T 1697
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Lactobacillus.
NCBL_TaxID=1597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning, sequencing and expression of the gene encoding the cell-envelope-associated proteinase from Lactobacillus paracasei subsp. paracasei NCDO 151.";
                                 -----GGTKIDEKGISFVDANGQAKANTPVLSANGL-----DLGGKVISNVGKGTK
                                                                                                         DTDAANVQQL--NEVRNLLGLGNDN---ADGNQVNIADIKKDPNSGS-SSNRTVIKAGTV
                                                                                                                                                                                               -----VW-----VKTQKD
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                                                                                                                                                                                                                                                               1987 PTAPPMPKAPELDLRGHTLESAEGRKIFGEYKKLQGEYEKAKMAVQAVEAYGEATRRVHD
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                     LTIKGGQ - - - - TDTNKLFDNNIGVVAGTDGFTVKLAKDLT - - - - - NL - NSVNA - - - -
                                                                                  1749 GELTVKAONITNKRAALIEAGGNARLTAAVALLNKLGRIRAGEDMHLDAPRIENTAKLSG
                                                                                                                                                                                                                                          ----GSKKALLATYNAAGQTNYVTNNPAEAIDRINE
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020470;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1998 (Rel. 26, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
11-TYPE PROPEINASE PRECURSOR (EC 3.4.21.96) (LACTOCEPIN)
ASSOCIATED SERINE PROPEINASE) (LP151).
                                                                                                                                                    L----GGKGNNDTEKLATGGVQVGVDKDGNANGDLSN-
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MEDLINE=92381481; PubMed=1512565;
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SEQUENCE FROM N.A.
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                                                                                                 Naes H., Nissen-Meyer J.; "Purification and N-terminal amino acid sequence determination of the cell-wall-bound proteinase from Lactobacillus paracasei subsp.
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DYNKLNKVQQQDTYVDVIVQMSAAPASENGTLRTDYSSTAEIQQETNKVIAAQASVKAAV 138
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                                                                                                                                                                            paracasei.";
J. Gen. Microbiol. 138:313-318(1992).
J. Gen. Microbiol. 138:313-318(1992).
GROWTH OF THE BACTERIA ON MILK.
-!- CATALYTY ENDOPEDFIOASE ACTIVITY WITH VERY BROAD SPECIFICITY, ALTHOUGH SOME SUBSITE PREPERENCE HAVE BEEN NOTED, E.G. LARGE HYDROPHOBIC RESIDUES IN THE P1 AND P4 POSITIONS, AND PPO IN THE P2 POSITION. BEST KNOWN FOR ITS ACTION ON CASEINS, ALTHOUGH IT HAS BEEN SHOWN TO HYDROLYSE HEMOGLOBIN AND OXIDIZED INSULIN B-CHAIN.
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EXTRACELLULAR (POTENTIAL).
MEMBRANE ANCHOR (BY SIMILARITY).
CYTOPLASMIC (POTENTIAL).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. CELL WALL. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS SUBTILASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 1902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell wall; Zymogen; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; PR001899; -.
InterPro; PR001899; -.
Pfam; PF00746; Gram_pos_anchor; 1.
Pfam; PF007082; Peptidase_S8; 3.
PRINTS; PR00723; SUBTILISIN.
PROSITE; PS00136; SUBTILIASE_ASP; 1.
PROSITE; PS00138; SUBTILIASE_HIS; 1.
PROSITE; PS001343; GRAM_POS_ANCHORING; FALSE_NBG.
HYDOLIASE; Serine protease; Cell wall; Zymogen: S1c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.3e-07;
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Gen. Microbiol. 138:1353-1364(1992)
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                                               SEQUENCE OF 189-196.
MEDLINE=92226694; PubMed=1564442;
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PIR; B44858; B44858.
HSSP; Q99405; IMPT.
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0	142	GGDVLAEGDASIAIGSDDLYLPKNLDLKNEFHKLIHGHEILKKIQTSTDG 191	
. q	199	KYKG	
Οy	192	KIKYRRTRAQGHASTAVGAMSYAQG-HFSNAFGTYATAEAAYSLAVGLAAQA 242	
QQ	253	RYFTSKVPYGFNYADNNDTITDDTVDEQHGMHVAGIIGANGTGDDPTKSVVGVAPEAQLL 312	
Qy	243	VALGFGSQILDRDNNTDASAY  :   :	
qq	313	AMKVETNSDTSATIGSATLVSAIEDSAKIGADVLNMSLGSDSGNQTLE 360	
ΟŸ	297	VPLGKTLADQYKATRQGDSTDIFSIGNSNNNNSSIRRKIINVCAGSRDT 345	
qq	361	GTSGSATOG	
ΟŸ	346	DAVNVAQLKLVEELANRKITFKGDGDNNSVERGLGNTLTIKGDAQTNALTEANIGVYT 405	
qq	41.5	GATTVASAENT-DVISQAVTIT-DGKDLQLGPETIQLSSNDFTGSFDQKKFYVVK 467	
ογ	406	AELQSGGLTFSPITGTKTDKTVYS	
qq	468	LNFADKQKYAQA	
οy	464	IDGLKFTNDSNSIATKGTTRITKKKIGFAGINDGVDESKPY 504	
QQ	509	AGAAGLIIVNNDGTATPLTSIRLTTTFPTFGLSSKTGQKLVDWVTAHPDDSLGVKIALTL 568	
ογ	502	LDNEKLKVGNSTLNSGSLTVNNTTGNKOLQVGANGIKFATVANNVANTSATVG 557	
qq	569	LPNQKYTEDKMSDFTSYGPVSNLSFKPDITAPGGNIWSTQNNNGYTNMSGTSMASPFIAG 628	
δλ	558	TARITEEKIGFAGTNDGVDEQAP-YLDKERLKVGRVEITTDSGINAGNHKITG 609	
рр	629	SQALLKQALN676	
ΟŸ	610	LINGIANTDAVIIKOLKDAKPILNAGDGISINSNNGDLVDSSGNITTPTYNISVKTTK 667	
QQ	677	- NNVIVSPRROGAGLYDVKAAIDALEKNPSTVVAENGYPAVELKDFTSTDKTFK 729	
٥y	899	LN-SNGTSGNNKFSVSNAHDNNSLVTAKDLADYLNKVNETADSALPSFKVQNGDNS 722	
QQ	730	LTFTNRTTHELTYQMDSNTDINAVYTSATDPNSGVLYDKKIDGAAIKAGSDITVPAGKTA 789	
٥٧	723	NNAITVGKDINGKTFNILKLKGENGVNITINRATGIVIFGIDQSNGL 769	
QQ	790	QIEFTLSLPKSFDQQQFVEGFLNFKGSDGSRLNLPYMGFFGDWNDGKI	
Οy	770	TTPKLTVGSDTNGNRLVIEQVPSADGNSTKNIIKGLSPTLPSIASPSGRNIALGN 824	
qq	850	GGNY	
δŷ	825	TIEEKDKSNAASIDDVLNAGFNLKNNGKDKDFVSTYDTVDFIDGNATTATVTYDEANQTS 884	
Dp	895		
Qy	885	KVAYDVNVDEKTIELIGDNGKKOLGVKTIKLTETSTNGNATTFSTDDDHALVKASDIAGN 944	
QQ	936	KTYYDAHGN 965	
QY	945	LNTLAEEIHTT	
QQ	996	IRTADDGSYTYRISGVPEGGBKRQVFDVPFKLDSKAPTVRHVALSAKTE 1014	4
Qy	966	TLKLKGKNGLDIKTDKDGTVTFGINTOSGLKAGDSTTLNNNGLSIKNTASNEQ	æ ·
q	1015	NGKTQYYLTAEAKDDLSGLDATKSVKTAINEVTNLDATFTDAGTTADGYTKIETPLSDEQ	<del>.</del>
οy	1049	IQVGADGVKFAMVNNGVVGAGIDGTTRITRDEIGFTGTNGSLDKSKPHLSKDGINAGG	، ب
οp	1075	AQALGNGDNSAELYLTDNASNATNQDASVQKPGSTSFDLIVNGGG 1119	o,

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ONSCHEFS    :::  GKKHDLN	IDQTKGL1	KDEDKTR?       AALDAQH	NJ   FGANEFN	ANKFAL-   :   OKPFGVV	VIYDSTDI : :    ITGTATDI	KQGIN   :      KLLEGKN	TIKGGQT    : :  TTEPAKT	NGQAKAN 	VNIADIKKDPNSGSSS 	IVWVKTQK	NGIDSSA   1   1   1	VVVAGKHS  :  \VLAKLAE	AHLOALQ	VGASGAERRIQNVAAGEV     :   :   : -GKDKGDEGSQPSSGGNIPT	
SSTAKTA     DGTYTDA	IKGVVRVG	rteggnii    : : rvnvgdfv	/NFANG         /TFDQGVK	rrrsrgrg       -	rvdadgnk   : : rtndpnfq	EQVNDANK   HMAIDQPV	AKKLGETI S	KGISFVD?  ::   AGVT-VT?	DNADGNO	NANGDLSI    1  GANRDLQI	QEPVVQGI    : QLQSVKA!	SIAIGTGI  :  SLAKVLD	VALGSN-	AVSVGASO      GKDI	
KTELENKI : SGTYPAAV	TTKVN     KHEDTKVE	NDKGSVR] :  :  SDTKJ	PDVLKNA	TT: : NDLTFSF:	QANNSAG:	VKSVINKI :   INSGKPG	AGDTGTT	TKIDE : TYQDVPA	NLLGLGN	VGVDKDG     ASVDSLT	FHVNDGN	AAQATGDQ       LQA	TTVTESNS   :     :     OTLTSGQA	FAGQTAVG 	
GGKIYDLI         GGGTYTF	AGENGI-	NTLANVT  :  KVTGTVS	DFVSTYD  :   TITSSYD	SKVVYDVNVDDTTIEVKDKKLGVKTTTLTSTGTGANKFALSNQ ::           ::         ATITGKVKHPTTTLQVDGKQISIKNDLTFSFTLDLGTLGQKPFGVVVGDTTQNK	OTAKGAS    SST	OGTLAQMN   :  \SQYADIN	/AQTPLTF : 1 KYEPKKTL	NIGVVAGTDGFTVKLAKDLTNLNSVNAGGTKIDEKGISFVDANGQAKANTPVLSANG 	VOOLNEVE :  LOTAKOAL	NRTVIKAGTVLGGKGNNDTEKLATGGVQVGVDKDGNANGDLSNVWVKTQKDGSKKALL 	ATYNAAGGTNYVTNNPAEAIDRINEGGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAI 	GEQAKADGEAAVAIGRQTQAGNQSIAIGDNAQATGDQSIAIGTGNVVAGKHSGAIGDPST 	VKADNSYSVGNNNQFTDATQTDVFGVGNNITVTESNSVALGSNSALSA 	GTHAGTQAKKSDGTAGTTTTAGATGTVKGFAGGTAVGAVSVGASGAERRI 	
SHDAVT-::	KTSDVITE  : AQVDLYAD	DNTITGLS:     EATI	GNGEAV         GNTTTEOF	DDTTIEVE   ::  PTTTLQVI	LNTLSGD]       -PTLSLD9	VAQAQTPI AINGSHV?	TVGDLNAV	AKDLTNLI :   SAD	KDTDAAN         KADDPAQ	NNDTEKL  :   TOKA	PAEAIDR	ROTOAGN   111 QAQAGT	TDATQTD     -DAATGK	GTTTTAG   :  GTSDKGG	47 51
OSGEIAKI :  TTG	YSSYDTSI ::   :: VTNADYA	VINSQNGC:SDQTS:	Q	CVVYDVNV :   ITGKVKH	ASDIVAH	EVAKDKL	KTKNAAV     :   UTTTKKI	rDGFTVKL     : \TGETVQY	ISNVGKGT :: : /TNI	STVLGGKG     -TALAAA-	TINYVINN: 1: :	SEAAVAIC   DLVA	SVGNNNQE      EVGNAK	HAGTQAKKSDGTAGT 	19
KKITNIOSGEIAKNSHDAVT-GGKIYDLKTELENKISSTAKTAONSLHEFSVA-DEQG 	NNFTVSNPYSSYDTSKTSDVITFAGENGITTKVNKGVVRVGIDQTKGLTTPKLT  :     :-    :-	GNNNGKGIVINSQNGQNTITGLSNTLANVTNDKGSVRTTEQGNIIKDEDKTRAASIVDVL     :  :	SAGFNL	DDTSKTSK   : : DPKTGIAT	ATGDALVKASDIVAHLNTLSGDIOTAKGASQANNSAGYVDADGNKVIYDSTDNKYYQAKN 	DGTVDKTKEVAKDKLVAQAQTPDGTLAQMNVKSVINKEQVNDANKKOCIN	LEKAASDNKTKNAAVTVGDLNAVAQTPLTFAGDTGTTAKKLGETLTIKGGOTDTNKLTDN :	NIGVVAGI   AAA	LDLGGKVISNVGKGTKDTDAANVQQLNEVRNLLGLGNDNADGNQV	NRTVIKA( :   DATT	ATYNAAG       AKLPADK	GFQAKADO 	VKADNSY:     	GTHAGTO   AVEAAKT	SATSTD ::     KPATTTSTSTD
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Geme J.W., Cutter D. III, Barenhamp S.J.;
"Characterization of the genetic locus encoding Haemophilus influenzae type b surface fibrils.";
J. Bacteriol. 178:6281-6281-6281.
EMBL; U41852; AAC44560.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 ESTNASSFTYSLKKDLTDLTSVATEKLSFGANGDKVDITSDANGLKLAKTGNGNVHLNGL 178
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Haemophilus.
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Last annotation update)
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Similarity 23.8%; Pred. No. 1.1e-42;
27; Conservative 295; Mismatches 853;
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_	1104 WTAKADKYADGESEGETDQEVKAGDKVTFKAGKNLKVKQSEKDFTYSLQDTLTGLTS	5	163
	6	KKITNI  :  :	1112
_	1164 GGTANGRNDTGTVINKDGLTITLANGAAAGTDASNGNTISVTKDGISAGNKEI		1219
٠. ٥	1113 QSGEIAKNSHDAYEGKIYDLKTELEBKISESYRATADNAL 		1270
. ~	TBESVADEGGNNFTVSNPYSSYDTSK		1183
0	1271 HTVIIDVAEAKVGDGLEKDTDGKIKLKVDNTDGNNLLTVDATKGASVAKGEFNAVTTDAT		1330
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<sub>х</sub> д			1450
<b>×</b>	1223		1269
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<u> </u>	1270 AASIVDVLSAGFNLQGNGEAVDFVSTYDTVNFANGNTTTAKTYDDTSKT 		1319 1569
9 ;	0161		1365
<u> </u>	19 1320 SNYTLDYNYCOTTETTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT		1613
: ≿	1366		1418
q	1614 NGLVTAKAVIDAVNKAGWRVKTT-GANGQNDDF		1667
Σy	1419 QAKNDGTVDKTKEVAKDKLVAQAGTPDGTLAQMNVKSVINKEQ 		1467 1716
ą	1668		52
λ G	1468 KOGINEDNAFVKGLEKAASJONIANAAVIVOLANA NASTALIA   1   1   1   1   1   1   1   1   1		76
à	1528		1578
음		KITKDGLT	1814
ó	1579 FVDANGQAKANTPVLSANGLDLGGKVISNVGKGTK	DTDAAN	1619
g	1815 ITPANGAGAAGANTANTISVTKDGISAGNKAVTNVVS	VALLEBARIT	, ,
δά		 .:! :NAQVRNAN	1934
9 8	1660	5Ač	1687
<u>3</u> 8	1835 EVKFKSGNGINVSGKTLNGTRVITFELAKGEVV	(VGDMYYSK	1994
ò	1688 VDKDGNANGDLSNVWVKTQKDGSKKALLATYNAAGQTN	INNPAEAID	1736
g	1995	IGNQVAD	204
Qy	1737	ADGEA	1785
g	2047 AIAKSGFEL	ATCHECTOR	1837
δý	1786 AVAIGROTQAGNOSIAIGDNAQATGDQSIAIGTGNVVAG	KHSGALGDESIVA ::    :   -NTDANGNKTVKK	21
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NESIAIGGDVLAEGDASIAIGSDDLYLPKNLDLKNEFHKLIHGHEILKKIQTSTDGKIKY 195

RRTRAQGHASTAVGAMSYAQGHFSNAFGTYATAEAAYSLAVGLAAQATKQSSIAVGSNAK

-TLGGSLY - - - - VNSGQVGV 114

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NSVERGLGNTLTIKGDAQTNALTEANIGVVTDGNGLKVKLAKELTGLTSVSATNKITVSN 434

-----GWNLTASG-----ANSGNVAPGSSVDLKNTDKNLTITKAIGSNDVOF--

TNNNNAELQSGGLTFSPITGTKTDKTVYSIDGLKFTNDSNSIATKGTTRITKKKIGFAGT

STDIFSIGNSNNNNSSIRRKIINVGAGSRDTDAVNVAQLKLVEBLANRKITFKGDGDNNS

----VSIGDVSSTNLK-TRQLSGLAAGTSNTDAVNVAQLKVVDEIASR------

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--NLNKDVK------VTTLAVGDALLNTDGIALGTDV-SLSTTGLA-ITD---GPAVT 393

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394 ASGIDAGSKVISH----VAAGAVSETSTDAVNGSQLNAVQVQAS--QPVTFTGNEGAVKR 447
                                                                                                                                                                                                                                                                                                                                                                                                                       256 ANA-FAATAIGGNTVVNLGRGVALGFGSQILDRDNNTDASAYVPLGKTLADQYKATRQGD 314
                                                           79 TNKINNTLKGDALATGEASIAFGS---LSKAQGSQAIAIGSVKPDPNNGSNGNVGSHAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                218 VIVPDGAVALGLNSVASTGKGLS---GYDPKTKTTSTDASA-----AWKSTLAA-
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76 VTGYARFFGPSG--TAAEQQGASRNL--
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165 ARAIAIGAKASADGVDTVALGS-
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Ra Alvarenga R., Alves L.M.C., Arraya J.E., Bala G.S., Baptista C.S.,
Ra Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Bithones M.R.S.,
Ra Berros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Bithones M.R.S.,
Ra Benro M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa Neto C.M.,
RA Collauto L.L., Cristofani M., Dlas-Neto E. Docena C., El-Dorry H.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Franca E.C., Franco M.C., Frohme M., Furlan L.R.,
RA Frieger J.E., Kuramae E.E., Langret F., Lambais M.R., Leite L.C.C.,
RA Lemos B.C., Lenos M.Y.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B., Madeira H.M.F., Matsukuma A.Y.,
RA Machado M.A., Madeira A.B., Martins E.M.F., Matsukuma A.Y.,
RA Machado M.A., Madeira A.B., Martins E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Monn D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Goliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Goliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA de Souza A.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.,
RA The genome sequence of the plant pathogen Xylella fastidiosa.";
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                               ADNSY SVGNNNQFTDATQTDVFGVGNNITVTESNSVALGSNSA I SAGTHAGTQAKKSDGT
                                                                                       ADGKW-----YELNADGTASNKEVTLGNVDANGKK-------VVKVTENG
                                                                                                                                                  ACTTTTAGATGTVKGFAGQTAVGAVSVG------ASGAERRIQNVAAGEVSATS
                                                                                                                                                                                                          ADKWYYTNADGAADKTKGEVSNDKVSTDEKHVVRLDPNNQSNGKGVVIDNVANGEISATS
                                                                                                                                                                                                                                                                     TDAVNGSQLY - - - KATQSIANATNELDHRIHQNENKANAGISSAMAMASMPQAYIPGRSM
                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                        2003 VTGGIATHNGQGAVAVGLSKLSDNGQWVFKINGSADTQGHVGAAVGAGFHF 2053
                                                                                                                                                                                                                                                                                                                                                                                                                          2303 VAIAGSSYQGQNGLAIGVSRISDNGKVIIRLSGTTNSQGKTGVAAGVGYQW 2353
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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SEQUENCE 2059 AA; 2040
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1009 T 999 999 1069 G 1069 G 1126 T 1126 T 1135 G 1135 TDKDGTVTFGI :    :  -NTDGNLTIS-	, ,	FGGKIYDLKT   :: :: GSQLNAVQV	AGENGITTKN :  : :   SGGN-LKSV	ANVTNDKGS	GNTTTAKVT	ANKFALSNO               	DNKYYQAKN	CPVTFTG-N KQGINEDNA	FGNVVING											
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Gaps 128;
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1936 VAAGEVSATSTDAVNGSOLYKATQSIANATNELDHRIHQNENKANAGISSAMAMASMPQA 1995
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                                                     ------ARIAALAVIVIG------ARIAALAVIVIG---
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                                                                                                                                                                                                                                                       Pasteurella multocida.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
NCBI_TaxID=747;
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"Evolutionary origins of the autotransporter proteins.";

"Evolutionary origins of the EMBL/GenBank/DDBJ databases.

Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ777636; CAC14203.1; --

SEQUENCE 2712 AA; 276154 MW; 3F5579D6F32FFA3D CRC64;
                                                                                                                                                     "O9F3X5 PRELIMINARY; PRT; 2712 AA. 09F3X5; C1-MAR-2001 (TrEMBLrel. 16, Created) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) MAPB PROTEIN.
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9.3%; Score 966.5; DB 2;
Best Local Similarity 22.0%; Pred. No. 1.6e-32;
Matches 629; Conservative 338; Mismatches 932;
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GTYAGT	DIE   LGLDAV	одоны	IKYDTV	ANIGVV     TGINPV	LQSGGI       LDDGVP	ESKPYL : VDR	RITEER : : SKSEGQ	VGRVE1 :  LGNTNS	AKPTLN   IYVT	FSVSNA        NT	NTLKLK	NST      NSTLSN	AKTLSN	VDE  : TDAVNV	ASDIA- :  KLEIGI	KVNTLK    :  AVITVK	DSTTLA : 1: TANTVW	DEIGFT
536	317	327	360	399	442	500	560	589	628 1061	679	738	796 1228	846	892 1346	938	993	1029	1079
qq	Qy Db	Qy Db	oy D	Qy Db	Qy	Qy Db	Qy Db	Oy Dp	VQ Db	yo go	o O	Oy Dp	Qy Db	Oy Db	Qy Db	Oy Db	Oy Db	ογ

1395 1432 2112 1690 1742 2379 1191 ITTKVNKGVVRVGIDQTKGLTTPKLTVGNNNGKGIVINSQNGQNTITGLSNTLANVTNDK 1250 1670 VNTKV-----VD-------GQNGGKALEVSL---ANQLTLGKGPEANVPNAT 1706 1251 GSVRTTEOGNIIKDEDKTRAASIVDVLSAGFNLQGNGEAVDFVSTYDTVNFANGNTTTAK 1310 1433 ------AKDKLVAQAQTPDGTLAQMNVKSVINKEQVNDANKKQ- 1469 1553 1554 KLAKD------LINLNSVNAGGTKIDEK----GISFVDANGQAKANTPVLSANGLDL 1600 1601 GGKVISNVGKGTKDTDAANVQQLNE-----VRNLLGLGNDNADGNQVNIADIKK 1649 2271 2322 2493 1570 D--GLTITQGDNTVS---LTDDGLDNGNKQIKNVASGLTTTNGTATTSLDDAVQTNGVNV 1624 1131 YDLKTELENKISSTAKTAQNSLHEFSVADEQGNNFTVSNPYSSYDTSKTSDVITFAGENG 1190 1873 GAVINKDGLTITEGDKTVKLTEKGLDNGGNQIINVDSGLKKTDGSVVALKDAEGSVLTNG 1932 1933 VNVGDLKNAIKDVTSATNGGFGLKDKAGAEFKQDLGTTAQITGDKNINTKVIDVPNSNDK 1992 . 1993 ALEISLANDITLGKNGADGVDGSLGVNGKDGASVVLNGKDGSIGLTGPRGQDGSDGKSAT 2052 -----KGLEKAASDNKTKNAAVT-----VGDLNAVAQTPLTFAGDTG-TTAKKLGE 1523 1743 -IRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAK--ADGEAAVAIGRQTQA-GNQ 1798 1799 SIAIGDNAQATGDQSIAI----GTGNV-----VAGKHSGA-IGDPSTVKADNSYSVGN 1846 1847 NNOFTDATQTDVFGVGNNITVTESNSVALGSNSAISAGTHAGTQAK-KSDGTAGTTTAG 1905 2494 GNSKTRIVYTKPNGEBEQV-ATMNDGLVFGADKGTEHKAKLGTTVKVKGDDKNIETEVAG 2552 1906 ATGTVKGFAGQTAVGAVSVGAS-----GAERRIQN-----VAAGEVSATSTDAVNGSQLY 1955 1344 ----TTTLTSTGTGANKFALSNQATGDALVKASDIVAHLNTLSGDIQTAKGASQAN----2053 ISVKDGKAGVDGKDGKTRIVYETKDATGKPVVEEVATLNDGMKFVGNDGKEVTRKLNE 2216 ----ITNVTAGVDDKDAVNVSQLKDGLAKATTKVEAGKNMTVTPTVNQDGSTTYTVATED : | : | : | : | | 2272 NVNF----TITVTTGNTVM----NDGVKVGDNVALINEGLKAGDVTVTTAGINAGNKKV 1311 VTYD----DTSKTSKVVYDV-NVDDTTI--------EVKDKKLGVK----1691 DGNANGDLS-----NVWVKTQKDGSKKALLATYNAAGQTNYVTNNPAEAIDRINEQG 2437 GISI --- VGKDGKDAVAISGKDGVGTIGLTGPAGADGKNANAIIGVNDSVKGLDGNDGKD TLTIKGG-----QTDTNKLTDNNIG-------------------------VVAGTDG--FTV ------LATGGVQVGVDK-----KNDGTVDADGNKVI-----YDSTDNKYYQA-----KNDGTVDKTKEV----1650 DPNSGSSSNRTVIKAGTVLGGKGNNDTEK------1470 1479 1707 1396 1524 qq q q q q QQ q Q qq g g q οy δλ Q δ δ δ qq ŏ ò g δ à qq ŏ δ g ò õ g ç δy δ ò á

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 GHEILKKIQTSTDGKIKYRRTRAQGHASTAVGAMSYAQGHFSNAFGTYATAEAAYSLAVG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 LAAQATKQSSIAVGSNAKANAFAATAIGGNTVVNLGRGVALGFGSQILDRDNNTDASAYV 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 KPDPNNGSNGNVGSHAKGNESIAIGGDVLAEGDASIAIGSDDLYLPKNLDLKNEFHKLIH 177
1956 KATOSI---ANATNELDHRIHQNENKANAGISSAMAMASMPQAYIPGRSMYTGGIATHNG 2012
                                     2612 KVQQQVNNQATAINKLGDHINKVDKDLRAGIAGATAVAFLQRPNEAGKSIVSLGVGSYRS 2671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 ------GNTG------VSGDDKYCFYNASSQS----VIC 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MNHIYKVIFNKATGTFWAVAEYAKSHSTGGGSCATGQ---VGSVRTLSFARIAALAVLVI 57
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7.2%; Score 742; DB 2; Length 1299;
Best Local Similarity 21.1%; Pred. No. 1.7e-23;
Matches 448; Conservative 231; Mismatches 546; Indels 902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Henderson I.R., Nataro J.P., Cappello R., Stein C.; "Evolutionary origins of the autotransporter proteins."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AJ277655; CAC14202.1; "SEQUENCE 1299 AA; 130963 WW; BBCCEOEBE6GDB428 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                   2013 QGAVAVGLSKLSDNGOWVFKINGSADTQGHV--GAAVG 2048
                                                                                                                                                                        2672 ESAIAVGYARNSDNNKISIKLGGGMNSRGDVNFGGSIG 2709
                                                                                                                                                                                                                                                                                                                                                              PRT; 1299 AA.
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Pasteurella multocida
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SEQUENCE FROM N.A.
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09F3X6;
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1688 VDKDGNANGDLSNVWVKTQKDGSKKALLATYNAAGQTNYVTNNPAEAIDRINEQGIRFFH
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                                                                                                          ---GDTTYNPETGEYAN-----TNIGGTGASTI---
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987 KDGTSGKVNTLKLKGKN---GLDIKTDKDGTVTFGINTQSGLKAGDSTTLNN---NGLSI 1040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           379 KTTDSNDVTFNLATALKVDSLTTGNTAMTTDGVTVGKRVTLDSTGLVIAEG-----PSV
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de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E., da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr., de Salva E.R., Silva W.A. Jr., de Sulva A.P., Tarenzi M.L.Z., Siqueira W.J., de Souza A.A., de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L., zapo M.A., Zatz M., Meidanis J., Setubal J.C.; Vertore A.L., The genome sequence of the plant pathogen Xylella fastidiosa."; Nature 406:151-159(2000).

EMBL: AE004017; AAF84783.1; -. SEQUENCE 1190 AA; 118446 MW; 756741B0C8D787CC CRC64;
                                                                                                                                                                                                                                                                                                                                    Length 1190;
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                                                                                                                                                                                                                                                                                                                                 6.8%; Score 704.5; DB 2; 22.9%; Pred. No. 5.7e-22;
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Matches 360; Conservative 179; Mismatches 508;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SA--ISAGTHA-----GTQAKKSDGTA-GTTTTAGATGTVKGFAGQTAVG-----A 1921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SATPIAAGVDATAIGVGATASGADSIAMGNKASASADNAV-----AIGNHSVADRANT 1064
                                                                                                                                                                                                                                                                                                        EAIDRINEQGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGRQ 1792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-NONTYPEABLE STRAIN 11;
MEDLINE-96332658: Pubmed-8730864;
Barenkamp S.J., St Geme J.W. III;
Barenkamp S.J., St Geme J.W. III;
"Identification of a second family of high-molecular-weight adhesion
proteins expressed by non-typable Haemophilus influenzae.";
Mol. Microbiol. 19:1215-1223(1996).
                                                                                                                                                                                                                                                     DTEKLAT -- GGVQVGVDKDGNANGDLSNVWVKTQKDGSKKALLATYNAAGQTNYVTNNPA 1732
                                                                                                                                                                                                                                                                                                                                                            1793 TQA-GNQSIAIGDNAQATGDQSIAIGTG------NVVAGKHSG------AIGDPS 1834
                                                                                                                                                                                                  TDAANVQQLNEVRNLLGLGNDNADGNQVNIADIKKDPNSGSSSNRTVIKAGTVLGGKGNN 1674
                                                                                                                                                                                                                                                                                                                                                                             VSVGASGAERRIQNVAAGEVSATSTDAVNGSQLYKATQSIANATNELDHRIHQNENKANA
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                                                                                                                                                                -----TAMAGSGAK
                                                                                                                                                                                                                                                                                                                                   -----GATGTRSIAVGVGTLASAEGATAVGSG
                                       1448 LAQMNVKSVINKEQVNDANK--KQGINEDNAFVKCLEKAASDNKTKNAAVTVGDLNAVAQ
                                                                                                                    SOLOAVSSTASKGWNLLASGANSSNVAPGESVDLKNTDGNIVISKESGSNDVLFNLSSSL
     1506 TPLIFAGDICTTAKKL----GETLTIKGGQTDTNKLIDNNIGV--VAGTDGFTVKLAKDL
                                                                  -----SAGNOKITNVAAGTADTDAVNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophlus.
NCBI_TaxID=727;
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Last sequence update)
Last annotation update)
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     SNVVPGESVDLKNSDGNLLITKTTDS---
                                                                     662 TVGSNVTLGSTGLVITDGPSVTSSGI---
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01-NOV-1996 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTLAQMNVKSVINKEQVNDANKKQGINEDNAFVKGLEKAASDNK---TKNAAVTVGDLNA 1502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .284 Q-----GNGEAVDEVSTYDTVNFANGNTTTAKVTYDDTSKTSKVVYDVNVDDTTIEV 1335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KDKKLGV-KTTTLTSTGTGANKFALSNQATGDALVKASDIVAHLNTLSGDIQTAKGASQA 1394
                                                                                                                                                                                                                                                                                                                               .112 IQSGEIAKNSHDAVTGGKIYDLKTELENKISSTAKTAQNSLH--EFSVADEQGNNFTVSN 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       438 TTALTVN------DGKNANNPKGKVADVASTDEKKLVTAKGLVTA--LNS 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 HLN------GIGSTLTDTL--VGSPATHIDGG---DQSTHYTRAASIKDVLNAGWNI 266
                                                                                                                                                                                                                                                                                               ---QVKHA-----KGGVQVTS 152
                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267 KGVKAGSTTGQSENVDEVHTYDTVEELSADTETTTVTVDSKENGKTEVKIGAKTSVIKE
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                                                                                                                                                             HTKCASATVAVAVLATLLSATVEANNTPVTNKLKAYGDANFNFTNNSIADAEKOVQEAY
                                                                                                                                                                                                                            KGLLNLNEKNASDKLLVEDNT------AATVGNLRKI,GWVLSSKNGTRNEKSQ-
                                                           Length 1098;
                                                                                                                              953 HTTKGTANTA---LQTFTVKKVDENDKADDTNAITVGKDGTSGKVNT----
          D977335A89F7333D CRC64
                                                           Ouery Match
6.7%; Score 690; DB 2; L.
Best Local Similarity 24.7%; Pred. No. 2.1e-21;
Matches 314; Conservative 151; Mismatches 439;
EMBL; U38617; AAC43721.1; -. SEQUENCE 1098 AA; 114100 MW;
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	PREJULT 7	QY         1081         IGFTGTNGSLDKSKPHLSKDGINAGGKKITNIOSGEIAKNSHDAVTGGKIYDLKTELENK         1140           B         174         LLMDAASGTFSASRNGSASKITNLAAGTLAADSTDAVNGSQLFDTNEKVDQN         225           QY         1141         ISSTAKTAQNSLHEFSVADEQGNNFTVSNPYSSYDTSKTSDVITF-AGENGIT         1192           B         1161         1   1   1   1   1   1   1   1   1   1

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                                                                                                                                                                                                                                                                                                                                                                                                                        SLGSIVFLSTGPVFAADITVSTQAELS----AALSNGTYDKIILGADITLIGSLTVNMTS 116
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                             -----STGGGSCATGQVGSVRTLSFARIAALA-----VLVIGA--TLNGSAYAQQIT 71
                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QITDGIDNTTTIGN-EIQLNAEN---ATAINFLGSSSKTLNNNGTIKGSVIFAGVAD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQAPYLDKERLKVGRVEITTDSGINAGNHKITGLTNGIANTDAVTIKQLKDAKPTLNAGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDNNSNSVERGLGNTL--TIKGDAQTNALTEANIGVVTDGNGLKVKLAKELTGLTSVSAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGTGVNVLASAILNLFGGTINTSATANGITFAG----TEGGHTLTDLTINLLG-TGIALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NKITVSNTNNNNAELQSGGLTFSPITGTKTDKTVYSIDGLKFTNDSNSIATKGTTRITKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----NTT--GNKQIQVGANGIKFATVANNVANTSATVGTARITEEKIGFAGTNDGVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAGDITAATGISATHNGTGTV--KIKNDGTITSTTAGIAISSASIKEISVDNTDGTITAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     488 KIGFAGTNDGVDESKPYLDNEKLKV------GNSTLNSGSLTVN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               556 GIGIAATNTELNT----FDAEALDINVNGAGIGIQATGGGVNLSASNLIINVANTLGTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 TGRFHVTHTGSSVISEVSTGGANNISIMDFASGADVKIDRTGSTGDLTSTGVNAFAYTFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGASFELIANQNVFSGTTTNRGLEIGSYNSID-GFGSGVKIVLQSRSDGSIISGNGIDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 TAVNVIYNNIDFLGSSQLIYMGAYGAATNSIMTFGDIL--NDVVVNDRAQBIGEVNKLAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KNEFHKLIHGHEILKKIQT-----STDGKIKYRRTRAQGH-ASTAVGAMSYA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 ------QGHFSNA-----FGTYATAEAAYSLAVGLAAQATKQSSIAVGS---NA
                                                                                                                                                                                                                                                                                                                  1 MNTIFKVIWNASLNVWVVVSELAKGRIKTKSSRNLISEGVLPKFEQSMVSKLFRKNLLAL
                                              Yersinia pestis.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                 631;
                                                                                                                                                                                                                                  Length 3705;
                                                                                                            SEQUENCE FROM N.A.
STRAIN=CO-92 BIOVAR ORIENTALIS;
Henderson I.R., Nataro J.P., Cappello R., Stein C.;
Henderson I.R., Nataro J.P., Cappello R., Stein C.;
"Evolutionary origins of the autotransporter proteins.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, A4277631; CAC1427.1;
EMBL, A4277631; CAC1427.1;
EQUENCE 3705 AA, 370756 MW; 714FDF16455968C9 CRC64;
                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                         1 MNHIYKVIFNKATGTFMAVAEYAKSH------
Last annotation update)
                                                                                                                                                                                                                                     Query Match
6.4%; Score 658.5; DB 2;
Best Local Similarity 21.8%; Pred. No. 2.3e-19;
Matches 523; Conservative 325; Mismatches 925;
  01-MAR-2001 (TrEMBLrel. 16,
                                                                                    NCBI_TaxID=632;
                   YAPH PROTEIN.
                                                                            Yersinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  370
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KGGQTDTNKLTDN--NIGVVAGTDGFTVKLAKDLTNLNSVNAGGTKIDEKGISFVDANGQ 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1420 AKNDGTVDKTKEVAKDKLVA------QAQTPDGTLAQMNVKSVINKEQVNDANKKQ 1469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NANNLDLLVDGTAITSGTQGVESAIQQGGSTVANAIHNYGLTSSNGNGGSGLYVNYTLS- 1693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1466 -----TIDIADATLNLDDIALFNHVLTGNGLLNVAKNDASTAFDFGSTVGGAFSGIVNL 1519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1178 KISDVITFAGENGITTKVNKGVVRVGIDQTKGLTTPKLTVGNNNGKG-----IVINSQNG 1232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FNLQGNGEAVDFVSTYDTVNFAN-----GNTTT------AKVTYDDTSKTSKVVYD 1325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1326 VNVDDTTIEVKDKKLGVKTTTLTS---TGTGANKFALSNQAT----GDALVKA-SDIVAH 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKNSHDAVTGGKIYDLKTELENKISSTAKTAQNSLHEFSVADEQGNNFTVSNPYSSYDTS 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VV---GAGID----GTTRITRDEIGFTGTNGSLDKSKPHLSKDGINAGGKKITNIQSGEI 1117
                                                                                                                                                                                                                                                                                                                                                                                                                          981 ALNSGTVNITGSG-----SWDNTDPLATNVSILEQDRAGSTLELINATNVTGD 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1029 IDALDLLVNGTAITSGTQGVQSAIQQGGSTVANAIHNYGLASSNSNGDSGLYVNYTLSAL 1088
                                                                                                                                                                                                                                                                                                                                          NVDEKTIELTGDNGKKOLGVKTIKLTETSTNGNATIFS-TDDDHA-----LVKASDIAGN 944
                                                                                                                                                              781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQANGVVIVTDLALNSGTISITGAGNWENEHPVTPPNVSLLEQDRGDILLELINAANVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1470 GINEDNAFVKGLEKAASDNKTKNAAVTVGD--LNAVAQTPLTFAGDTGTTAKKLGETLTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1378 LNT------LSGDIQTAKGASQANNSAGYVDADGNKVIYDSTDNKYYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1233 QNTITGLSNTLANVTNDKGSVRTTEQGNIIKDEDKTRAASIVDVLS------AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -------FGINTQSGLKAGDSTTLNNNGLSIKNTASNEQIQVGADGVKFA--MVNNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GELILGANGAFGQTSLLDIASGASANINGYSQTVGAVTNVGTVTLGSGGVLTSGLLTNGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNIALFNHV--LIGNGTLNVAKNLATTAFDFGSTVGGAFSGIVNLTKTTFALSADNAAAL
                                                                                                                                                                                     GNRLVIEQVPSADGNSTKNIIKGLSPTLPSIASPSGRN----IALGNTIEEKDKSNAASI
                                                                                                                                                                                                                                                                                                                     DDVLNAGFNLKNNGKDKDFVSTYDTVD-FIDG-NATTATVTYDEA---NQTSKV--AYDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LNTLAEEIHTTKGTANT------ALQTFTVKKVDENDK------
                                                                                                       GKTFNTLKLKGENGVNITTNRAT------GTVTFGIDQSNGLTPKLTVGSDTN-
G-ISINSNNGDLVDS----SGNITTPTYNISVKTTKLNS-NGTSGNNKFSVSNAHDNNSL
                         VTAKDLADYLN-----KVNETADSALPSFKVQNGDNSNNAI-----
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123 TSIITGVGTKTFSNIDFAGKNATLQINKDLN-----ITTKID------NTVAG--- 164

qq	Qy Dp	λσ ———	oy da	λo da	yo da	Oy GD	y d	λο qα	Qy	a ko	qq	φγ	qa	λo	g 20	G qq	δ.	qa	40	qu	Qy	qa	δλ	qa	
Db 1694ALELLANGANALLLATESGLTANRYLNAELFGVGGLVVDAQNGALTLANGN 1744	QY 1586 AKANTPVLSANGLDLGGKVISNVGKGTKDTDAANVQQLNEVRNL 1629  1745 NRYEGTTTVTAGELILGANGA-FGQTSLLNIASGASANINGYRQTVGAVTNSGAVT 1799	QY 1630 LGLGNDNADGNQVNIADIKKDPNSGSSSNRTVIKAGTVLGGKGNNDTEKLATGGVQVG 1687	QY 1688 VDKDGNANGDLSNVWVK-TQKDG-SKKALLATYNAAGQTNYVTNNPAEAIDRINEQ 1741	QY 1742 GIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGRQTQAGN 1797	QY 1798 QSIAIGDNAQATGDQSIAIGTGNVVAGKHSGAIGDPSTVKADNSYSVGNNNQFTDATQTD 1857	QY 1858 VFGVGNNITVTESNSVALGSNSAISAGTHAGTQAKKSDGTAGTTTTAGATGTVKG 1912	QY 1913 FAGQTAVGAVGASGAERRIQNVAAGEVSATSTDAVNGSQLYKATQSIANATNE 1967	OY 1968 -LDHRIHONENKANAGISSAMAMASMPOAYIPGRSMYTGGIATHNGQGAVAVGLSK 2022          : :       : :	2023 LSDN 2026	Db 2148 LSDD 2151	RESULT 9	USZUSI ID QSZD91 PRELIMINARY; PRT; 2340 AA. AC OGYDG1.	DT 01-MAY-1999 (TrEMBLrel. 10, Created) DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)	01-MAY-2000 (TrEMBLrel. 13, CELL SURFACE ANTIGEN (SCA3).					KA Andersson S.G.E., Zomorbour A., Andersson J.O., RA Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., DA Erikegon A. G. Ginblow U. D. Windland A. C., Anderson A. C.		A1 MILOCHOLDIA 1	SEQUENCE 2340 AA; 247862		Similarity 21.5%; Pred. No. 8.2e-17; 4; Conservative 307; Mismatches 839; Indels	

35 TGQVGSVRTLSFARI---AALAVLVIGATLNGSAYAQQITTKIEIGQTNKINNTLKGDAL 91

õ

989 GQIGTPQNFTIQVNNKNLTLVSSVNSSINFGDANSQLILSAPVDQTIKFINNLNETGGGI 1048 263 314 IKGNNN---KDILNFKVHGTNLDNEMIIPAPQK-----THGTLNFKGNATLNGNINNLNI 365 542 943 944 TL-----EFNGNNTYNL------NAIIVNGQNGILNAFTNLKASDDTIGTVKIINI 988 92 ATGEASIAFGSLSKAQGSQAIAIGSVKPDPNNGS----NGNVGSHAKGNESIAIGGDVL 146 324 SNNNNSSIRRKIIN--VGAGSRDTDAVNVAQLKLVEELANRKITFKGDGDNNSN----- 375 425 SATNKITVSNTNNNNAELQ-SGGLTFS-PITGTKT-----DKTVYSID----GLKFTNDS 473 504 543 ATVANNVANTSA-----TVGTARITEEKIGFAGTNDGVDEQAPYLDKERLKVGRVE 593 657 696 LA-------DYLNKVNE--TADSALPSFKVQ-NG-------DNSNNAITVGKD 731 829 TGTIIAHGGLVGDIDFNNKAGKFILGDGAMIDGSVLCNGGVAGTLDFIGDGNVTQNIGAD 888 732 TNGKTFNTLKLKGENGVNITTNRATGTVTFGIDQSNG-----LTTPKLTVGSDTNGN 783 784 RLVIEOVPSADGNSTKNIIKGLSPTLPSIASPSGRNIALGNTIEEKDKSNAASIDDVLNA 843 844 G-----FNLKNNGKDKDFVSTYD-TVDFIDGNA-----TTATVTY-DEANQTSKVA 887 147 AEGDASIAIGSDDLYLPK--NLDLKNEFHKLIHGHEILKKIQTSTDGKIKYRRTRAQGHA 204 264 IGGNTVVNLGRGVALGFGSQILDRDNNTDASAYVPLGKTLADQYKATRQGDSTDIFSIGN 323 376 -SVERGLGNTLTIKGDAQTNALTEANIGVVTDG----NGL-----KVKLAKELTGLTSV 424 -----IKO 624 | :| | :| | :| | :| | :| | | 485 AKIIFEGADSMLALINTGVTADRTFTIYNNLNQSGNDEYGIVKIEAIKKVITIANQSGPY 889 -NANSISTINIQGDNTKNVTI--ANDIFVDNIHFTNGGILQLGGNLTTHNIDFGA--NGG 205 STAVGAMSYAQGHFSNAFGTYATAEAAYSLAVGLAAQATKQSSIA-VGSNAKANAFAATA 474 NSIATKG-----TTRITKKK-----IGFAGTND-GV------DESKPY 505 L...DN-EKLK------VGNSTLNSGSLTVNNT---TGNKQIQVGANG-IKF---625 LKDAKPTLNAGDGIS-INSN-------NGDLVDSSGNITTP-----658 -----TYNISVKTTKL-----NSNGTSGNNKFSVSNAHDN---NSLVTA----KD 888 YDVNVDEKTIELTGDNGKKQLGVKTIKLTETSTNGNAT-TFSTD------D 193 GNGEAKI-----YAPEANNITINAKNINLTHNNSIL----TLCDGNI------594 ITTDSGINAGNHKITGLTN-----GIANTDAVT----165 ----рp ŏ

991 1144	1039 1199	1089 1253	1132 1311	1179	1207	1237 1490	1287 1541	1340	1393	1449	1498	1558	1598 1863	1649 1916	1692 1976	1728	1788
$\infty - \infty$	rn ı	S L						VKDKKL 	AKGASQ   :   SADDTAT	TPDGTLA	NAAVTVG   : : NGLLTI-	SFTVKLAKD :    -IKIKAHSD	LTDTGRD	GLGNDNADGNQVNIADIKK   ::	VDKDG:1: LDRLSNR	-TQKD-GSKKALLATYNAAGOTNYVT       :   :   :   :   :   : FTAKEIGNRLEELSDANTVNGLNKTNTLL	DGEAAVA : : : 1 NSKNS-P
TNAITVC	-LKAGDSTTLNNNGLS : ::!!! LITDTNKLTIDNNG	RD-EIGE' :   : KDIELNE'	GTLNFNG	TSKT :   INKTGGQ	NKGVVRV   1 NNNVTAT	THESNAT	LSAGFNI    EI	DTTIE	SGD-IQI	CLVAQAQ7   : CFM	ASDNKTKI :     YTGNVTHI	VAGTDGE	ANGL       ANGLVLL	DGNQVNI 	TGGVQVG    PNRVTET	TYNAA        ANTVNGI	IGFQAK?
DENDKADDTN::	3LK/     : :	DGTTRIT :   ENVTLNI	SGELAKNSHDAVTG   : :     EIDGSVTSTGNVNG	NNFT-VSNPYSSYDTSKT-      :   :   :       GNNNLTFAANSHLTTDINKTG	-ENGITTKVNKGVVRVGID-QT :	GTLQAQN	AASIVDV    	VYDVNVI	-KASDIVAHLNTLSGD-IOTAKGASQ :: : : : : : : : PRSLSLFNYFTDIKADNLNFADDTAT	FKEVAKDI  :    EIASDI	VKGLEKA. 1 NYELK	TDNNIGV       -DNLI	ANTPVLS   FVKWVAD	GLGNDNA   ::  GGSSS	INDTEKLA      :: INDLGFMS	SKKALLA:::  :	SGKHSVI  -   TGIWGMS
QTFTVKKVDENI  : : ::  -TYTLDAINDN	NTQSG-       DPGNNQFGI	VGAGI    : LKVGINV	-SGELAK   : IDGSVTS	NNFT - VS	SCAIVIS	NGQNTIT 	CKDEDKTE   :   CGDAN-NE	OTSKTSKI 	KASD	NDGTVDK'   :  NANII	INEDNAF       IVLDLA-	OTDTNKL   :   NVDMSDL	DANGQAK :     ASEEQNK	NEVRNLL     SNEA+	VLGGKGN      TTDAGKLI	-TOKD-GS    :  : FTAKEIG	RNGIDSSA   : DEDNI
TANTALO'      GA'	GTVTFGI  :  ITLTSAL	VNNGV ::   IDNGAIA	NIQ  :  NLNDDIE	DEQG	NESNILK	GIVINSC      G-TIEVA	-QGNIIKDEDKTRAASIVDVLSAGFNLQGNG- 	TITAKVIYDDISKISKVVYDVNVDDTIIEVKDKKL 	DALV    : DALIDLDV	YYQAK : : ! WLTQEIK	DANKKOG : ITNLNVRD	TLTIKGG   :   ILVSQGS	EKGISFV : : OTKVIIC	ANV OOI   : SNISNNSS	RTVIKAG1   HVKDFGNJ	IAINMDN	QEPVVQGI   :   QAIIAAGI
DHALVKASDIAGNINTLAEEIHTTKGTANTALQTFTVKKVDENDKADDTNAITVGKDGT   :	GKVHAGDSTTLNNNGL:	-SNEQIQVGADGVKFAMVNNGVVGAGIDGTTRITRD-EIGFTGTNGS	LDXSKPHLSKDGINAGGKKITNIQSGEIAKNSHDAVTGGKIYD 	LKTELENKISSTAKTAQNSLHEFSVADEQGNNFT-VSNPYSSYDTSKT		KGLTTPKLTVGNNNGKGIVINSQNGQNTIT	-GLSNTLANVTNDKGSVRTTEQGNIIKDEDKTRAASIV   ::	EAVDEVSTYDTVNFANGNTTTAKVTYDDDTSKTSKVVYDVNVDDTT1EVKDKKL	TINSPHYYSSITTANNAQONYALNIEGGIIIDDGSALDGGARAGUTANGGARAGU GVKTTTLTSTGTGANKFALSNQATGDALVKASDIVAHLNTLSGO-IQTAKGASQ I	AN-NSAGYVDAD-GNKVIYDSTDNKYYQAKNDGTVDKTKEVAKDKLVAQAQTPDGTLA 	QMNYKSVINKEQVNDANKKQGINEDNAFVKGLEKAASDNKTKNAAVTVG QMNYKSVINKEQVNDANKKQGINEDNAFVKGLEKAASDNKTKNAAVTVG	DLNAVAQTPLTFACDTGTTAKKLGETLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKD	LINLNSVNAGGTKIDEKGISFVDANGQAKANTPVLSANGL	DLGGKVISNVGKGTKDT-DAANVOOLNEVRNLLGLGNDNADGNQVNIADIKK-	DDNSGSSSNRTVIRAGTVLGGRGNNDTEKLATGGVQVGVDKDG	NANGDLSNVWVKTYNAAGQTNYVT	NNPAEAIDRINEQGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVA 
NLNTLAE  :   XIN	LKGKNGL    :  LKNSSNT	JEQIQVGA :: HMLK	SINA    NINGHVDE	FAKTAQNS ::: AGDVSLS#	SDV	'TPINITS'	NDKGSVR' :: TAGNNIH	EAVDFVSTYDTVNFANGN-	TTANNAQ TGANKFA     RGDNNMN	D-GNKVI	ADNANLVI	rFAGDTGT  :  YFDT	Vh	NVGKG	SG:       NNYVASG	DLSNVWVK  :: : VVGLNGIEVENF	NEQGIRF    INL
DHALVKASDIAGNLN'   :            :  DOSLTSAKIKNIN	NTLE	IKNTASNEQIQ'     :  :: NVAYTLGTANHMLK	LDKSKPHLSKDGINA:	LENKISS: : : IVMLQAG	OLSOSAS	KGLTTPKL         ANNGTLKLNNH	NTLANVT: : :  :	VDFVSTY	TTLTSTC TTLTSTC GKTINFC	SAGYVDA   :   CDAVVIDA	QMNVKS    : : QKNIKAATLIA	AVAQTPLTF1::1:	LTNLNS :  :   ITNITSDTKH	DLGGKVIS     : : DTGGRDDTRG		-NANG      INVNGLNEGV	NNPAEAIDRI 
DHALA   :	GKV	IKNTA-     NVAY	LDKSI :   : FNKN	LKTE   LINN													
932	992	1040	1090	1133	1180	1208	1238	1288	1542 1341 1602	1394	1450	1499	1559	1599	1650	1693	1729 2037
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DECUENCE FROM N.A.

REP SEQUENCE FROM N.A.

REP SEQUENCE FROM N.A.

REP SEQUENCE FROM N.A.

REP STAIN-BERFELELY:

RAMAIN-BERFELELY:

RAMAIN-BERFELEY:

RAMAIN-BERFELT:

RAMAIN-BERFELT:

RAMAIN-BERFELT:

RAMAIN-BERFERT:

RAMAIN-BERFELT:

RAMAIN-BERFERT:

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                                                                                                                                                                                                                                                                    1932 RIQNVAAGEVSATSTDAVNGSQL----YKATQSIANATNELDHRIHQNENKANAGISSA 1986
1789 IGROTQAGNQSIAIGDNAQATGDQSIAIGTGNVVAG---KHSGAIGDPSTVKADNSYSVG 1845
                                   2083 SGYQSNTGGGIIGFDYNI----DNSIVIGAAYTWADSKVKHKNDKNGDRTKAKSNIYSIY 2138
                                                                                     -----NNNQFTDA------TQTDVFGVGNNITVTESNSVALGSNSAIS 1882
                                                                                                                   2139 GLYNWLTNNFFVBAIGVYGRNKIKNYEKRITTITDQIAIGKFINTFYSYELLGGYNYLIS 2198
                                                                                                                                                                            1883 AGTHAGT------QAKKSDGTAGTTTTAGATGTVKGFAG--QTAVGAVSVGASGAER 1931
                                                                                                                                                                                                                                                                                                            -----THYLSQDIIIKPELHWFINYQCKNKLPNIDARLD-------GIDEP 2287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Colosopila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                       ---HRTTITPMFGMRYATFKNNGYKENNTTFQNLSIKKNYYDKFETILGLNSV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                1987 MAMASMPQAYIPGRSMVTGGIATHN 2011
                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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NCBI_TaxID=7227;
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Q9VTK8
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Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O., Glibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
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EMBL, AE003544, AAF50040.2;
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Flybase; Fspn0036181; CG1831.
SEQUENCE 2586 AA, 260194 MW; BEBB2435A9FEAE5B CRC64;
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                                                                                                                                                                                                                                                                                      50 AALAVLVIGATLNGSAYAQQ----ITTKIEIGQTNKINNTLKGDALATGEASIAFGSLS 104
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                                                                                                                                                  Query Match 5.4%; Score 559.5; DB 5; Best Local Similarity 19.2%; Pred. No. 2.1e-15; Matches 463; Conservative 312; Mismatches 998;
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                                                                                                                                                                                                                        -----SNGDGNSTQSSTTTTITTTSSD---GDQST------TSSDPVVEVS 1067
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 ASPSGRNIALGNTIEEKDKSNAASIDDVLNAGFNLKNNGKDKDFVSTYDTVDFIDGNATT
                             877 RCPRORTTTTTTSSDGGESTTLS-DPVVEV--SQGTNGGNSSTQSS-----SSTT
                                                             ATVTYDEANQTSKVAYDVNVDEKTIELTGDNGKKQLGVKTIKLTETSTNGNATTFSTDDD
                                                                                                                            HALVKASDIAGNLNTLAEEIHTTKGTANTALQTFTVKKVDENDKADDTNAITVGKDGTSG
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Oy 143 GDVLAEGDASIAIGSDDI	200 A	TTVVNLG      TANN	369	Oy 421 LTSVSATNKITVSNTNNNA ::	QY 470 TNDSNSIATKGTTRITKKKI		211	Db 565 GGNILKQVLFNGAK	Oy 633 NACDGISINSNNGDI   :   :   :   :   :     :     Db 616 TANNGIVGAVTTANNNTGT	QY 686 DNNSLVTAKDLADYLNKV-	Db 663 SNVATIDATTVTINNVA Qy 741 KLKGENGVNITTNRATGTV	Db 708GAVTTANNNTGTL	Qy 801 II-KGLSPTLPSIASPSGR ::     ::     ::       ::	854	Db 791IAGAVII	QY 909 -GVKTIKLTETSTNGNATT	DD 884NNNTG	OY 1024 GLKAGDSTTLNNNGLSIK!	DD 919 NVATIDATTVTINNVAAN	7	DD 9/3 TRANSVILLAND OV 1137 LENKISSTAKTAQNSLHE
	1710 SKKALLATYNAAGQTNYVTNNPABAIDRINEQGIRFFHVNDGNQEPVV 1757                    100	1902 SRKNNNGSSILVGE ESSELLINGS TO THE PROPERTY OF THE PR	1869	1927	1977	2026	Db 2238 IDLSLPKLDASLNVNG 4253	RESULT 11 09XC47 DEPT.INTNARY: PRT: 2106 AA.	0950.47; 01-NOV-1999 (TrEMBLrel. 12, Cr 01-MAR-2001 (TrEMBLrel. 16, La		GN OMPA. OS Rickettsia australis. OS Rickettsia Proteobacteria; alpha subdivision; Rickettsiales; OC Rickettsiaceae; Rickettsieae; Rickettsia. OV NCRT Tax TD-787.				int. J. Syst. Evol. Microbiol. 30:1///-1//2007/. R. BMBL; AF149108; AAD39531.2;			IMLSSSGAWGVAAGVI-SVNDAAFSNRAVANN	Qy 53 -AVLVIGATLNGSAYAQQITTKIEIGQTNKINNT 85	60 WNEITAGGAANGNHADGPQDNEAFTYGGNHTITADEAGRIITAINVAGTIFVALNSIQNI	OY 86 LKGDALATGEASIANGCSCARACOSCARIOSON   1   1   1   1   1   1   1   1   1

KPHLSKDGINAGGKKITNIQSGEIAKNSHDAVTGGKIYDLKTE 1136 HEFSVADEQGNNFTVSNPYSSYDTSKTSDVITF-AGENGITTKV 1195 KNTAS---NEQIQYGADGVKFAMVNNGVVG----AGIDGTTRI 1076 NAITVGKDGTSGKVNTLKLKGKNGLDIKTDKDGTVTFGINTQS 1023 AN------VTAAGAITAAVNFAADGALTANNGIVGAVTTA- 883 ATNVTINNAAANVTAAGAITAAVNFAADGALTA----NNG-- 790 TTATVTYDEANQTSKVAYDVNVDEKTIELTGDNGKKQL---- 908 TTFSTDDDHALVKASDIAGNLNTLAEEIHTTK----GTANTAL 963 --NETADSALP---SFKVQNGDNSNNA1TVGKDTNGKTFNTL 740 VTFGIDQSNGLTTPKLTVGSDTNGNRLVIEQVPSADGNSTKN 800 RNIALGNTIEEKDKSNAA-----SIDDVLNAGFNLKNNGKD 853 RVEITTDSGINAGNHKITGLTNGIANTDAVTIKQLKDAKPTL 632 : | : | | : | | | ASNVAT---IDATNVTINNAANVTAAGAITAAVNFAADGAL 615 DLVDSSGNITTPTYNISVKTTKLNSNGTSGNN--KFSVSNAH 685 (IGFAGTNDGVDESKPYLDNEKLKVGNSTLNSGSLTVNNTTG 529 --GAIGVNGG-NILKQVLFNCASNV--ATIDATTVTINNVAA 510 AELOSGGLTFSPITGTKTDKTVYSIDG------LKF 469 AANVTAAGAITAAVN-----FAADGALTANNGIAGAVTT 457 KGDAQTNALTEANIGV-----VTDGNGLKVKLAKELTG 420 : | | | : | : | : | : | : | : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | NVGAGSRDT-DAVNVAQLKLVEELAN------RKITFKG 368 GDVLAEGDASIAIGSDD----LYLPKNLDLKNEFHKLIHGHEILKKIQTSTDGKIKYRRTR 199 ALGFGSQILDRDNNTDASAYVPLGKTLADQYKATRQGDSTD 317 257 SNA-FGTYATAEAAYSLAVGLAAQATKOSSIA-VGSNAKAN

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101	1196	124	1083	130(	113	136(	116	141	120	147	124	153(	127	157	133	162	138	168	142	172	1478	178	150	1838	155	188	160	192	166	197	172	201	1777
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Gaps 121;
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SEGUENCE FROM N.A.
SEROGROUP B;
MEDLINE-20175755; PubMed=10710307;
Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
Mason T., Clecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,
Cotton M.D., Utterboack T.R., Khouri H., Qin H., Vamathevan J.,
Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,
Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
"Complete genome sequence of Neisseria meningitidis serogroup B strain
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                                                                                                                                                                                                                                                                               Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2514 AA; 265615 MW; 95643A671B3BC268 CRC64;
                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
HEMAGGLUTININ/HEMOLYSIN-RELATED PROTEIN.
                                          2514 AA
                                             PRT;
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EMBL; AE002526; AAF42109.1; -.
TIGR; NMB1768; -.
                                          PRELIMINARY;
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ARLAIDTDTLNNQGKLSQTGSQKLHIDAQGKMDNRGRMGLQDTAPTASNGSSNQTGN 489	SGSLTVNNTTGNKOIQVGANGIKFATVANNVANTSATVGTARITEEKIGFAGTNDGVDEQ 578    : :::	APYLDKERLKVGRVEITTDSGI-NAGNHKITGLTNGIANTDAVTIKQLKDA 628	KPTLNAGDGISINSNNGDLVDSSGNITTPTYNISVKTTKL	NSNGTSGNNKFSVSNAHDNNSLVTAKDLADYLNKVNETADSAL 711	LNNQNGEIATNQOLI - IHDGQQSIAVIENTILIKEGENGVNITTNRATGTVTFGIDQSPSFKVQNGDNSNNAITVGKDTRKTFNTLKLKGENGVNITTNRATGTVTFGIDQS										GLTTP : I TVLVP			
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2091 RTVSQDFSKNVQQANTEINQHLDKLKADKEAAETAAAEALANG-DMETAKRKAHEAQDAA 2149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2031 NTRNIQITDEAAQIRLIGKTAAQIKADIDINNYTDIAERHSGSLKNTFNKEAVQSELDLO 2090
                                                                                                                                                                                                                                                                                                                                                                                                                                      1779 AKA-----DGEAAVAIGRQTQAG---NQSIAIGDNAQATGDQSIAI 1816
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1860 VNAKNLSIQSVQDRETYQSKQQNASAQVTVGYGFSAGGDYSQSKIRADHVSVTEQSGIYA 1919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1920 GEDGYQIKVĞNHTDLKGGIITSTQSAEDK----GKNRFQTATLTHSDI----KNHSQYKG 1971
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                                                                                                                                                                                                                                                                                         1695 ANGTTENEROVSIS-----TTYGEDONROTTQVQANQAQASQIQAGGK----TTLIATGAA 1745
                                                                                                                                                                                                                                                                                                                                                                                 1721 AGQTNYVT--NNPAEAIDRINEQGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQ 1778
                                                                                                                                                                                                                                                                                                                                                                                                  1802 GGWSLGVTAGGNVGKGYGNGDSITHRHSHIGDKGSQTLIQ--SGGDTTIKGAQVRGKGVQ 1859
                                                                                                                                                                                                                                                                                                                            Q-----VGVDKDGNA-----LLATYNA 1720
                                                                                                                                                                                                                                                                                                                                              -----VLSANGLDLGGKVIS-----NVGKGTKD----TDAANV--QQLNEVRNLLGL 1632
                                                                                                                                                                                                                                       1635 EOKGLTVAFSSPVTDLAQQAIAVAQSSKQVGOSKNDRVNAMAAANAGWQAYQTGKSAQNL 1694
                                                                                                                                                                                                                                                                        1633 GNDNADGNQVNIADIKKDPNSGSSSNR--TVIKAGTV-----LGGKGNNDTEKLATGGV 1684
                                                    NKEQVNDANKKQGINEDNAFVKGLEKAASDNKTKNAAVTVG------DLNAVAQTPL 1508
                                                                                                          1509 TFAGD-----TGTTAKK-----1537
                                                                                                                                                            TDNNIGVVAGTDGFTVKLAKDLTNLNSVNA---GGTKIDEKGISFVDANGQAKANTP--- 1591
                                                                                                                                                                                  1405 GNKVIYDSTD---NKYYQAKNDGTVDKTKEVAKDKLVAQAQTPDGTLA-----QMNVKSVI 1457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----HRIHQNENKANAGISSAM-----AMASMPQAYIPGRSMVTGGIATHNGQGAV
                                                                        1457 NTTHVDDASKHTGRSGGGNKLVITDKAQSHHETAQSSTFECKQVVLQAGNDANILGSNVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2017 AVGLSKLSDN---GOWVFKINGS---ADTQGHVGAAVGA------GFHF 2053
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Hacheria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Hacmophilus.
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Q9ZHLO;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
LARGE SUPERNATANT PROTEIN 2.
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SEQUENCE FROM N.A.
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1409 --IYDST-----DNKYYQAKN-----DGTVDKTKEVAKDKLVAQAQT-----PD 1445 1296 |:|: | |:: | |:: | |:: | |:: | |:: | |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: | 1106 GK------KIT-----NIQSGEIAKNSHDAVTGGKIYDLKTELENKISS 1143 1625 --TGDILSQRLSKLVGKKGLESTGVTYVDETGATKVRKARIKSEGHIYLETDKDKNVDLT 1682 1048 QIQVGADGVKFAMVNNGVVGAGIDGTTRITRDEIG--FTGTNGSLDKSKPHLSKDGINAG 1105 1144 TAKTAQNSLHEFSVADEQGNNFTVSNPYSSYDTSKTSDVITFAGE---NGITTKVNKGVV 1200 1172 TFKT--NGTHPVYL-----NFKSNNNEKKYRNSENTKNFKSIGDLINEALSDSAPEAIE 1223 1297 DTVNFANG---NTTTAKVTYDDTSKTSKVYYDVNVDDTTIEVKDKKLGVKTTTLISTGTG 1353 1683 ASELKGNTGQIKAKDLNLNDIYETSYKYKYEKLFGKNGGEIGDRVTQTSQAKSVGTDASF 1742 1000 KGKNGLDIKT-DKDGTVT-----FGINTQSGLKAGDSTTLNNNGLSIKNTASNE 1047 1446 GTLAQMNVKSVINKEQVNDANKKQGINE---DN-----AFVKGLEKAASDNKTKNAA 1494 ------ 1524 829 -DGKLISIKNL-----NISSEADFINNGTLLGIEALKIATKGNFTNKEKAILASNSLL 880 881 DISVAEGKKTFNNGTIESGKNLNITNTGAF-LNVDNATI------RSFGVLNITSTGN 931 968 VKKVDENDKADD--TNAITV------GKD------GTSGKV-----NTLKL 999 TFGIDQSNGLTTPK-LTVGSDTN----GNRLVIEQVPSADGNSTKNIIKGLSPTLPSIAS 81.4 815 PSGRNIALGNTIEEKDKSNAASIDDVLNAGFNL------KNN--GKDKDFVSTYDTV 863 864 DF--IDGNATTATVTYDEA---NQTSKVAYDVNVDEKTIELTGDNGKKQLGVKTIKLT-E 917 918 TSTNG-----NATTFS--TDDDHALVKASDIAGNINTLAEEIHTTKGTANTALQTFT 967 787 T----NSGNLTTVKTLDVGDIQNFTNKGNLTVGEDLHIKSKTKITN--------1246 -----VTNDKGSVRTTEQGNIIKDEDKTRAASIVDVLSAGFNLQGNGEAVDFVSTY 1278 KVLKOKWEDFKKDKGASKMLD---LYPNTDKEKAKIFAGIIRNGNDTISDVESEDFKKKY 1354 ANKFALSNQATGDALVKASDIVAHL--NTLSGDIQTAKGASQ------1201 RVGIDQTKGLTTP---KLTVGNNNGKGIVINSQNGQNTITGLSNTLAN------1495 VTVGDL-----NAVAQTPLTFAGDTGTT--------1394 -----ANNSAG-----YVDADGNKV------ANNSAG-----160 1518 g Q q Db qq g g ŏ Q δ g òγ g δ g ŏ g ò Ω g qq ó Dp δ q ò δy Qγ ò οy Ω οy οy

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SKDGIN--AGGKKIT----NIQS-GELAKNSHDAVTGGKIYDLKTELENKI--SSTAKTA 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1149 QNSLHEFSVADEQGNNFTVSNPYSSYDTSKTSDVITFAGENGITTKVNK----GVVRVGI 1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTSGKVNTLKLKGKNGLDIKTDKDGTVTFGINTQSGLKAGDSTTLNNNGL-----SIKN 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1043 TASNEQIQVGADGVKFAMVNNGVVGAGIDGTTRITRDEIGFTGTN-----GSLDKSKPHL 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KASDIAGNLNTLAEEIHTTKGTANTALQTFTVKKVDENDKADDTNA---ITVGK-----D 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         622 GAIDNIGN------ANNGIVTFTGDST-VTGNIGNTNALATVNVGAGIATLE 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     819 NIALGNTIEEKDKSNAASIDDVLNAGFNLKNNGKDKDFVSTYDTVDFID--GNATTATVT 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NTGNANNGIVTETGDSTVTGNIGNTNALA-----TVNVGAGLLQVQGGVVKANTIN 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVDSSGNITTPTYNISVKTTKLNSNGTSGNNKFSVSNAHDNNSLVTAKDLADYLNKVNET 706
                                                                                                                                                                                                                                                                                                                                                                                                                                      TTKLTNAASVLTLTNVNAVL-----TG------TG---------AIDNTT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RITKKKIGFAGTNDGVDESKPYLDNEKLKVGNSTLNSGSLT----VNNTTGNKQIQVGA 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 TVVGSIITGGNLLPVIINAGKSLTL-----NGNNADAANHGFDAP----ADNY--- 163
                                                                                                       IGGDVLAEGDASIAIGSDDLYLPKNLDLKNEFHKLIHGHEILKKIQTSTDGKIKYRRTRA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              777 ANNGIATFTGDSTVTGDIGNTNALATISVGAGKATLGGAIIKATT---TKLTDNASAVTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TFGIDQSNGLTTPKLTVGS-DTNGNRLVIEQVPSADGNSTKNIIKGLSPTLPSIASPSGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             519 -ATLGGAIIKATTT------KLTDNASAVTFTNPVVVTGAIDNTGNANNGIVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               877 YDEANQTSKVAYDVNVDEKTIELFGDNGKKQLGVKTIKLFETSTNGNATTFSTDDDHALV
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MEDLINE=94171067; PubMed=8125327;
MEDLINE=94171067; PubMed=8125327;
Crocquet-Valdes P.A., Welss K., Walker D.H.;
"Sequence analysis of the 190-kba antigen-encoding gene of Rickettsia conorii (Malish 7 strain).";
Gene 140:115-119(1994).
ERML; U01028; AAA17405.1; -.
SEQUENCE 2021 AA; 203366 WW; BE943FBA3BDD5C43 CRC64;
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NCBI_TaxID=781;
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Local Similarity 22.4%; Pred. No. 3e-14;
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                                                                  FVSTYDTVNFANGNTTTAKVTYDDTSK---TSKVVYDVNV--------DDTTIEV
                                                                                                                                                                                                                                                                                                     989 Y -- - YFKGAIANGNNAILNVNTKSLTASHLTIGTVAEINIGAGNLFAIDASAGDVTILNA
                                                                                                                                                                                                                                                                                                                                                       KD---KKLGVKTTTLTSTGTGANKFALSNQATGDALVKASDIVA----HLNTLSGDIQT
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                   834 TNPVVVTGAIDNTGN--
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EMBL; D90836; BAA15799.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  440 AELQSGGLTFSPITGTKTDKTVYSIDGLKFTNDSNSIATKGTTRITKKKIG-----FA 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  544 TVANNVA-NTSATVGTARITEEK------IGFAGTND-GVDEQAPYLDK----ERL 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     582 TRHEGVQDITLSDWKDN------GDGSYTQILTTGAMSGTLTLMPQLNGVDAAKAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 EASIAFGSLSKAQGS-----QAIA-----IGSVKPDPNNGSNGNVGSHAKGNESIAIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 AMTDWLSRFGTARITLGVDE-----DFSLKNSQFDFLHPWYETPDNLFFSQHTLHRTDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285 LDRDNNTDASA----YVPLG-KTLADQYKATRQGDSTDIFSI-----GNS----NNNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 PAQVSEKKLTPPPGNSSDNLEQQIASTSQQIGSLLAEDMNSE--QAANMARGWASSQASG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 EAAYSLAVGLAAQATKQSSIAVGSNAKANAF--AATAIGGNTVVN--LGRGVALGFGSQI
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2349;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 22.0%; Pred. No. 4.5e-14;
Matches 523; Conservative 302; Mismatches 933;
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                                                                                                                                                                                             MEDLINE=97251358; PubMed=9097040;
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PRINTS; PR00B10; BCTERIALGSPC.
PRINTS; PR01369; INTININ.
NON_TER 2349 2349
SEQUENCE 2349 AA; 247433 M4
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Dp	632	AVVNIISVSSSRTHSSIKIDKDRYLSGNPIEVTVELRDENDKPVKEQKQQLNNAVSIDNV 691
٥y	588	KVGRVEITTDSGINAGNHKITGLTNGIANTDAVTIKQLKDAKP 630
QQ	692	
Qy	631	TLNA-GDGISINSNNGDLVDSSGNITTPTYNISVKTTKLNSNGTSGNNK 678
QQ	749	•
δλ	619	
qq	807	GDSSTAQVDLQKSKNEVVADG
Qy	730	SDINGNR 78
qq	865	76
Qy	785	LVIEQVPS-ADGNSTKNIKGLSPTLPSIASPSGRNIALGNTIEE
qq	923	
οy	830	DKSNAASIDDVLNAGFNLKNNGKDKDFVSTYDTVDFIDG
8	982	FOT ACMICANC
Qy	873	ATVTYDEANQTSKVAYDVN-VDEKTIELT-GDNGKKQLGVKTIKLT 910
QQ	1042	MTEVADKDRAVVVLQTSKAEIIGNGVDETTLTATVKDPSNHPVAGITVNFTMPQDVAANF
Qy	917	F
qq	1102	TLENNGIAITQANGEAHVTLKGKKAGTHTVTATLGNNNTSDSQPVTFVADKASAQVVLQ-
٥y	996	FTVKKUDENDKADDTNAITVG-KDGTSGKUNTLKLKGKNGLDIKTDKDGTVTFGI
qq	1161	ISKDEITGNGVDSATLTATVKDQFDNEVNNLPVTFSSASSGLTLTPGVSNTNESGLAQ
δý	1020	NTQSGLKAGDSTTLNNNGLSIKNTASNEQIQVGADGVKFAMYNNGVVGAGIDGTTRI 107
QQ	1219	ATLAGVAFGEKTVTASLANNGASDNKTVHFIGDTAAAKIIELAPVPDSIIAGTPQ-
δλ	1077	TRDEIGFTGTNGSLDKSKPHLSKDGINAGGKKITNIOSGEIAKNSHDAVTGGKIYDLKTE
QQ	1274	ATVVDNNGFPVKGVTV 129
٥y	1137	LENKISSTAKTAONSLHEFSVADEQGN-NFTVSNPYSSYDTSKTSDVITFAGENGITT 119
qq	1298	NFTSNAATAEMTNGGQAVTNEQGKATVTYTNTRSSIESGARPDTVEASLENGSSTLS 135
ογ	1194	KVNKGVVRVGIDQTKGLTTPKLTVGNNNGKGIVINSONGONTITGLSN
Dp	1355	TSINVNADASTAHLTLLQALFDTVSAGETTSLYIEVKDNYGNGVPQQEVTLSVS
QY	1242	TLANVINDKGSVRTT-EQGNIIKDEDKTRAASIVDVLSAGFNLQGNGEAVDFVSTYDTVN
qq	1409	PSEGVTPSNNAIYTTNHDGNFYASFTATKAGVYQLTATLENGDSMQTVTY-VPN
QY	1301	FANGNITTAKVTYDDISKISKVVYDVNVDDITIEVKDKKLGVKTTTLISTGIGANKFALS
q	1463	VANAEITLADLTTLT
QΥ	1361	NOATGDALVKASDIVAHLNTLSGDIQTAKGASQANNSAGYVDADGNKVIYDSTDNKYYQA
qO	1501	NTEVTFTLPEDVKANFTLSDGGKVITDAEG
Qy	1421	KNDGTVDKTKEVAKDKLVAQAQTPDGTLAQMNVKSVI 145
QO	1531	KAKVTLKGTKAGAHTVTASMTGGKSEQLVVNF1ADTLTAQVNLNVTEDNF1AN-NVGMTR
Qy	1458	NKEQVNDANKKQGINEDNAFVKGLEKAASDNKTKNAAVTVGDLNAVAQTPLTFAGDTGTT  .
qa	1590	0 LOAIVIDGNGNPLANEAVIFILPADVSASFILGGGGS-AIIDINGKAEVILSGTK 1643

TNL 1562  : TDA 1701	ISN 1607							APV 1931			*ITV 1867	3LTV 2007	AVSV 1924	MQTV 2057	KANA 1981	KVSE 2106		TTIQ 2166		
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AKKLGETLTIKG-GQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNL:	NSVNAGGTKIDEKGISFVDANGQAKANTPVLSANGLDLGGKVISN	STEVGLKTVS	VGKGTKDTDAANVQQLNEVRNLLGLGNDNADGNQVNLADIKKUPNSGSSSSNK1	-DQFGNPVAH	VIKAGTVLGGKGNNDTEKLATGGVQVGVDKDGNANGDLSN-VWVKTQKDG	(ASLPNGASLE	SKKALLATYNAAGOTNYVTNNPAEAIDRINEQGIRFFHVNDGNQEPV	SVTPEGATLSC	1757 VQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGRQTQAGNQSIAIGDNAQATGDQSIAI		GTGNVVAGKH-SGAIGDPSTVKADNSYSVGNNNGFTDATQTDVFGVGNNITV	DLSTLKATVE	TESNSVALGSNSAISAGTHAGTOAKKSDGTAGTTTTAGATGTVKGFAGOTAVGAVSV	SVKGAMTGSV	GASGAERRIONVAAGEVSATSTDAVNGSQLYKATQSIANATNELDHRIHQNENKANA	L	GISSAMAMASMPQAYIPGRSMVTGGIATHNGQGAVAVG	GEGIATLIPV	4.5	2199
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FNK   : TKQVTLIADA	dv	TLSSTSVETD	EVRNLLGLGN : :	IPEGQVMVAQ	KLATGGVQVG	GVAEVTMT	VINNPAEAIC	ATLTSANGTE	AIGFQAKADO I	TASF	DESTURADORS	DPSTIAATN-	ISAGTHAGTQA	.:. VI	AGEVSATSTD	KSNRSSLKGD	Bd	SAIDYSLNIN		CTLDTTTTD
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AKKLGETI :   : SGTYPVTV	NSVNAGGT	NGNPVEG	VGKGTKD	LLNASAD	VIKAGIV	IISQNTV	SKKALLA	ASSPLIG	VQGRNGI	VL	GTGNVVA									
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1 22 AX079922 6942 bp DNA TION Sequence 10 from Patent W00107619. TON AX079922 N AX079922.1 GI:13159441	SC		n ce	2286 a 1621 c 19	Query Match 100.0%; Score 6942; Best Local Similarity 100.0%; Pred. No. 0; Matches 6942; Conservative 0; Mismatches
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4381 GGTGGGCAA 4441 gatggcttC 4441 GATGGCTTC 4501 gGcACCAG 4501 GGCACCAG 4561 aacaccCG 4561 aACACCCCC	4621 ggtgcagc                     4621 GGTGCAGC   4681 acggtcaa   1                   4681 ACGGTCAA   4741 gatgccaa	-6 6-6 6-	4861 CCCATCAC 4921 ggtcatca 1111111 4921 GGTCATCA 4981 aagtcca	49 50 50 51	5101 5161 5161 5221	5221 G 5281 g 5281 C 5341 t	/ 5401 aaccccc                   5401 AACCCC.   5461 GCGGTA'   5461 GCGGTA'
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Oy 5521 atccaaggcaaagataacagcagcatcacctaagcaaagatgggctgaatgtaggcggt 5580  Db 5521 ATCCAAGGCAAAGATAACAGCATCACCCTAAGCAAAGATGGGCTGAATGTAGGGGGT 5580  Oy 5581 aaggtcatcagcaatgtgggtaaaggcacaaaagacaccgacgctgccaatgtacaacag 5640  Illillillillillillillillillillillillilli	Qy         5761 actgtcatcaaagcaggcacggtacttggcggtaaaggtaataacgataccgaaaaactt 5820           Db         5761 ACTGTCATCAAAGCAGCACGCTACTTGGCGGTAAAAGCTAATAACGATAACGATAACGATAACGATAACGATAACGATAACGATAACTTT 5820           Qy         5821 gccactggtggtgtacaagtgggcgtggataaagacggcaacgctaacggcgatttaagc 5880           Db         5821 GCCACTGGTGTACAAGTGGGCGTGATAAAAGCGCAACCTAACGGCGATTTAAGC 5880           Qy         5821 GCCACTGGTGTACAAGTGGGCGTGATAAAAGACGCAACCTAACGCGATTTAAGC 5880           Qy         5881 aatgtttgggtcaaaaaccaaaaagatgcagcaaaaaagccctgctcgccacttataac 5940	Db 5881 AATGTTTGGGTCAAAAAGATGGCAGCAAAAAAAGCCTGGTCGCCAGTTATAAC 5940  QY 5941 gccgcaggtcagaccaactatttgaccaacaacccgcagaagccattgacagaataaat 6000  LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		Oy         6181 atcgccatcggtgataacgcacaagccacaggcgatcaatccatcgccatcggtacaggc.6240           Db         6181 ATCGCCATCGGTGATAACGCACAAGCCACGGGCGATCAATCCATCGCTACGGTACAGGC.6240           Oy         6241 aatgtggtaacaggtaagcactctggtgccatcggcgacccaagcactgttaaggctgat.6300           Oy         6241 aatgtggtaacaggtaagcactctggtgccatcggcgacccaagcactgttaaggctgat.6300	6301 aacagttacagtgtgggtaataacaaccagtttatcgatgccacccagacgtcttt [111111111111111111111111111111111	Db 6361 GGTGTGGGCAATAACATCACCGTGACCGAAAGTAACTCGGTTGCCTTAGGTTCAAACTCT 6420 Oy 6421 gccatcagtgcaggcacacaggaggcacacaagccaaaaatctgacggcacaggaggt 6480 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 6481 acaaccaccacagggggcaacaggttcaaaggctttgctggacaaacggcggtt 6540

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Loosmore, S.M., Sasaki, K., Yang, Y.P. and Klein, M.H.
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Patent: WO 0107619-A 8 01-FEB-2001.
CONNAUGHT LABORATORIES LIMITED (CA)
Location/Qualifiers
1. 6159
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Sequence 8 from Patent WO0107619.
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a S	1342 ACCTTTAGCCCAAT	tactactcgtatcaccaaagat 14	443
g ç	1402 AAGTITACIAATGA		461
οy	1444 aaaattggttttag	aaaacaaaccttatcttgataaa 15	503
Οp	1462 AAAATTGGTTTTGC	AAAGCAAACCTTATCTTGACAAC 15	521
Qy d	1504 gacaagctaaaagt 	gtgottgactgttaataacacc 15 	581
3 8	1564 attggtggtagcaa	atggcattaaatttgccgatgtg 16	623
d d		ATGGCATTAAATTTGCCACAGTC 16	635
δy	1624 aatgttaatgtatc	ctactcgtattaccgaagaggaa 10	
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ζ <u>α</u>	1816 AAGATTACCGGAC		1875
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qq		TCAGTATTAATAGTAATAACGG 1	1935
QY	1921 ggtcaggaattta		1952
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qq	2056 GATAACAATAGCT	SACTATCTAAATAAAGTCAATGAA 2	2115
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· 6	2116 ACGGCTGACAGTG	AACGGTGATAATAGCAACAACGCC	2175
Ωÿ	1953ta	gagaccatcacctttgcaggtgaa 3	0
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QY	2002 aacggcatcagta	aaagtcaaagttggtattgaccca	9
qq	2236 AACGGTGTTAATA	ACAGITACCITTGGCATTGACCAA	Ö
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3442 GCACAAAACTCATTACACGAATTCTCAGTA			3424 aaaggettaaccacgectaagetgaccgtg 	3484 gacagtaaagatggtcaaaataccatcaca 	3544 aatgatggtgcaggacacgcacta 	3598 accogtgccgccagcattggtgatgtgcta 	3658 gaagcggttgactttgtctccacttatgac 	3718 accgctaaggtgacctatgatgacacaagc 	3778 gtggataataaaccattgaagtgacaagt 	3838 ctgaccaaaacaagtgctaatggtaatgca 	3895 gccttgttaaagccagtgatatcgccacc 	3955	4015 aaggtcatctatgacagtaccgataagaag 	4075 gacaaaaacaaagaagttgccaaagacaaa 	4135	4195 aaaaagcaaggcatcaatgaagacaacgcc 	4255 gacaccaaaaccaaaaacgccgcagtaact 	4315 ccgctgacctttgcaggggatacaggcaca 
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	gcaggtgaggtcagtgccaccagcaccgatgcggtcaatggtagccagttgtacaaagcc 6654 	acccaaggcattgccaacgcaaccaatgagcttgaccatcgtatccaccaaacgaaat 6714 	aaagccaatgcaggatttcatcagcgatggcgatggcgtccatgccacaagcctacatt 6774 	cctggcagatccatggttaccgggggtattgccacccacaacggtcaaggtgcggtggca 6834 	.gtgggactgtcgaagctgtcggataatggtcaatgggtatttaaaatcaatggtcagcc 6894 	gatacccaaggccatgtagggggggggttggtgcagttttcacttt 6942 	3 AX067457 62909 bp DNA PAT 24-JAN-2001 N Sequence 32 from Patent WO0078968. AX067457 AX067457. GI:12545077		MOIASELIA.  1 (bases I to 62909)  Lagace, R.E., Patterson, C. and Berg, K.L.  Nucleotide sequences of moraxella catarrhalis genome  Patent: WO 0078968-A 32 28-DEC-2000;  Incyte Genomics, Inc. (US)	Location/Qu 162909 /organism='	18449 a	Query Match 41.1%; Score 2852.4; DB 10; Length 62909; Best Local Similarity 69.3%; Pred. No. 0; Matches 4853; Conservative 0; Mismatches 991; Indels 1156; Gaps 25;	1 atgaatcacatctataaagtcatctttaacaaagccacaggcacatttatggccgtggca 60	61 gagtgcgccaaatcccacagc-ggaggagtagcagtagtaccgcaggacaggtgggcag 119 	ctetectgteatecgectgaetegtgteaegetegetatectagtgateggtgegae 179 	getcaatggcagtgcttatgctcaaaataatagcaagatcgcattggtaccacaggcaa 239 	240 caatgacaatgcctcggctagcaatgaagcatccattgctattggtagtcttgctaaggc 299
Db 5752	Qy 6595 Db 5812	Qy 6655 Db 5872	Qy 6715 Db 5932	Oy 6775 Db 5992	Qy 6835 Db 6052	Oy 6895 Db 6112	RESULT 3 AX067457 LOCUS DEFINITION ACCESSION VERSION	REIWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL	FEATURES SOURCE	BASE COUNT ORIGIN	Query Match Best Local Matches 485	0y Db 4263	Oy 6 Db 4269	Qy 120 Db 42750	Oy 180 Db 42810	Qy 24

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Oy Dp	2061	aatcaatggtotcaccacgcottaagctgaccgtgggtagcgataaagatggtaaaactca :	2120 44735
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5702	3 aaacgaagtacgcaacttgttgggtcttggtaatgctggtaatgataacgctgacggcaa	564	δy
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5582	3 ccaaggcaaagataacagcagcatcaccctaagcaaagatgggctgaatgtaggcggt	552	Οy
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5522	3 ggtatttaaatccaaagatggtacaactactaccacagtaagctctgatggcatcagtat	546	Qy
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5462	3 ccccaatgctggtaaaggcagtacaggcgatgcagtggctcttaataacttatcaaaagc	540	Qγ
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5402	3 actaaaagcaggcaaatcagccagtgatgccaaaactccaactggtctaagccttgttaa	534	O
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5342	3 gcttatcaaaagccaaagatggtaagttctacaaagcagacgacctcatgccaaacggctc	528	Qy
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47169	0	4717	qa
5222	3 taccgtcaactttgtcaatggtacaggtgccgacatcacaagcgtgcgt	516	Qy
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/db_xref="taxon:480"
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Pred. No. 0;
0; Mismatches 1105;
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Loosmore, S.M., Sasaki, K., Yang, Y.P. and
Recombinant high molecular weight major
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CONNAUGHT LABORATORIES LIMITED (CA)
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Sequence 6 from Patent WO0107619.
AX079918
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Moraxella catarrhalis
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1989 2047 2106 2253 1929 2137 2313 1881 2154 2433 1614 1761 1821 1974 1675 ACTTTAAACGCAGCGCTGGCATCAGTGTCACTGAAATATCAGTTGATGCTAAG 1734 ggcaacagcaccctaaacaacggtggcttgactgttaataacaccattggtggtagcaat gcaacggacgataccgatgcagtcacttataaacagcttaaacaagtccaacaagacgcc 2035 GTTGCTACCAAAAAAGATGGTACGTTACCTTTGGGCTTAGCCAAGATAGCGGTCTGACC 2095 ATTGGCAAAAGCACCCTAAACAACGATGGCTTGACTTAAAGATACCAACGAACAAATC 2395 AGCATTGCCGATCAAAGTAGC --- CGCAACATAGAACTGGGCAATACAATACCA --- AGAC 2254 gaagacaaatccaaagccgccagtatcggtgatatattaaatacaggctttaacctaaaa 1555 AGTGTTGCAATTACCATAGACAATGGCATTGATGCAGGTAATAAAAAGATCAGTAATCTT 1639 aatgeegeaaaatteggeactaetegtattaeegaagaggaaattggetttgetgatget gacggtgccctacaa-----agcttctctattcgtgatgaaaaggtcaggaa 1990 tttgcaggtgaaaacggcatcagtatcagcaatgacatagccaaaggtaaagtcaaag aatgccaccaccgctaaggtaacttacgatgaaaccaatcaaaccagtaaagtaacttat 1579 aaacaaatccaagtcggtgctgatggcattaaatttgccgatgtgaatgttaatgtatca 1735 AGIGGCAATGITACCGCCCCAACITACAACATIGGCGTGAAAACCACCGAGCTIAACAGI 1855 GCCGAACATTTGGCAAGCTATCTAAATGAAGTCAATCGAACGGCTGACAGTGCTCAAAA 1762 aaaattaccaaagacagtggcattaatgcaggtgatcaaaagatcagtaatgttaaagat 1975 ACGACAAAAAATGCCGGCGCGCTCAGCATCTTAAAACTCAAAGGTAAAAACGGTCTAACG 1930 tttacgattagtaacttgtattctaatggtaataccccaaatacctttgagaccatcacc 2155 CAAGTCGGTGCTAATGGCATTAAATTTACTAATGTGAATGGTAGTAATCCAGGTACTGGC -ttggtattgacccaatcaatggtctcaccacgcctaagctgaccgtgggtagcgataaa 2275 GTTGATACAAACCTTATCTTGATCAAGACAAGCTACAAGTTGGCAATGTTAAGATT agcattaccaatgcaggtggcgtacgcaccacagaacagggcaatacaatcaccagcgac aataatagcaactccgttggctttgtctccacttataacactgttgactttatcgatggc 2314 1716 2048 2194 1699 1882 2107 1517 g q Ωp g g QQ δ Op q Qγ Op ŏ òγ Ω Ω g δy òγ Op οy δy q οy ò g οy Dp δ g οŻ QQ οy ò δý

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Moraxella catarrhalis
Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
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Best Local Similarity 66.9%;
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29; 973) ess,R.E., Loosmore,S.M. and Klein,M.H. coding high molecular weight major outer membrane aatgggtatttaaaatcaatggttcagccgatacccaaggc 6906 tcagaaggcaggttccacgccaaaggtaaagagtccatcgc 404 agc-ggaggagtagcagtagtaccgcaggacaggtgggcag 119 tgctcaaa-----ataatagcaagatcgcatttggt---- 228 661 Gaps 29-SEP-1999 2%; Score 2580.6; DB 9; Length 6973; 9%; Pred. No. 0; 0; Mismatches 1104; Indeis 1270; PAT ب 1620 24-A 1 15-SEP-1998; n/Qualifiers 3 bp DNA patent US 5808024. sm="unknown" c 1533 g 9600096

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                                        Loosmore, S.M., Sasaki, K., Yang, Y.P. and
Recombinant high molecular weight major
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Bacteria; Proteobacteria;
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GAAGCTGTCGGATAATGGTCAATGGTATTTAAAATCAATGGTTCAGCCGATACCCAAGG
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1 (bases I to 5976)
Loosmore,S.M., Sasaki,K., Yang,Y.P. and Klein,M.H.
Recombinant high molecular weight major outer membrane
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Pred. No. 0;
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                                 Klein,M.H.
outer membrane
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/db_xref="taxon:480"
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Loosmore, S.M., Sasaki, K., Yang, Y.P. and
Recombinant high molecular weight major
                                                  Patent: WO 0107619-A 12 01-FEB-2001;
CONNAUGHT LABORATORIES LIMITED (CA)
Location/Qualifiers
       Moraxella catarrhalis.
Moraxella catarrhalis
Bacteria; Proteobacteria;
                                                                                                           Query Match
Best Local Similarity 66.7%;
Matches 4674; Conservative
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                                               gamma subdivision; Moraxellaceae;
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                        gtacaggcaatgtggtaacaggtaagcactctggtgccatcggcgacccaagcactgtta
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outer membrane
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CONNAUGHT LABORATORIES LIMITED (CA)
Location/Qualifiers
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WO0107619.
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Moraxella catarrhalis
Bacteria; Proteobacteria;
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                                             DB
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746 c 741 g
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71.1%;
                                                           Conservative
                                                   Similarity
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              1011
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2y do	7	aacttggegtcaaaaccaccacactgaccaaaacaagtgctaatggtaatgcaacc 38 	o. e
yy Ob	3871 1039	gccgccgatggcgatgccctt 	0 8
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oy Ob	3991 1159		0 8
Oy Db	4051	agtggacaaaaacaaagaagttgccaaagacaaactggtc 41 	10 78
O.Y	4111	gcccaagcccaaaccccagatggcacattggctcaaatgaatg	70 38
Qy Db	4171	aaagagcaagtaaatgatgccaataaaaagcaagcatcaatgaagacaacgcctttatc 42 	30 98
QY	23	aaagggcttgaaaacgccgcaaagacaccaaaaccaaaaacgccgcagtaactgtgggt 42. 	96
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δy	4711	tcaggtgcgtcattaccctttgtggtaaccgatgccaatggcaagcccatcaatggca	7.0
QQ	1771		70
ογ	4771	gtaaatactatcacgccaacgcc 4	Ċ.
qq	1771	1	70

ΟY	4831 aacggcgtacctgtggacaags	tggcaagcccatcaccgatgcggacaaacttgccaat	4890
Dp	177		1770
Qy	4891 ctggcagctcatggcaaacccct	tgatgcaggtcatcaagtggtggcaagcctaggcggc	4950
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Ор	177	1	1770
QY	501	gcaagcccaaagtctgcccagcctatcagcagcacag	5070
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qa	177		1770
οy	516	tgctgatggcacgatgagtaacatcaccgtcaacacc	5250
QΩ	177		1770
Οý	525	ıtggcaatgtgcttatcaaagccaaagatggtaagttc	5310
QQ	177		1770
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qα	17.		1770
Οy	53,	goottgttaaccccaatgotggtaaaggcagtacaggc	5430
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Qy	54	atcaaaagcggtatttaaatccaaagatggtacaact	5490
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qq	1981 GCTAAAGGTA	AACTTGCCACTGGTGGTATACAAGTGGGCGTGGA	04
QY	5851 aaagacggca	taagcaatgtttgggtcaaaacc 	σ,
q	2041 AAAGACGCCAACGCTAACGGC	atttaagcaatgtttgggtcaaaacccaaaagatgg	-
ογ	y 5911 agcaaaaagccctgctcgcca	cttataa	5970

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RESULT 11

9 Toward 1 to 2448) sometre. S.M., Sasaki,K., Yang,Y.P. and Klein,M.H. sasaki,K., Yang,Y.P. and klein,M.H. 3219 atggogtgaagtttgccaaggt---tgataagggtaattcaagcactggcattgat 2979 caageegtateaceaaagateaaattggetttaetggggetaatggeteacttgat 3039 tcaacagtgctgctaaaaacagcacaaaactcattacacgaattctcagtagcagat 3279 cggttacctttggcattaacacccaaagcggtcttaaagccggcgacagcaccact 2862 3460 aataatggcaaaggcattgtcattgacagtaaagatggtcaaaataccatcacaggacta 3519 441 57 Gaps 22-FEB-2001 oraxella catarrhalis cteria; Proteobacteria; gamma subdivision; Moraxellaceae; oraxella. gcaatgatgctgtgacaggcggtcgggtttatgatttaaaaaaccgaacttgaaagc DB 10; Length 2448; 54; 0; Mismatches 187; Indels PAT /organism="Moraxella catarrhalis" /db\_xref="taxon:480" 1 569 c 556 g 497 t 20.5%; Score 1421.8; 87.2%; Pred. No. 0; tent: WO 0107619-A 47 01-FEB-2001; NNAUGHT LABORATORIES LIMITED (CA) Location/Qualifiers .079959 2448 bp DNA quence 47 from Patent W00107619. .079959 GI:13159466 raxella catarrhalis. Conservative imilarity raxella 826 ó

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                           682 AGCAACACTCTAGCTAATGTTACCAATGATAAAGGTAAGGTACGCACCACAGAACAGGGC
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1699 TITGTAGACTCAAGCGGTCAAGCCAAAGCAAACCCCCTGTGCTAAGTGCCAATGGGCTG 1758
                                                                                                                                  PMU277635 3900 bp DNA BCT 21-0CT-2000 Pasteurella multocida mapA gene. AJ277635 AJ277635 AJ277635 AJ277635. G:10945096 MapA protein. Pasteurella multocida pasteurella multocida Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae; Proteobacteria; Gamma subdivision; Pasteurella.
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Submitted (25-APR-2000) Henderson I.R., Center for Vaccine
Development, University of Maryland School of Medicine, 685
Baltimore St, MD 21202, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     function-"putative autotransporter protein"
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Henderson, I.R., Nataro, J.P., Cappello, R. and Stein, C. Byolutionary origins of the autotransporter proteins Unpublished
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complement (2415., 6314)
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PAKSVVIGFGATNDGETNVALGAKSKSSKAASIAIGDNAKALDNQAIAIGQNATANSD
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NLATLLGGNAQNTNGNVAMTDIGGTGKNNINDAIKASRNEVKQGKNMVVTPTTGANGQ
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/gene="yfkJ"
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                                                                                                                                                                                                                                                                                                                                   /db_xref="GI:12721960"
                                                                          GGKTKLRAVVQAKIELIND
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/transl_table=11
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                                                                                                                                   /note="PM1567"
868. .1467
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/codon_start=1
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                                                                                                                        6588 tgtggcagcaggtgaggtcagtgccaccagcaccgatgcggtcaatggtagccagttgta 6647
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Direct Submission
Submitted (24-027-2000) Department of Veterinary Pathobiology,
University of Minnesota, 1971 Commonwealth Ave., St. Paul, MN
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Pasteurella multocida PM70 section 161 of 204 of the complete
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Pasteurella multocida
Bacteria: Proteobacteria: gamma subdivision; Pasteurellaceae;
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May, B.J., Zhang, Q., Li, L.L., Paustian, M.L., Whittam, T.S.
Kapur, V.
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Proc. Natl. Acad. Sci. U.S.A. 98 (6), 3460-3465 (2001)
                  Length 3900;
                                                                        Indels
                  1.3%; Score 90.8; DB 3; 55.5%; Pred. No. 2.1e-09; ative 0; Mismatches 152;
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91. .804
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AE006194.1 GI:12721958
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91. .804
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                                                                          Conservative
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07-0CT-1997

PAT

DNA US 5646259

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2601 ACCACAAGCGTATATCCCTGGTAAGAGCATGGTTGCAGCGGGCACTTACAAAGG 2542
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2781 TATTGCAAAAGGTGACATTTCTGAAACAGTACTGATGCTGTGAATGGTAGCCAGCTATA 2722
                                                                                                                                                                                                                                                                                                                                                                                                                                                          gccacaagectacatteetggcagatecatggttacegggggtattgeeaeceacaaegg
                                                                                                                                                                                                                                                                                                                                                           tcaaggtgcggtggcagtggactgtcgaagctgtcggataatggtcaatgggtatttaa
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St. Geme, J.W. III and Barenkamp, S.J.
DNA encoding haemophilus adhesion proteins
Patent: US 5646259-A 1 08-JUL-1997;
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608 c 835 q
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Sequence 1 from patent U:
155122
155122.1 GI:247*^^
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DWHTPDEGGETKGLNGDILVMNPILERAFELSSMGIRVDETARKQLALTNRBDRKF
DWHQDLVNGKLPLSIGGGIGRRSRVMLLQKKHIGEVOSSVWFKWVHBQFDNIL"

2124 c 2065 g 3349 t
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GYDLGPRYDGYVSGKYRHFGGSLKOWODLNYNNFEMESATLFTMCSALGLRAGMVAGA
IVNRTQGEIPNBAAVKDIEKNAVEIVVKAAAYLL"
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ALGMSRISDNGKVIIKLTGNTNSRGDFGASIGAGYQW"
COMPlement(6493. .7833)
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55.5%; Pred. No. 2.3e-09;
tive 0; Mismatches 152; Indels
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                                                                                                                         complement(6493. .7833)
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Best Local S
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ORIGIN
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                                                                                                                                                             2863 GATGAAAAACACGTTGTCAGCCTTGATCCAAATGATCAAAAGGTAAAAGGTGTCGTG 2922
                                                               6640 cagitgiacaaagccacccaaggcatigccaacgcaacc----aaigagcitgac
                                                                                                                                                                                                                                                                                                                           6691 catcgtatccaccaaaacgaaaataaagccaatgcagggatttcatcagcgatggggatg
                                                                                                                                                                                            2803 AAAGCIGACGGTACTGCGGATAAAACCAAAGGCGGAAGTGAGCAATGATAAAAGTTTCTACC
Length 3294;
                                    Indels
 Score 82.8; DB 10;
Pred. No. 1.2e-07;
0; Mismatches 237;
        1.2%;
                        Best Local Similarity 49.8
Matches 244; Conservative
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Gaps 6 tgtggcagcagtgaggtcagtgcaccagcaccgatgeggtcaatggtagccagttgta 6647

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Search completed: September 12, 2001, 23:14:38 Job_time: 38100 sec
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Barenkamp, S.J. and St Geme, J.W. 3rd.
Identification of a second family of high-molecular-weight adhesion
proteins expressed by non-typable Haemophilus influenzae
Mol. Microbiol. 19 (6), 1215-1223 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTNVTFASGNGTTATVTNGTDGITVKYDAKVGDGLKLDGDKIAADTTALTVNDGKNAN
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VTFKAGKNLKVKQEGANFTYSLQDALTGLTSITLGTGNNGAKTEINKDGLIITPANGA
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EBGLADEADAKRAPDKTKALSAGTTEIVNAHDKVRRANGLNTKVSAATVESTDANG
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NVDSDGKKVVKDDNDGKWYHAKADGTADKTKGEVSNDKVSTDEKHVVSLDPNDQSKKKG
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EDNTAATVGNLRKLGWVLSSKNGTRNEKSQQVKHADEVLFEGKGGVQVTSTSENGKHT
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TVHLNGIGSTLTDTLVGSPATHIDGGDOSTHYTRAASIKDVLNAGWNIKGVKAGSTTG
QSENVDFVHTYDTVEFLSADTETTVTVDSKENGKRTEVKIGAKTSVIKEKDGKLFTG
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TNLDEKGTDKQTPVVADNTAATVGDLRGLGWVISADKTTGGSTEYHDQVRNANEVKFK
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3103 TCACAGTTACCACAAGCCACTATGCCAGGTAAATCAATGGTTGCTATTGCGGGAAGTAGT 3162
                                                                                                                                                                     3223 ATTATTCGCTTGTCAGGCACAACCAATAGTCAAGGTAAAAACAGGCGTTGCAGCAGGTGT:3282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    St.
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Haemophilus influenzae adhesin (hia) gene, complete cds.
U38617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 3700)
Barenkamp, S.J.
Barenkamp, S.J.
Direct Submission
Submitted (16-OCT-1995) Stephen J. Barenkamp, Pediatrics, Suniversity School of Medicine, 1465 South Grand Boulevard, Louis, MO 63104-1095, USA
                                                                                     cacaacggtcaaggtgcggtggcagtgggactgtcgaagctgtcggataatggtcaatgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /standard_name="Haemophilus influenzae adhesin"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus influenzae strain=Nontypeable strain 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Haemophilus influenzae"
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1. .3700
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251. .3547
/gene="hia"
251. .3547
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RBS
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VERSION
KEYWORDS
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AUTHORS
TITLE
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MEDLINE
REFERENCE
AUTHORS
TITLE
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VVIDNVANGDISATSTDAINGSQLYAVAKGVTNLAGQVNNLEGKVNKVGKRADAGTAS
ALAASQLPQATMPGKSMVAIAGSSYQGQNGLAIGVSRISDNGKVIIRLSGTTNSQGKT
GVAAGVGYQM"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     3233 CAGTTGTATGCTGTGGCAAAAGGGGTAACCAAACCTTGCTGGACAAGTGAATAATCTTGAG 3292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atccaaaatgtggcagcaggtgaggtcagtgccaccagcaccgatgcggtcaatggtagc
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                                                                                                                                                                                                                                                                                                                                                                                                 6520 tttgctggacaaacggcggttggtgcggtctccgtgggtgcctcaggtgctgaacgccgt
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6
                                                                                                                                                                                    Length 3700;
                                                                                                                                                                                    Score 82.8; DB 3;
Pred. No. 1.2e-07;
0; Mismatches 237;
                                                                                950
                                                                                882
                                                                                                                                                                                 Query Match
1.2%;
Best Local Similarity 49.8%;
Matches 244; Conservative (
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Haemophilus influe
M. catarrhalis str
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Plasmodium falcipa Moraxella outer me Haemophilus adhesi Haemophilus influe

DNA

influe

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New nucleic acid encoding Moraxella catarrhalis outer membrane protein, useful in protective vaccines and for diagnosis
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200kDa outer membrane protein; antibacterial; immunogenic; infection;
otitis media; detection; ds.
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standard; DNA; 6942
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Score 6942

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Post-processing:

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The present invention describes an isolated and purified nucleic acid (I) catched the accodes a 200 kba outer membrane protein of Moraxella acturhalis.

The 200 kba outer membrane protein (II) has antibacterial activity and the 200 kba outer membrane protein (II) has antibacterial activity and can be used in vaccines. (II), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarhalis immunoassays for detecting specific antibodies (Ab), and to antigen in immunoassays for detecting specific antibodies (Ab), and to antigen in immunoassays for detecting specific antibodies (Ab), and to fragments are used as probes for identifying/cloning 200 kba protein fragments are used as probes for identifying/cloning 200 kba protein fragments are used as probes for identifying/cloning 200 kba protein (I) makes possible production of large amount of recombinant immunogens. (I) makes possible production of large amount of recombinant immunogens. (I) makes possible production of large amount of recombinant immunogens. Characts the Escherichia coll host. The present sequence represents the towards the Escherichia coll host. The present sequence represents the confirmation in the exemplification of the present invention. Fig 7; Claim

T; 0 other; 1471 ö C; 1564 Sequence 6942 BP; 2286 A; 1621

ö 720 480 480 009 360 420 360 180 240 300 300 Gaps 9 9 gagtgcgccaaatcccacagcggaggagtagcagtagtaccgcaggacaggtgggcagc tetectgteatecgectgaetegtgttgceaegetegetatectagtgateggtgegaeg catgocaatcaagctattgctatcggtggtagcaaaccagatcctcgtaatcaagcggct atgaatcacatctataaagtcatctttaacaaagccacaggcacatttatggccgtggca 6942; ö Length Indels 22; ö DB Score 6942; 1 Pred. No. 0; ; Mismatches ; Query Match Best Local Similarity 100.0%; Matches 6942; Conservative 0 481 541 601 661 661 121 481 541 501 361 421 301 241 301 181 ~ 121 121 181 Db g ŏ Db οy ò qq õ Q ολ qq ò οy g Qγ QCI δ qq ò qq g ŏ δ

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26-JUL-2000; 2000WO-CA00870.

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The present invention describes an isolated and purified nucleic acid (I) that encodes a 200 kba outer membrane protein of Moraxella catarrhalis. The 200 kba outer membrane protein of Moraxella catarrhalis. The 200 kba outer membrane protein (II) has antibacterial activity and can be used in vaccines. (II), and its truncated versions, are used as infections, particularly otitis media in humans. (II) is also used as antigen in immunoassays for detecting specific antibodies (Ab), and to generate Ab. (I) are used for recombinant production of (II) and its caraments are used for recombinant production of (II) and its genes from other strains, and for diagnostic detection of M. catarrhalis. (I) makes possible production of large amount of recombinant immunogens. Expression of truncated versions of (II) reduces toxicity of the protein towards the Escherichia coll host. The present sequence represents the examplification of the present in the sequence of the protein or examplification of the present in the complete of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the process
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                                                                                                                                                                                                                                        outer
                                                                                                                                                                                                                                        New nucleic acid encoding Moraxella catarrhalis
useful in protective vaccines and for diagnosis
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Matches 5085; Conservative
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δλ	1953	
Db	2056	ataacaatagcttagttaccgccaaagatttggcagactatctaaataaa
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qq	2116	gtccaaaacggtgataa
δλ	1953	taatggtaataccccaaatacctttgagaccatcacctttgcaggtg
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οy	2002	cggcatcagtatcagcaatgacatagccaaaggtaaagtcaaagttg
qq	2236	  acggtgttaatattacgaccaatagagccacaggtacagttacctttggcattgacca
Qy	2062	ccacgcctaagctgaccgtgggtagcgataaagatggtaaaactcaa
QQ	2296	gtaatggtctcaccacgcctaagctgaccgtgggtagcgatacaaatggtaatcga 2
δy	2122	gttattgagcaagtggctagcggtaacgacaccaaaaacat
qa	2353	tggttattgagcaagtccctagcgctgacggtaacagcaccaaaaacatcattaaagg
Οy	2176	gtccccaacactgccttagcattaccaatgcaggtggcgtacgcaccacagaacagg
QQ	2413	illililililililililililililililililili
Qy	2236	aatcaccagcgacgaagacaaatccaaagccgccagtatcggtgatattaa
QQ	2470	atacaatcgaagaaaaagacaaatccaacgctgccagcattgatgatgtgctaaat 252
Qy	2296	ctttaacctaaaaataatagcaactccgttggctttgtctccacttataacact 235
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5695 gacggcaatcaggtaaacattgccgacatcaaaaagacccaaattcaggttcatcatct	4972 aaccgcactgtcatcaaagcaggcacggtacttggcggtaaaggtaataacgataccga. 5815 aaacttgccactggtggtgtacaagtgggcgtggataaagacggcaacgctaacggcga. 5815 aaacttgccactggtggtgtacaagtgggcgtggataaagacggcaacgctaacggcga.	5875 traagcaatgtttgggtcaaaacccaaaagatggcagcaaaaagcctgctcgccact	5935 tataacgccgcaggtcagaccaactatttgaccaacaccccgcagaagccattgacaga	5995 ataaatgaacaaggtatccgcttcttccatgtcaacgatggcaatcaagagcctgtggta	6055 caagggcgtaacggcattgactcaagtgcctcaggcaagcactcagtggcgataggtttc	6115 caggccaaggcagatggtgaagccgccgttgccataggcagacaaacccaagcaggcaac	tocatcgccatcggtgataacgcacaagccacg	6235 acaggcaatgtggtaacaggtaagcactctggtgccatcggcgacccaagcactgttaa 	tgataacagttacagt 	355 gtctttggtgtgggcaataacatcaccgtgaccgaaa 	6415 aactctgccatcagtgcaggcacacacgcaggcacacagg 	6475 gcaggtacaaccacagcaggtgcaacaggtacggtt 	6535 gcggttggtgcggtctccgtgggtgcctcaggtgctgaacgcc	5 gcaggtgaggtcagtgccaccag 	cccaaggcattgccaacgcaaccaatgagcttgaccatcgtatccaccaaaacgaaa; 	tcagcgatggcgatggcgtccatgccacaagcc 	6775 cctggcagatccatggttaccgggggtattgc
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ctetectgteatecgeetgaetegtgttgeeaegetegetatectagtgateggtgegae

120

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aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. caterrhalis is known to cause acute, localised infections such as otitis media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprising of a combination of 41 nucleic acid molecules (see ARZ8814-ARZ8854). The library has a number of uses described in the specification e.g. is useful for aidentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a Moraxella catarrhalis genomic library
                                                                                                                                                                                                                                                                                                         otitis media; sinusitis;
                                                                   6111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucleic
                                                      gtgggactgtcgaagctgtcggataatggtcaatgggtatttaaaaatcaatggttcagcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 62909 BP; 18449 A; 13798 C; 12744 G; 17918 T; 0 other;
                                                                                                           gatacccaaggccatgtaggggcggcagttggtgcaggtttcacttt
                                                                                                                                                                                                                                                                                                      pacteria; human upper airway; endocarditis; meningitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 293-308; 545pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0140121
                                                                                                                                                                                                                                                                                                        bacteria;
                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patterson C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INCY-) INCYTE GENOMICS
                                                                                                                                                                                                                                                                                                                                                Moraxella catarrhalis
                                                                                                                                                                                                                                                                            Genomic fragment #32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-041427/05
                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                        bronchopulmonary;
                                                                                                                                                                                                                                                                                                      library;
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Best Local Similarity Matches 4853; Conserv

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Query Match

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Length 62909;

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The present invention describes an isolated and purified nucleic acid (I) that encodes a 200 kDa outer membrane protein of Moraxella catarrhalis. The 200 kDa outer membrane protein (II) has antibacterial activity and can be used in vaccines. (II), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarrhalis infections, particularly otitis media in humans. (II) is also used as antigen in immunoassays for detecting specific antibodies (Ab), and to generate Ab. (I) are used for recombinant production of (II) and its fragments are used as probes for identifying/cloning 200 kDa protein (I) makes possible production of large amount of recombinant immunogens. Expression of truncated versions of (II) reduces toxicity of the protein towards the Escherichia coll host. The present sequence represents the
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or diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                            catarrhalis strain 4223 genomic 200kDa coding sequence SEQ ID NO:6.
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200kDa outer membrane protein; antibacterial; immunogenic; infection;
otitis media; detection; ds.
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useful in protective vaccines and for
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The present invention describes an isolated and purified nucleic acid (I) that encodes a 200 kba outer membrane protein of Moravella catarrhalis. The 200 kba outer membrane protein of Moravella catarrhalis. The 200 kba outer membrane protein of Moravella catarrhalis. The used in vaccines. (II), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarrhalis infections, particularly outlis media in humans. (II) is also used as antigen in immunoassays for detecting specific antibodies (Ab), and to generate Ab. (I) are used for recombinant production of (II) and its fragments are used as probes for identifying/cloning 200 kba protein genes from other strains, and for idagnostic detection of M. catarrhalis. (I) makes possible production of large amount of recombinant immunogens. Expression of truncated versions of (II) reduces toxicity of the protein towards the Escherichia coil host. The present sequence represents the moral strain 4223 genomic 200kba gene, which is given in the
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P-PSDB; AAB69134.
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0; Mismatches 1104; Indels 1270;
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                                                                                                                                                             membrane protein; OMP; immunogen; vaccine; otitis
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                                      Score 2580.6;
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P-PSDB; AAW04505.
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Best Local Similarity
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Oy :	5886 ttgggtcaaaacccaaaagatggcagcaaaaagcctgctcgccacttataacgccgc 5945 	RESULT 7 AAF59100 ID AAF59100 standard;
Oy 5	5946 aggicagaccaactattigaccaacaaccccgcagaagccatigacagaataaatgaaca 6005 	AA AC AAF59100; XX XT 24-APR-2001 (first
o yo	6006 aggtatccgcttcttccatgtcaacgatggcaatcaagagcctgtggtacaagggcgtaa 6065 	M. cata
Oy 6	6066 cggcattgactcaagtgcctcaggcaagcactcagtggcgataggtttccaggccaaggc 6125 	KW 200KDa Outer membran KW Otitis media; detect XX OS Moraxella catarrhali:
Oy 6	6126 agatggtgaagccgcttgccataggcagacaaacccaagcaggcaaccaatccatcgc 6185 	XX
Oy 6	6186 catcggtgataacgcacaagccacgggcgatcaatccatcgccatcggtacaggcaatgt 6245 	XX PF 26-JUL-2000; 2000WO XX PR 27-JUL-1999; 99US
oy da	6246 ggtaacaggtaagcactctggtgccatcggcgcccaagcactgttaaggctgataacag 6305 	XX PA (CONN-) CONNAUGHT LA XX XX T LOOSMORE SM, Sasaki
Oy 6	6306 ttacagtgtgggtaataacaaccagtttatcgatgccactcagaccgatgtctttggtgt 6365 	WPI; 2001-159722/ P-PSDB; AAB69133.
Oy 6	6366 gggcaataacatcaccgtgaccgaaagtaactcggttgccttaggttcaaactctgccat 6425 	PT New nucleic acid enco XX Example 3; Fig 2A-W;

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                                                                                                                    is strain 4223; major outer membrane protein;
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                            i K, Yang Y, Klein MH;
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The present invention describes an isolated and purified nucleic acid (I) that encodes a 200 kba outer membrane protein of Moraxella catarrhalis. The 200 kba outer membrane protein of Moraxella catarrhalis. Can be used in vaccines. (II), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarrhalis infections, particularly otitis media in humans. (II) is also used as antigen in immunoassays for detecting specific antibodies (Ab), and to generate Ab. (I) are used for recombinant production of (II) and its fragments are used as probes for identifying/cloning 200 kba protein genes from other strains, and for diagnostic detection of M. catarrhalis. (I) makes possible production of large amount of recombinant immunogens. (I) makes possible production of (II) reduces toxicity of the protein towards the Escherichia coll host. The present sequence represents the towards the Escherichia coll host. The present sequence represents the contract of the protein co the exemplification of the present invention.

Sequence 6973 BP; 2265 A; 1555 C; 1533 G; 1620 T; 0 other;

29; 1078 578 agtaggtettaccgccaaagccgaaaaaggatatacaatcgctattggttetaatgcaca 758 tegtaateaageggetaateagaaggeaggtteeeaegeeaaaggtaaagagteeatege 404 179 721 228 781 284 841 344 868 661 9 Gaps tgtcaatggaagcagtttggataagataggtaccgatgctacgggtcaagagtccatcgc acattigotigateageatggtaateetaaacateegaaaggtaetetgattaaegatet tattaacggccatgcagtattaaaagaaatacgaagctcaaaggataatgatgtaaaata atatttggataggaatagcactaactctaaatatccaaatgg---tcttcttagcactct tattcaaaaccatacagtattacgccaaatacgagactcaaatggttctca---gaaata tagtettgetaaggeacatgecaateaagetattgetateggtggtageaaaceagatee tgaaaatgctaacgcacagggcggtcaagccatcgccatcggtagtagtaa---taaaac gagtgcgccaaatcccacagc-ggagggagtagcagtagtaccgcaggacaggtgggcag atgaatcacatctataaagtcatctttaacaaagccacaggcacatttatggccgtggca Length 6973; Score 2580.6; DB 22; Length 6973 Pred. No. 0; 0; Mismatches 1104; Indels 1270; Query Match 37.2%; Best Local Similarity 66.9%; Matches 4803; Conservative 1199 019 1079 669 465 579 842 345 668 959 522 285 405 -602 120 662 722 229 782 61 80 qq ò g qq Ω qq ò qq ò qq οy Ob õ pp ò g δŽ qq Q ò δ 8 g ò

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ВР

AAF59101 standard; DNA; 5979

(first entry)

24-APR-2001

DXXXI

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The present invention describes an isolated and purified nucleic acid (I) that encodes a 200 kba outer membrane protein of Moraxella catarrhalis. The 200 kba outer membrane protein of Moraxella catarrhalis. The 200 kba outer membrane protein (II) has antibocterial activity and can be used in vaccines. (II), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarrhalis infections, particularly olitis media in humans. (II) is also used as antigen in immunoassays for detecting specific antibodies (Ab), and to generate Ab. (I) are used for recombinant production of (II) and its fragments are used as probes for identifying/Cloning 200 kba protein genes from other strains, and for idagnostic detection of M. catarrhalis. (I) makes possible production of large amount of recombinant immunogens. Expression of truncated versions of (II) reduces toxicity of the protein towards the Escherichia coli host. The present sequence represents the M. catarrhalis strain 4223 lambdabenals clone 200kpa coding sequence, which is used in the exemplification of the present invention.
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strain 4223 lambdaEMBL3 clone 200kDa coding sequence #2.
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                                                                    Moraxella catarrhalis strain 4223; major outer membrane protein; . 200kDa outer membrane protein; antibacterial; immunogenic; infection; otitis media; detection; ds.
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P-PSDB; AAB69133.
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ф	3727	ccaccgctaaggtgacctatgatgacacaagcaaaaccagtaaagtggtctatgatgt
oy da	3775	aatgtggataataaaaccattgaagtgacaagtgataaaaacttggcgtcaaaaccacc 3834 
6	. 60	cactaaccaaaacaadtactaataataaaaccaaattaataccaccaataa 340
: <b>q</b>	84	ggcacaggtgctaatatatgccctaagcaatcaagctactggc 390
Οy	3892	atgccttgttaaagccagtgatatcgccacccatctaaataccttggctggc
QΩ	3904	ing filli ang fillilitititi i fillili i lilit i lilili i torgetyaceteaaecaccttatctggcgaca tgcgcttgtcaaggccagtgatatcgttgctcatctaaacaccttatctggcgaca
Qy	3952	gatgctgatg
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Qy	4012	acaaggtcatctatgacagtaccgataagaagtactatcaagtcaatgacaaggtca
qq	4024	taaggtcatctatgacagtaccgataacaagtactatcaagccaaaaatgatgg
ÓΫ	4072	gtgacaaaaacaaagaagttgccaaagacaaactggtcgcccaagccccaaaccccagat 4131
qa	4084	ttgataaaaccaaagaagttgccaaagacaaactggtcgcccaagcccaaaccccaga
٥y	4132	ggcacattggctcaaatgaatgtcaatcagtcattaacaaagagcaagtaaatgatgcc 4191
qa	4144	gcacattggctcaaatgaatgtcaatcagtcattaacaaagaacaagtaaatgatgc
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qq	4264	ataacaaaaaccaaaaacgccgcagtaactgtgggtgatttaaatgccgttgccca
Qγ	4312	acaccgctgacctttgcagggatacaggcacaacggctaaaaaactgggcgagactttg 4371
Dp	4324	cogetgacetttgcaggggatacaggcacaacggctaaaaaactgggcgagacttt
οy	4372	gtgggcaaacagacaccaataagctaaccgataataacatcggtgtg
qq	4384	ccatcaaaggtgggcaaacagacaccaataagctaaccgataataacatcggtggt ccatcaaaggtgggcaaacagacacccaataagctaaccgataataacatcggtggt
QY	4432	caggtactgatggcttcactgtcaaacttgccaaagacctaaccaatcttaacagcgt
ΟĐ	4444	ggtactgatggcttcactg
Oy	4492	catctctttgtagacgcaaacg
qq .	4504	atgcaggtggcaccaaaattgatgacaaaggcgtgttttttgtagactcaagcggtca
ογ	4552	gccaaagcaaacacccctgtgctaagtgccaatgggctggacctgggtggcaaacgcatc 4611
qq	4564	ccaaagcaaacacccctgtgctaagtgccaatgggctggacctgggtggc
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Db 4615		Qy	6592 gcagcag
Oy 5512 ggcatca	catcagtatccaaggcaaagataacagcagcatcaccctaagcaaagatgggctgaat 5571	qa	5626 gcagcaggtg
Db 4615		Qy.	6652 gccacccaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein,
                                                                                                                                                                                                                                            Moraxella catarrhalis strain Q8; major outer membrane protein;
200kDa outer membrane protein; antibacterial; immunogenic; infection;
otitis media; detection; ds.
           5866 gcagtgggactgtcgaagctgtcggataatggtcaatgggtatttaaaaatcaatggttca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid encoding Moraxella catarrhalis outer membrane useful in protective vaccines and for diagnosis
                                                          Sequence 6259 BP; 2067 A; 1414 C; 1393 G; 1385 T; 0 other;
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Gaps

35.8%; Score 2484.8; DB 22; Length 6259; 66.7%; Pred. No. 0;

0; Mismatches 1067; Indels 1269;

Conservative

Best Local Similarity Matches 4674; Conserv

Query Match

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gta	caa   ata	nctgataattet             ctaataatgea	gttttagcaata          ggctttgctcga	aagttg 	gtaat	gtag      cca8	aatgtatcaaa      qatgctaagag	gctgatg	ttag	ggtggt     gctcta	ttaa 	caaga ggtct	aggtcagg	ac ac	gt to	tagoga       Egatgg	 tgt	aacact
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ΟŸ	4673 ttgccaaaacg	gtcaacaacctaaaccaaagtaactcaggtgcgtcattaccctttg 4732
qq	4615	4614
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qq	4615	4614
Qy	5333 caaacggctca	ctaaaaagcaggcaaatcagccagtgatgccaaaactccaactggtctaa 5392
qq	4615	4614
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The present sequence represents a Haemophilus influenzae adhesin (Hia) gene from the non-typeable Haemophilus influenzae (NTHI) strain M407. Hia genes and proteins have antiinflammatory, auditory and antibacterial activities, and can be used in the production of a vaccine. An immunogenic composition comprising an Hia gene, a polypeptide encoded by an Hia gene, or a recombinant Hia polypeptide is useful for inducing protection against disease caused by Haemophilus strains in a susceptible host, preferably a human. An Hia protein is useful as an
                                                                                                                                                                                                                                                                                                                                                                              Hia; adhesin; Haemophilus influenzae adhesin; NTH1; infection; vaccine; non-typeable Haemophilus influenzae; antiinflammatory; auditory; antibacterial; meningitis; epiglottitis; septicaemia; otitis media; diagnosis; immunogenic; antigen; ds.
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p-PSDB; AAB23857.
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antigen, in immunogenic preparations including vaccines, as a carrier for other immunogens, and in the generation of diagnostic reagents. His is useful for treating diseases caused by the infection of Haemophilus influenzae such as meningitis, epiglotitis, septicaemia and otitis media. Recombinant production of Hia favours high recovery of the protein compared to the low recovery of native protein from Haemophilus influenzae species. A truncated protein has a significantly higher amount of recovery than a full-length protein.
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                                                                                                                                                                                                                                                                         12;
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The present sequence represents a Haemophilus influenzae adhesin (Hia) gene from the non-typeable Haemophilus influenzae (NTHi) strain 33.

Hia genes and proteins have antiinflammatory, auditory and antibacterial activities, and can be used in the production of a vaccine. An immunogenic composition comprising an Hia gene, a polypeptide encoded by an Hia gene, or a recombinant Hia polypeptide is useful for inducing protection against disease caused by Haemophilus strains in a susceptible host, preferably a human. An Hia protein is useful as an antigen, in immunogenic preparations including vaccines, as a carrier for other immunogens, and in the generation of diagnostic reagents. His is useful for treating diseases caused by the infection of Haemophilus is a useful for treating diseases.
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es 188;
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Pred. No. 3.4e-
0; Mismatches
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                                                                                                                                           Klein
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Best Local Similarity 58.4%;
Matches 281; Conservative
                 2000WO-CA00289
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                                                                                                 (CONN-) CONNAUGHT LAB
                                                                                                                                           Yang Y,
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gene from the non-typeable Haemophilus influenzae (NTH1) strain K9.

Hia genes and proteins have antiinflammatory, auditory and antibacterial
activities, and can be used in the production of a vaccine. An
activities, and can be used in the production of a vaccine. An
interpolation composition compliance in a polypeptide is useful for inducing
by an Hia gene, or a recombinant Hia polypeptide is useful for inducing
by an Hia gene, or a recombinant Hia polypeptide is useful for inducing
protection against disease caused by Haemophilus strains in a
susceptible host, preferably a human. An Hia protein is useful as an
antigen, in immunogens, and in the generation of diagnostic reagents. His
for other immunogens, and in the generation of diagnostic reagents. His
is useful for treating diseases caused by the infection of Haemophilus
influenzae such as meningitis, epiglotitis, septicaemia and otitis
media. Recombinant production of Hia favours high recovery of the
protein compared to the low recovery of native protein from Haemophilus
influenzae species. A truncated protein has a significantly higher
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acid encoding Hemophilus influenzae adhesin protein, fuse as antigens and vaccines and for treating Hemophilus influenzae
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                                                                                                                                                                наеmophilus influenzae adhesin (Hia) gene from NTHi strain К9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3354 BP; 1082 A; 639 C; 866 G; 767 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tch al Similarity 57.8%; Pred. No. 6.7e-27 278; Conservative 0; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amount of recovery than a full-length protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 22; 275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                           Klein MH;
                                                                                               ВЪ.
                                                                                              AAA92495 standard; DNA; 3354
                                                                                                                                                                                                                                                                                                                                                           99US-0268347.
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                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                          Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-618897/59.
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                                                                                                                                               17-JAN-2001
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           6940 t 6940
                                  3023 t 3023
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The present sequence represents a Haemophilus influenzae adhesin (Hia) gene from the non-typeable Haemophilus influenzae (NTHI) strain K22.
Hia genes and proteins have antilnflammatory, auditory and antibacterial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3212 caaaatyyttayctatcygyytatcacyaatttccyataatyycaaaytyattattcyc 3271
                                                                                                                                                                                                                                                                             6128
                                                                                                                         2984 atccaaaacgtcgcggcaggcgaaatttccgccacttccaccgatgcgattaacggcagc 3043
                                                                                                                                                                                                                                                                                                                                                                                                                        3152 ccacaagectetatgecaggtaaateaatggtttetattgegggaagtagttateaaggt 3211
3044 cagitgiaigcigiggcaaaaggggtaacaa-----atcitgciggacaagig 3091
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                                                                                                                                                                           cagitigiacaaagccaaccaaggcatigccaacgcaaccaaigagcitgaccaicgiaic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haemophilus influenzae adhesin (Hia) gene from NTH1 strain K22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA92498 standard; DNA; 3342 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klein
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P-PSDB; AAB23859.
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Klein MH

Υ,

Yang

Sasaki K,

Loosmore SM,

WPI; 2001-159722/16.

2000WO-CA00870.

26-JUL-2000; 27-JUL-1999;

01-FEB-2001

WO200107619-A1.

99US-0361619

(CONN-) CONNAUGHT LAB LTD

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                immunogenic composition comprising an Hia gene, a polypeptide encoded by an Hia gene, or a recombinant Hia polypeptide is useful for inducing protection against disease caused by Haemophilus strains in a susceptible host, preferably a human. An Hia protein is useful as an antigen, in immunogenic preparations including vaccines, as a carrier for other immunogens, and in the generation of diagnostic reagents. His is useful for treating disease caused by the infection of Haemophilus influenzae such as meningitis, epiglottitis, septicaemia and otitis media. Recombinant production of Hia favours high recovery of the protein compared to the low recovery of native protein from Haemophilus influenzae species. A truncated protein has a significantly higher amount of recovery than a full-length protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggcaaacgtgcagatgcaggtacagcaagtgcattagcagcttcacagttacc----a 3142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6460 aaatctgacggcacagcaggtacaaccaccacaggtgcaaggtgcaacaggtacggttaaaggc 6519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3032 cagitgiatgcigiggcaaaaggggiaacaaatciigc---iggacaagigaataaagig 3088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ccacaagcotacattcotggcagatccatggttaccggggggtattgccaccacaacggt 6819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           caaggtgcggtggcagtgggactgtcgaagctgtcggataatggtcaatgggtatttaaa 6879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tttgctggacaaacggcggttggtgcggtctccgtgggtgcctcaggtgctgaacgccgt 6579
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200kDa outer membrane protein; antibacterial; immunogenic; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tttgccggtgcaacggcacggtgcggtttctgtcggcgcaagcggcgaagaagacgt
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                                                                                                                                                                                                                                                                                                                                                                                                 DB 21; Length 3342;
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activities, and can be used in the production of a vaccine.
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                                                                                                                                                                                                                                                                                                                           Sequence 3342 BP; 1072 A; 641 C; 865 G; 764 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.9%; Score 132.6; DB 21; Best Local Similarity 57.8%; Pred. No. 1.4e-24; Matches 278; Conservative 0; Mismatches 194;
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Moraxella catarrhalis.

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The present invention describes an isolated and purified nucleic acid (I) that encodes a 200 kDa outer membrane protein of Moraxella catarrhalis. The 200 kDa outer membrane protein (II) has antibacterial activity and can be used in vaccines. (II), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarrhalis infections, parktuolarly ofitis media in humans. (II) is also used as antigen in immunoassays for detecting specific antibodies (Ab), and to generate Ab. (I) are used for recombinant production of (II) and its fragments are used as probes for identifying/cloning 200 kDa protein genes from other strains, and for diagnostic detection of M. catarrhalis. (I) makes possible production of large amount of recombinant immunogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               towards the Escherichia coll host. The present sequence represents a
M. catarrhalis strain 4223 200kDa partial nucleotide sequence, which is
                                                                                                                                                                                                                                                                             New nucleic acid encoding Moraxella catarrhalis outer membrane protein, useful in protective vaccines and for diagnosis
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Pred. No. 1e-20;
0; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 720 BP; 201 A; 142 C; 140 G; 237 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                   Example 14; Fig 17; 247pp; English.
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78.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.7
Best Local Similarity 78.2
Matches 140; Conservative
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                                                                                                                                                                Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface.
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1.6%; Score 110.6; DB 22; Length
Best Local Similarity 1.0%; Pred. No. 4.5e-19;
Matches 8; Conservative 472; Mismatches 301; Indels
                                                                                                                                                                                                                                                                                                                                          Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;
                                                                                                                                                                                                                            Example 6; Page 127; 159pp; English.
                                                                                               (CLIN-) CLINICAL MICRO SENSORS INC
                                  26-JUL-2000; 2000WO-US20476
                                                          26-JUL-1999; 99US-0145695
17-MAR-2000; 2000US-0190259
                                                                                                                                                 WPI; 2001-159728/16.
          01-FEB-2001
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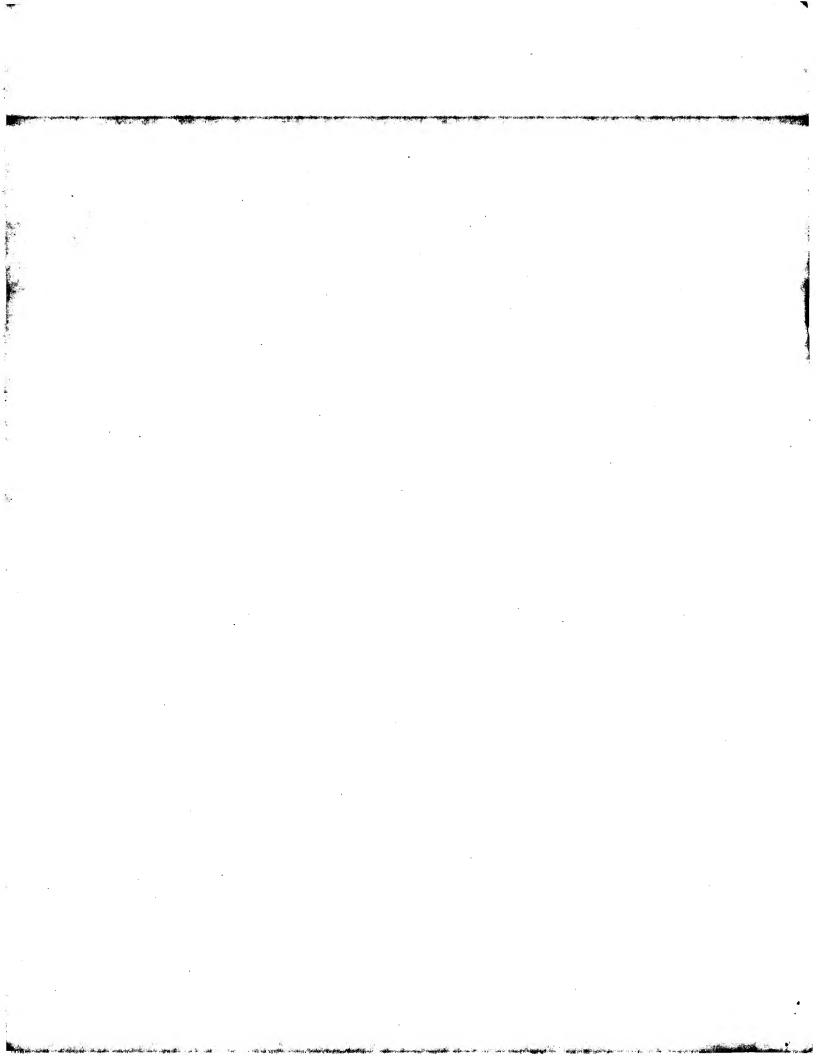
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1820 atgcaacggacgataccgatgcagtcacttataaacagcttaaaacaagtccaacaagacg 1879
                                                                                                      1880 ccgacggtgccctacaaagcttctctattcgtgatgaaaaaggtcaggaattacgatta 1939
1760 ttaaaattaccaaagacagtggcattaatgcaggtgatcaaaagatcagtaatgttaaag 1819
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Search completed: September 12, 2001, 13:49:19 Job time: 4181 sec

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Appl Appl

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; Mismatches 1104; Indels 1270;
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Sequence 1, Application US/08478370

Patent No. 5808024

GENERAL INFORMATION:

APPLICANT: SASAKI, Ken

APPLICANT: HARKNESS, Robin E.

APPLICANT: LOCSMORE, Sheena M.

APPLICANT: KLEIN, Michell H.

TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER

TITLE OF INVENTION: MEMBRANE PROTEIN OF MORAXELLA

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSES: SIM & MCBUTHEY

STREET: SOILE 701, 330 University Avenue

CITY: Toronto

STATE: Ontario

CITY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2580.6; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patentin Release #1.0, Version #1.30
US-08-852-344D-28
US-08-344-639E-28
US-08-844-639E-7
US-08-852-344D-7
US-08-852-344D-7
US-08-467-969A-7
US-08-467-961A-7
US-08-467-961A-7
US-08-001-554A-7
US-08-771-134-5
US-08-728-323A-1
US-08-728-323A-1
US-08-757-669A-20
US-08-757-669A-20
US-09-197-649-7
US-09-363-1189B-3
US-09-363-118-117
US-08-473-446-117
US-08-473-446-117
US-08-473-446-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: PatentIn Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,370
FILING DATE: 07-JUN-1995
CLASSIFICATION: 407-JUN-1995
ATTORNEY AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE,DOCKET NUMBER: 1038-502
TELECOMMUNICATION INFORMATION:
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TELEFAX: (416) 595-1163
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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Matches 4803; Conservative
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US-08-478-370-1
   Query Match
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                                                                                                                          time 454.28 Seconds
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Sequence 14,
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US-08-913-942-1
US-08-913-995-3
US-08-478-370-4
US-09-377-155-12
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US-09-377-155-10
US-09-377-155-10
US-09-377-155-10
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US-08-838-189D-28
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Maximum Match 100%
Listing first 45 summaries
                                                                                       - nucleic search, using sw model
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Copyright (c) 1993
                                                                                                                                                                                         US-09-361-619-10
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atttacgattagtaacttgtattctaatggtaataccccaaatacctttgagaccatcac 1988 taaaattaccaaagacagtggcattaatgcaggtgatcaaaagatcagtaatgttaaaga 1820 2456 AAGCTTTACCGTTAAAGAAGAAGAACGATGATGACGCCAACGCTATCACCGTGGCTAAAGA 2515 2396 CGCCGAACATTTGCCAAGCTATCTAAATGAAGTCAATCGAACGGCTGACAGTGCTCTACA 2455 aaatgccgcaaaattcggcactactcgtattaccgaagaggaaattggctttgctgatgc 1697 2155 2156 riccialadraccadecralacerracerracerracarcelaacaccecaaacc 2215 tggcaacagcaccctaaacaacggtggcttgactgttaataacaccattggtggtagcaa 1577 cgacggtgccctacaa-----agcttctctattcgtgatgaaaaggtcagga 2516 TACGACAAAAAATGCCGGCGCGCAGTCATAAAACTCAAAGGTAAAAACGGTCTAAC 2276 GAGTGGCAATGTTACCGCCCAACTTACAACATTGGCGTGAAAACCACCGAGCTTAACAG tgalggtaaagttgataa-----2036 AGATGGTGATGTATGAAAAACACCACATATTTGGATAAAAAAACAACTTAAAGTGGG 1 2096 TAGTGTTGCAATTACCATAGACAATGCCATTGATGCAGGTAATAAAAAGATCAGTAATCT tcttgaaacagttagcaccaaaaacctaaccgccagcgagaagttacggtag---gtag 1881 2696 2576 2636 1761 1638 1698 1578 1518 1517 1736 1796 1113 1173 1233 à op δ qq δ Dp οy g ò Q οy qq Qγ qq Ω oy Oy ò òγ qq oy Op οy Dp qq QQ Ω qq Óγ ò g δ

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5 AATGAATGTCAAATCAGTCATTAACAAAGAACAAGTAAATGATGCCAATAAAAAGCAAGG CAtcaatgaagacaacaagagctttatcaaagggcttgaaaacgccgccaaagacaccaaaac	SATGCCAATAAAAAGCAAGG 4924 gccgccaaagacaccaaaac 4265 
CATCAATGAAGACACGC caaaaacgccgcagtaac 	432
6 tgcaggggatacaggcacaacggctaaaaaactgggcgagactttgaccatcaaaggtgg 	actttgaccatcaaaggtgg 4385 
6 gcaaacagacaccaataagctaaccgataataacatcggtgtggtagcaggtactgatgg 	gtggtagcaggtactgatgg 4445 
6 cttcactgtcaaacttgccaaagacctaaccaatcttaacagcgttaatgcaggtggcac 	gegttaatgeagtggeac 4505 
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agctgttgatgataacgatgcggtgaactttaagcagttta	atgaagttgccaaaacggt 408
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22	5321
86 cactttgccacaaattgacacaccaaacacaggtaatgccaat	gcagggcaagcccaaag 5
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26 gatgagtaacatcaccgtcaacaccgccttagcagcgaccga	tgatgatggcaatgtgct 52
22	5321

٥y	5286	atcaaagccaaagatggtaagttctacaaagcagacgacctcatgccaaacggctcact 5	345
qq	5322	5	321
Qy	5346	aagcaggcaaatcagccagtgatgccaaaactccaactggtctaagccttgttaaccc 5	405
qq	5322	9	321
Qy	5406	ygtaaaggcagtacaggcgatgcagtggctcttaataacttatcaaaagcggt 5	465
QQ	5322	\$	321
δλ	5466	atggtacaactactaccacagtaagctctgatggcatcagtatcca 5	525
Dp	5322	S	321
Qy	5526	99	282
Ор	5322	AAGGT 53	326
Qy		catcagcaatgtgggtaaaggcacaaaagacaccgacgctgccaatgtacaacagttaaa 56	645
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qq	5627	TIGGGTCAAAACCCAAAAAGGCAGCAAGCAAAAAAGCCCTGCTGCTATAAAGGCCGC 5	9899
Qy	5946	<u> </u>	5005
qq		AGGTCAGACCAACTATTTGACCAACAACCCGCAGAAGCCATTGACAGAATAAATGAACA 5	5746
Οy		aggtatccgcttcttccatgtcaacgatggcaatcaagagcctgtggtacaagggcgtaa 6	5909
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οy	9	cggcattgactcaagtgcctcaggcaagcactcagtggcgataggtttccaggccaaggc 6	6125
qq	5807	– ט	5866
QY	6126	agatggtgaagccgccgttgccataggcagacaaacccaagcaggcaaccaatccatcgc 6	6185
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qq	5927	CATCGGTGATAACGCACAAGCCACGGGGGATCAATCCATCGCTACGGTACAGGCAATGT 5	5986
δλ	24	96	6305
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                                                                                                                                                                             Length 9542;
                                                                                                                                                                                                       0; Mismatches 1041; Indels 1545;
                                                                                                                                                                         Score 2382.4; DB 4;
Pred. No. 0;
                                                                                                                                                                             34.3%;
         TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 9542 base pairs
(212) 869-8864
                                                                                                                                                                         Query Match 34.3
Best Local Similarity 65.2
Matches 4842; Conservative
                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                    TOPOLOGY: linear
                                                                                                               MOLECULE TYPE: DNA US-08-968-685A-9
 TELEFAX:
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APPLICANT: PLOSILA, LAURA
TITLE OF INVENTION: MORAXELLA CATARRHALIS OUTER MEMBRANE
TITLE OF INVENTION: PROTEIN-106 POLYPEPTIDE, GENE SEQUENCE AND USES THEREOF
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                             6725
                                                                                                                                                                         catggttaccgggggtattgccaccacaacggtcaaggtgcggtggcagtggactgtc
gggcaataacatcaccgtgaccgaaagtaactcggttgccttaggttcaaactctgccat
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                                                                                                                                              CACCACAGCAGGTGCAACCGGTACGGTTAAAGGCTTTGCTGGACAAACGGCGGTTGGTGC
                                                                                                                                                                                                                                                                                               tyccaacycaaccaatgaycttyaccatcytatccaccaaaacyaaaataaayccaatyc
                                                                                                                                                                                                                                                                                                                                                                                                                               6527 CATGGTFACCGGGGGTATTGCCACACACGGTCAAGGTGCGGTGGCAGTGGGACTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gaagctgtcggataatggtcaatgggtatttaaaaatcaatggttcagccgatacccaagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,685A
FILING DATE: NO. 6214981ember 12, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Baldwin, Geraldine F.
REGISTRATION NUMBER: 31,232
REFERENCE/DOCKET NUMBER: 7969-060
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/08968685A Patent No. 6214981 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: MC
TITLE OF INVENTION: PR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10036-2711
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  GAT 110	tta 939    GTA 116	ggt 987      GGT 122	ctg 104      CTG 128	g 11     13	aat 11     AAC 13	cta 12     TTA 14	taggt 12:		rgaa 15	ccca 13:	13	TAAC 16	actgat 13        GGTAAT 17		TCAA 1	at 1    GT 1	aaac 	AAAC	teggt 1       Teggr 1			ataaa      ATGCA	-tgtt 1
SCACCA	ggt     !ACGGAT	saatgtege 	ggagaat       GGTGAGG	gaaaaaa      AAAAGGT	cgataat 	taaaaac        TGAAAC1	1		GCATTGAT	0 - O	1	AAAAGT	aagtttac    AAAAATGG	cggcact	CGGTA	gtacagt      AAACAAA	sacce 1111	ACCC	caag        CAAG	caaaa 	GCATIG	ogtaaagttg             rggmcameg	
GGCCTATO	caatggt       CAAGAATGGTGCTACGGAT	tatcaagcgtaaaatcatcaat. 	cacagctaaaagcggtggagaatct 	actggcgttaagaaaaact                     AATAGAGTAGAAAAGGTTT	aagcggacaagctaaccgataat. 	aaacttgctaaaaacct 	agaaagt 		ATGAATG	gtttaad        GTCAAA		AGCTTAA	ggctta	8	AAACCAG	taaagctggtacagttg 	ggcaacago	GGCAACA	taaacaaatc              \CAAACAAATC	55 —	CI	gat AC	i
ATGTACG	gcaat      TCAAGAA	agcgtaa          GGCGTAA	agctaae           AGCTTA	ggtactgg      AATAATA(	reggacaa        CCAGCG	gaaagtta          GAAAGTTC	gccagcg 		TGAT	agcggtg       GCAGGTG		TATGGACAG	actgatg             AAAAGG		AATAACI	tttagcaata     GTTGATGTT	yctaaaagttggc 	SACCGIT	tagcaat        TAGTAAC	caatgtatcaaatg 	TAAGCCA	ctgatgct            CTAATAAT	gggtgg- 
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	cataaaatcy       aGACAACCGG	g I GTAATGG	tgaggataccgatgcgg                  GCGGATACCGATGCGG	it tt	taaa      CACA		rttagcad	STTACCA	CAGATA	aataaca       Gataaag		AGTAGATG	acagaca    -	GCTCTAC	AAAATCA	otegtateaceaaga                  	cttgata	CTTAACC	gttaat         GTTAAA	tttgcc	TTTACT(	gaagagi        AGAGAC	ggataaa 
I II I	tcaaaca      ccaatag	ggtagt          GTAAT	gaggata          3CGGATA	tcaaattao 	CO T		gaaacag	AAAATG	CTTA	tg 		SGTGT		,	SACAG	tegtate 	acctta	CTTTGG	cttgact          CTTATC	cattaaa	CATTAC	actcgtattaccgaaga 	caccatatttg
	aatggg      AACCAG	tccatt        TCCATT	gtta      GTTC	9969 	cgagactttaac 		oggt 	CAGC	AACCCG		20000	CITACIGCI	caacaaa 	<b>∡</b> ↓	aactctaat               GATGCTAAT	tactac	aaaca	. ¥	acggtgg          ACGATGG	ctgatgg	CTGATGG	oti C	- a
111 043 CAGO	892	40 tt     63 TT	88 g - 1	048 9	108 9	168 aa 400 AT	228 ag 	454 AC	1288 ag   	06	339	634	339	694 C	1399 ac	1420 ga	480 9	1874 A	1537 a	1597 g	1988 G	1657 a   2048 A	717
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3181 2427 3061 2487 3121 2828 ANIACCTAACCGATGCCACCAACGCAACAACAGGGCATGTAACTCAATTGGGTATCGTT 2887 2121 2648 AATGGTATAGCACTTGACGCACAACTTACATCACCAAAGACAAAGTTGGCTTTGCTAAG 2707 2288 CAAGTACCGCTGACCTTTGCAGGTGATACAGGTCCTAATGTCACCAAAAAACTGGGGGAG 2347 2468 CTTGATGCGGTTAATACTAAAACCCTAACTGCCAGCGATAAAGTTACCGTAGACAGTGGC 2527 2167 gacggtgccct-----acaaagcttctctattcgtgatgaaaaagtcagg 1927 2122 ttggttattgagcaagtggctagcggtaacgacaccaaaacatcatt------2708 CAAGATGGTTCACTTGATAAAAGCAAACCTTATCTTGATAAGGACAAGCTAAAAGTGGGT 2236 aatacaatcaccagcgac---atcaatggteteaceaegectaagetgacegtgggtagegataaagatggtaaaacteaa 2348 ATTTTAAAGGTTAAAAGGTGGTAAAACCACAGGTGATGATTTAACCAAAAATAACATCGGT 2408 GTGGTGGCTGATAGTACCGATAATAGCTTAAACCTTGCTAAAACTTTGAAACTTTAAGCGAT -----tctaatggtaatacccaaatacctttgagaccatcacctttgcaggtgaa aacggcatcagtatcagcaatgacatagccaaaggtaaagtcaaagttggtattgaccca 2108 AACAAACCCCGCCTAACCCCCAACTGGCATTAACGCAGGTGGTAAAGAGCTGACCAATGTC 2170 --agaggattgtccccaacactgc-------1951 -----aatttacgattagtaacttgtat-------2488 2002 2062 2588 1951 1882 1928 1822 QQ Ω ò qa. δ QΥ Вb οy g ŏ ò qq g ò qq δλ QQ ò g δy Db Q Dp QΥ Dp Q ογ q ò q δŽ οy

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3658 gaagcggttgactt 	3778 gtggataataaaa 	3838 ctgaccaaaacaac 	0 0	3955 accgccaaaggggg 	4015 aaggicaiciaiga 	4075 gacaaaaacaaage 	4135 acattggctcaaat 	4195 aaaaagcaaggcat 	4255 gacaccaaaaccaa               4877 GATAACAAAACCAA	2 2	4375 atcaaaggtgggc 	10 1	2 2	5 aa 7 AA	4615 aacatcggtgcag	4675 gccaaaacggtca	4735 gtaaccgatgccaa
40 AV	oy dg	Qy Db	qa qa	qa 3	da (	da 	QQ Pp	QY Db	QQ QD	Q7	Q7 Q0	OY Db	da Db	da da	δδ Op	QY	Qy
658 301 703	361 763 415	23 75	883 535	43 95	<b>33</b> 55	3063 3715	3123 3739	3183 3799	43 59	03	3363 3979	3423 4039	3483 4099	3543 4159	3597	57	62
gaaaatctaaacacctagcaaggaaattcacaccaaaggcacagcagacaccgcc	CTACAAACCTTTCAAGTCAAAAAGTCAAAGAAAATGGTGATGATGATAATGACGCTGAC 3 aCcatcaccgtgggtaaagatggtacacaaaacggcaagaccgtcaacactctaaaactc 2	aaaggtgaaaacggtctaacggttgctaccaataaagatggtacggttacctttggcatt 2823 	aacacccaaagcggtcttaaagccggcgacagcaccactctaaacaaagatggcttgtct 2	attaaaaacccgctagtaacgaacaaatccaagtcggtgctgatggcgtgaagtttgcc 294 	aaggttgataagggtaattcaagcactggcattgatggcacaagccgtatcaccaaagat 3003 	caaattggcttactggggctaatggctcacttgataccaccaacccacctaaccaaa	gacaagcttaaagtgggtgaagttgaaattaccaacactggcattaacgcaggtggtaaa 	aagattaccaacattcaatcaggtgatattacccaaaacagcaatgatgctgtgacaggc 	ggtcgggtttatgatttaaaaaccgaacttgaaagcaaaatcaacagtgctgctaaaaca 324 	gcacaaaactcattacacgaattctcagtagcagatgaacaaggtaatcactttacggtt 3303 	agtaaccttactccagttatgacacctcaaagacctctgatgtcatcacctttgcaggt 	gaaacggcattaccaccaaggtaaataaaggtgtggtgcgtgtgggcattgaccaaacc 	aaaggcttaaccacgcctaagctgaccgtgggtaataatagtgcaaaggcattgtcatt 	gacagtaaagatggtcaaaataccatcacaggactaagcaacactctagctaatgttacc	aatgatggtgcaggacacgcactaagccaagggcttgccaatgacaccgacaaa 	acccgtgccgccagcattggtgatgtgctaaacgcaggctttaacttgcaaggcaatggt	
	3302 7 2704 3362	y 2764 5 3416	7 2824 5 3476	7 2884 5 3536	7 2944 5 3596	7 3004 5 3656	y 3064 5 3716	y 3124 5 3740	y 3184 5 3800	y 3244 o 3860	y 3304 b 3920		y 3424 b 4040	y 3484 b 4100	y 3544 0 4160		0 4220
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aatggcaagcccatcaatggcaccgatggcaagccccaaaaagccatc 4794 cctgtgctaagtgccaatgggctggacctgggtggcaaacgcatcagt gctgttgatgataacgatgcggtgaactttaagcagtttaatgaagtt aacaacctaaacaaccaaagtaactcaggtgcgtcattaccctttgtg igtgctaatggtaatgca---accaaatttagtgccgccgatggcgat SCACAGGGGCTAATAAATTTGCCCTAAGCAATCAAGCTACTGGCGAT

gccgatggtaaatactatca cccatcaccgatgcggacaa ggttcatcaagtggtggcaag caaagtccactttgccacaaa aagtccactttgccacaaa ggtaccgtcaacttgtca ggtaccgtcaaagcaaag			5224	gatggtaaatactat	5224	ccgatgcg	5224	agtggtggca	5224	tccactttgccaca	5224	agtetgeecageeta	5224	atgtaggettta	5224	ccgtcaactttg	5224	cgatgagtaa	5224	cttatcaaagccaa	5224	ctaaaagcaggcaa	5224	cccaatgctggta	5224	gtatttaaatccaa	5224	ccaaggcaaaga	5224	aaggtcatcagcaatgtgggtaaaggcacaaaagacaccgacgctgccaatgta 5634	gtaatgataacgct 569	CAACAGTTAAACGAAGTACGCAACTTGTTGGGTCTTGGTAATGCTGGTAATGATAACGCT 5338	acggcaatcaggtaaacattgccgacatcaaaaagacccaaattcaggttcatcatct 5754 	atcaaaqcaqqcacqqtacttqqcqqtaaaggtaat	
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qq	5459 A	TAACGGCGAT 551
0y	875	ttaagcaatgtttgggtcaaaacccaaaagatggcagcagaaaaagcctggttggcagt 5934 
oy o		araacgegagggggggggacaacaatttgaccaacaacaccegagaagccattgacagg 599.
qa	5579 1	CAGACCAACTTTGACCAACAACCCGGAGAAGCCATTGACAGA 563
δλ	995	ataaatgaacaaggtatccgcttcttccatgtcaacgatggcaatcaagagcctgtggta 6054
a à	5639 7	Adreadantes introductions and a second secon
g 8	669	
δλ	6115	17
QQ	5759 (	AGGCCAAGGCAGATGGTGAAGCCGCCGTTGCCATAGGCAGACAAACCCAAGCAGGCAAG 581
Oy to	175	caatccatcgccatcggtgataacgcacaagccacgggcgatcaatccatcgccatcggt 6234
a ò	35	engocaatgtggtaacaggtaagcactctggtgccatcggcgacccaagcactgttaag 629
q	879	TAAG 593
Qy	6295	
qa	5939	CTGATAACAGTTACAGTGTGGGTAATAACAACCAGTTTACCGATGCCACTCAAACGGAT 599
Οy	6355	4.1
qq	5999	TCTTTGGTGTGGGCAATAACATCACGGTGACGGAAAGTAACTCGGTTGCCTTAGGTTCA 605
QY	6415	,
q	6029	ACTOTGCCATCAGTGCAGGCACACACGCAGGCACAGAAGCCAAAAAATCTGACGGCACA 611.
Qy	_	gcaggtacaaccaccacagcaggtgcaacaggtacggttaaaggctttgctggacaaacg 6534
qq	6119	CAGGTACAACCACCACAGCAGGTGCAACCGGTACGGTTAAAGGCTTTGCTGGACAAACG
ΟY	e.	gcggttggtgcggtctccgtgggtgctcaggtgctgaacgccgtatccaaaatgtggca 6594
qq	6119	CGGTTGGTGCGGTCTCCGTGGGTGCTCAGGTGCTGAACGCCGTATCCAAATGTGGCG
Qγ	6595	9
QC	6239	CAGGTGAGGTCAGTGCCACCAGCACCGATGCGTCAATGCTAGCCAGTTGTACAAAGCC 629
Qy	6655	717
qq	6533	CCAAGGCATTGCCAACGCAACCAATGAGCTTGACCATCGTATCCACCAAAACGAAAAT 8339
Οy	6715	77
QQ	6329	AAAGCCAATGCAGGATTTCATCAGCGATGGCGATGGCGTCCATGCCACAAGCCTACATT b41
Οy	6775	cctggcagatccatggttaccgggggtattgccacccacaacggtcaaggtgcggtggca 683
ΩD	6419	CTEGCAGATCCATEGTTACCGGGGGTATTGCCACCCACAACGGTCAAGGTGCGGTGGCA 647
Qy	6835	gtgggactgtcgaagctgtcggataatggtcaatgggtatttaaaatcaatggttcagcc 689
qo	6419	GTGGGACTGTCGAAACTGTCGGATAATGGTCAATGGTATTTAAAATCAATGGTTCAGG
Qy	6895	gatacccaaggccatgtaggggcggcagttggtgcaggtttcacttt 694;
qa	6239	GATACCCAAGGCCATGTAGGGGCGGCAGTTGGTGCAGGTTTTCACTT

us-09-361-619-10.rni

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6460 aaatctgacggcacagcaggtacaaccaccacagcaggtgcaacaggtacggttaaaggc 6519
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1910 AAGGTCAAAATGGTTTAGCTATCGGGGTATCAAGAATTTCCGATAATGGCAAAGTGATTA 1969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 3294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Flehr, Hohbach, Test, Albritton & Herbert
Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Barenkamp, Stephen I.
APPLICANT: Bt. Geme III, Joseph W.
TITLE OF INVORTION: Haemophilus Adhesion Proteins
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & He
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,995
FILING DATE: 24-MAR-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.2%; Score 82.8; DB 1; 1
49.8%; Pred. No. 8.4e-14;
lve 0; Mismatches 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: A 61053/RFT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEEX: 910 277299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3294 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STAIL:
COUNTY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"WEDIUM TYPE: Floppy disk
"WEFR: IBM PC COMPATIBLE
""C"FEM: PC DOS/MS-DOS
                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08409995 Patent No. 5646259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
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Best Local Similarity 49.8°
Matches 244; Conservative
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EDNESS: double
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STRANDEDNESS:
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US-08-409-995-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1790 AAGTGAATAAAGTGGGCAAAACGTGCAGATGCAGTACTGCAATAGCGGCTTCAC 1849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6695 gtatccaccaaaacgaaaataaagccaatgcagggatttcatcagcgatggcgatggcgt 6754
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                                                                                                                                                                                                       TITE OF INVENTION: HARMOPHILUS ADHESION PROTEINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS: ADDRESSEE: Flehr Hobbach Test Albritton & Herbert LLP
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                            APPLICANT: St. Geme, Joseph
APPLICANT: Barenkamp, Stephen J.
TITLE OF INVENTION: HAEMOPHILUS ADHESION PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A-61053-1/RFT/RMS/DAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,995
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/4031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/913,942
FILING DATE: 29-DEC-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US96/4031 FILING DATE: 22-MAR-1996 ATTORNEY/AGENT INFORMATION:
                                                            US-08-913-942-14; Sequence 14, Application US/08913942; Patent No. 6200578; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Vance, Dolly A. REGISTRATION NUMBER: 39,054
REFERENCE/DOCKET NUMBER: A-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2037 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: United States ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                            STREET: Four Embarca
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: DNA
US-08-913-942-14
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                                                         6520 tttgctggacaaacggcggttggtgcggtctccgtgggtgctcaggtgctgaacgccgt 6579
2803 AAAGCTGACGGTACTGCGGATAAAACCAAAGGCGAAGTGAGCAATGATAAAGTTTCTACC 2862
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STREET: Four Embarcadero Center, Suite 3400
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REGISTRATION NUMBER: A-61053-1/RFT/RMS/DAV
REPERBNCE/DOCKET NUMBER: A-61053-1/RFT/RMS/DAV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEPHONE: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: St. Geme, Joseph
APPLICANT: Barenkamp, Stephen J.
TITLE OF INVENTION: HAEMOPHILUS ADHESION PROTEINS
NUMBER OF SEQUENCES: 19
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COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,942
FILING DATE: 29-DEC-1997
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CLASSIFICATION: 514
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/409,995
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/4031
FILING DATE: 22-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-DEC-1997
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: San Francisco
STATE: California
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US-08-913-942-1
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                                         6691 categtatecaceaaaaegaaaataaageeaatgeagggattteateagegatggegatg 6750
                                                                                           3043 GGCAAAGTGAATAAAGTGGGCAAACGTGCAGATGCAGGTACAGGTACAGGATGCATTAGCGGCT 3102
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pred. No. 8.4e-14;
0; Mismatches 237; Indels
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Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08685467
Sequence 1, Application US/08685467
Patent No. 6060059
GENERAL INFORMATION:
APPLICANT: St. Geme III, Joseph W.
APPLICANT: Barenkamp, Stephen J.
TITLE OF INVENTION: HAEMOPHILUS ADHESION PROTEINS
NUMBER OF SEQUENCES:
CORRESPONDENCE S:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herber
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIRE: 94111-4187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A-61053-2/RFT/RMS
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APPLICATION NUMBER: US 08/409,995
FILING DATE: 24-MAR-1995
ATTORREY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPAX: (415) 781-1989
TELEFAX: (415) 398-3249
TELEFAX: 910 277299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-
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al Similarity 49.8%;
244; Conservative (
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Matches 244; Conserva
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6751 gcgtccatgccacaagcctacattcctggcagatccatggttaccggggggtattgccacc 6810
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Patent No. 5646259
GENERAL INFORMATION:
APPLICANT: Barenkamp, Stephen I.
APPLICANT: St. Geme III, Joseph W.
ATTLE OF INVENTION: Haemophilus Adhesion Proteins
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: A-61053-1/RFT/RMS/DAV TELECOMMUNICATION INFORMATION:
TELECHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                        CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US 08/409,995
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/4031
FILING DATE: 22-MAR-1996
ATTORNEY/AGGNT INFORMATION:
NAME: Vance, DOlly A.
REGISTATION NUMBER: 39,054
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52.78;
                                 29-DEC-1997
N: 514
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Matches 195; Conservative
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163..7221
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; LOCATION:
US-08-913-942-3
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US-08-409-995-3
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                                                                                                                                                                                                                   Length 3294;
                                                                                                                                                                                                                   Score 82.8; DB 4; Length 3 Pred. No. 8.4e-14; 0; Mismatches 237; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: St. Geme, Joseph
APPLICANT: BarenKamp, Stephen J.
TITLE OF INVENTION: HAEMOPHILUS ADHESION PROTEINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08913942 Patent No. 6200578
                                                                                                                                                                                                                   1.2%;
                                                     LENGTH: 3294 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA
US-08-913-942-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States ZIP: 94111-4187
                                                                                                                                                                                                                 Query Match
Best Local Similarity 49.8'
Matches 244; Conservative
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
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Query Match
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   ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400 CITY: San Francisco STATE: CA COUNTRY: USA
                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,995
FILING DATE: 24-MR-1995
CLASSIFICATION:
ATTORNEY/AGRNT INFORMATION:
NAME: S11va M. 38,304
REGISTRICATION NUMBER: 38,304
REGISTRICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEX: (415) 398-3249
TELEX: (415) 398-3249
TELEX: G10 277299
SEQUENCE CHARACTERICATICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 69.8; DB 1;
Pred, No. 9.1e-10;
0; Mismatches 137;
                                                                                                                            MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS OSTWARE: Patentin Polocies
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Best Local Similarity 52.6%;
Matches 152; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 5788 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                        ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
CORRESPONDENCE ADDRESS:
                                                                                                       94111-4187
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US-08-409-995-3
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3699 tategatggcaatgccaccaccgctaaggtgacctatgatgacacaagcaaaaccagtaa 3758
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC COMPATIBLE
COMPUTER: TBM PC POS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 22-JUL-1996
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION NUMBER: US 08/409,995
FILING DATE: 24-MAR-1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.0%; Score 69.8; DB 3;
52.6%; Pred. No. 9.1e-10;
tive 0; Mismatches 137;
                                                                                                                                                                                                                                                                                                           A-61053-2/RFT/RMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 38,304
REGISTRATION NUMBER: 38,304
REPERENCE/POCKET NUMBER: A-61(
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 398-3249
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 5738 base.pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)
US-08-685-467-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 52.63
Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Surrante
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US-08-478-370-4
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6689 accatogtatocaccaaaacgaaaataaagccaatgcagggatttoatcagcgatggoga 6748
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Pred. No. 2.6e-06;
0; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: DENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 14, Application US/08232463; Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                ; Sequence 4, Application US/09377155; Patent No. 6197312; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.8%;
Best Local Similarity 51.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Ver. 2.0
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US-09-377-155-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-232-463-14/c
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SEQ ID NO 4
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                                                                 COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,370
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 58.4; DB 4;
Pred. No. 8.7e-07;
0; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 58.4; DB 1;
Pred. No. 6.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: PEAK, Ian Richard Anselm APPLICANT: PEAK, Ian Richard Paul APPLICANT: JENNINGS, Michael Paul APPLICANT: JENNINGS, Michael Paul APPLICANT: MOXON, E. Richard TITLE OF INVENTION: NOVEL SURFACE ANTIGEN FILE REFERENCE: 065064/0128 US/09/377,155 CURRENT FILING DATE: 1999-08-19 PRIOR APPLICATION NUMBER: PCT/AU98/01031 PRIOR PILING DATE: 1998-12-14 PRIOR FILING DATE: 1998-12-12 NUMBER: OF SEQ ID NOS: 33 NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-502
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/09377155
Patent No. 6197312
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                   TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.8%;
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Matches 59; Conservative
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Best Local Similarity 52.0
Matches 131; Conservative
                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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; LOCATION: (1)..(1794)
US-09-377-155-12
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US-08-478-370-4
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                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
STOPPERSSEE: FOLEY F. G.
STOPPERSSEE: FOLEY F. G.
                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
APPLICATION NUMBER: US/07/935,313
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENTY Stephen A.
REGISTRATION NUMBER: 29,768
RECISTRATION NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1000PMATION:
TELEFAX: (703)683-4109
                                                                                                                                                  ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road,
CCITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                             CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-029
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
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STRANDEDNESS: single
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US-08-232-463-14
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Pred. No. 7.6e-06;
0; Mismatches 123; Indels
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Sequence 10, Application US/09377155

Patent No. 6197312

GENERAL INROMATION:
GENERAL INROMATION:
APPLICANT: DEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MONGN, E. Richard
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR FILING DATE: 1998-12-14
                                                                                                                                                           APPLICANT: PEAK, IAN Richard Anselm APPLICANT: PEAK, IAN Richard Anselm APPLICANT: JENNINGS, Michael Paul APPLICANT: JENNINGS, Michael Paul APPLICANT: JENNINGS, Michard Anselm STILE OF INVENTION: NOVEL SURFACE ANTIGEN FILE OF INVENTE: 065064/0128 CURRENT APPLICATION NUMBER: US/09/377,155 CURRENT FILING DATE: 1999-08-19 PRIOR APPLICATION NUMBER: PCT/AU98/01031 PRIOR FILING DATE: 1998-12-14 PRIOR FILING DATE: 1997-12-12 PRIOR FILING DATE: 1997-12-12 NUMBER OF SEQ ID NOS: 33 SOFTWARE: Patentin Ver. 2.0
1: ::: :: :: :: :: |||| | 1089 RRRRRRRRRRRRRRRRATCG 1063
                                                                                                                      Sequence 18, Application US/09377155
Patent No. 6197312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Neisserla meningitidis
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Best Local Similarity 51.2%;
Matches 129; Conservative (
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; LOCATION: (1)..(1767)
US-09-377-155-18
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PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 1776
TYPE: DNA
ORGANISM: Neisseria meningitidis
FRATURE:
MAME/KEY: CDS
LOCATION: (1)..(1773)
US-09-377-155-10
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Search completed: September 12, 2001, 13:00:35 Job time: 1257 sec

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        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                      OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Sequence:
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gb\_htc:\* em\_gss\_fun:\* em\_gss\_hum:\*

gb\_est110:\*

em\_gss\_hum5:\* em\_gss\_hum6:\* em\_gss\_hum7:\*

em\_gss\_hum2:\* em\_gss\_hum3:\* em\_gss\_hum4:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

JOURNAL Unpublished (1999) COMMENT Other_GSSs: Sheared DNA-46J23.TF Contact: Najib M. El.Sayed Department of Eukaryotic Genomics	The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0200 Email: nelsayed@tigr.org Email: nelsayed@tigr.org Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared DNA library constructed at TIGR. Clones will be available for distribution through ATCC. Sheared DNA end sequences search page: http://www.tigr.org/tdb/mdb/tbdb/.	<del></del>	Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared tog qive a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University press, 1999)."	Query Match  Query Match  Best Local Similarity  44.88; Pred. No. 6.2e-06;  Matches 248; Conservative  O; Mismatches 306; Indels  O; Gaps  O; 1315 agcggtggtttaacctttaccccaacaatgcaacacagacaaaccgtctatggc 1374.		Oy 1555 aataacaccattggtggtagcaataaacaaatccaagtcggtgctgatggcattaaattt 1614
Result Query Description	1 64.4 0.9 641 236 AQ946120 AQ946120 3 59.8 0.9 806 221 CNS04AEE AL281759 4 58 0.9 822 219 CNS0073W AL06784 AL06784 AL06784 AL076451 S 55.6 0.8 1101 219 CNS00175 AL0767874 AL076451 S 54.8 0.8 8101 219 CNS00175 AL0767874 AL0767874 S 53.6 0.8 895 219 CNS0071A AL0767874 AL0767874 S 53.6 0.8 894 245 AZ55059 AZ550	53.4 0.8 884 219 00800600 53.2 0.8 849 245 A254009 52.6 0.8 537 107 A0039635 52.6 0.8 537 107 A003415 51.8 0.7 861 219 CNS0075A 51.4 0.7 1183 220 CNS02GK 51 0.7 681 221 CNS02CK 51 0.7 568 219 CNS02EOD	20 50.0 0.7 1204 219 CNS010E2 ALL002222 2 50.0 0.7 1204 24 59 0.7 890 245 AZ530768 AZ540Z AZ550Z AZ540Z AZ550Z AZ540Z AZ550Z AZ540Z AZ550Z AZ540Z AZ550Z AZ540Z AZ550Z AZ550Z AZ550Z AZ550Z AZ540Z AZ550Z AZ	8 0.7 1101 219 CNS0100X 8 0.7 1101 219 CNS0100X 2 0.7 791 219 CNS006XT 2 0.7 791 219 CNS006XF 2 0.7 900 245 A5549980 2 0.7 1101 219 CNS006XF 6 0.7 1101 219 CNS006XF 6 0.7 546 156 CZ2974 6 0.7 546 195 CNS006XF 4 0.7 939 219 CNS0010I 2 0.7 500 107 AU08474	ALIGNMENTS	LOCUS LOCUS LOCUS LOCUS Sheared DNA-46J23.TR Sheared DNA Trypanosoma brucel genomic clone Sheared DNA-46J23.TR Sheared DNA Trypanosoma brucel genomic clone ACCESSION A0946120

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Tetracdon nigroviridis.
Tetracdon nigroviridis.
Eukaryota, Metazca; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Neoteleostel;
Actinopterygii; Neopterygii; Percomorpha; Tetracdontiformes;
Tetracdontidae; Tetracdon.
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Barin, W. and Weissenbach, J. Tanate provided by genome wide analysis using
Human gene number estimate provided by genome wide analysis using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted.(12-APR-2000) to the EMBL/GenBank/DDBJ databases Submitted.(12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a lar scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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t 40 others
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1795 gatcaaaagatcagtaatgttaaagatgcaacggacgataccgatgcagtcacttataaa 1854
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42.9%; Pred. No. 3.4e-05;
tive 23; Mismatches 282;
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/note="Genoscope
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Direct Submission

Submitted (02-JuN-1999) Genoscope - Centre National de Sequencage:
Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr
Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila malanogaster genome using these BACs. For further information please see http://www.fruitily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Piteter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo.

NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and bx to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers

Location/Qualifiers
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                                                                                                                                                                                                                                            1624 aatgitaaigiatcaaaigccgcaaaailcggcactacicgtaitaccgaagaggaait 1683
                                                                                                                                                                                                                                                                                                                                                              1684 ggcttigctgatgctgatggtaaagttgataaaagtcaccatatttggataaaaacaa 1743
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1507 aagstaaaagttggcaacagcacctaaacaacggtggcttgactgttaataacaccatt 1566
                                                                                                                 ggtggt---agcaataaacaaatccaagtcggtgctgatggcattaaatttgccgatgtg 1623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1804 atcagtaatgttaaagatgcaacggacgataccgatgcagtcacttataaacagcttaa 1862
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

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Tetraodon nigroviridis.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.

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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fishe
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
                                                                                      845 МИСИИАСМИАМСИМАСИМИАМАМИМИМИМИАМИАМОАСМАМИМАСАСМСАМИМИСИМИМ
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/organism="Tetraodon nigroviridis" /db\_xref="taxon:99883"

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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Determination of this BAC-end sequence was carried out as part of collaboration with the Barkeley Drosophila Genome Project (BDGP).
The BDCP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/clone_lib="G"
/note="Genoscope s
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Sheared DNA-42E21.TF Sheared DNA Trypanosoma brucei genomic clone
Sheared DNA-42E21, DNA sequence.
please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, Cancer Genetics at the Rosophila DNA provided by the BDGP from the ECORI digestion of Drosophila DNA provided by the BDGP from the ECORI digestion of Drosophila DNA provided by the BDGP from the 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 1 and 
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/organism="Trypanosoma brucei"
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/strain="Trypanosoma brucei"
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/db_xref="taxon:5691"
/clone_"Sheared DNA-42E21"
/clone_lib="Sheared DNA"
/note="vector: pUC18: Site_1: Smal; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb).
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb).
The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C.
(Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing Press, Decical Maproach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TiGR. Clones will be available for
bistribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/tbb/mdb/tbdb/.
Seq primer: M13-Forward
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45.2%; Pred. No. 0.0025;
Live 0; Mismatches 242; Indels 0;
                                                                                                                                                                  Kinetoplastida; Trypanosomatidae;
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• Web: www.genoscope.cns.fr.

• Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley prosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: on by sp, the same strain used for the BDGP's pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or fillters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                     CNSO071A 895 bp DNA GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR14B09 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
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Pterzyota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/clone_llb="betramoeba histolytica Sheared DNA"
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/rote="vector: PHOS1; Site_1: Bst I; Constructed at The
/rote="vector: PHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica: a
method dor isolate identification. Exp. Parasitol.
/rote="vector phosis of the phosis of tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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Eukaryota; Entamoebladae; Entamoeba.

I (bases 1 to 884)

Loftus, B., Van Aken, S. and Fraser, C.

Determination of clone end sequences from Entamoeba histolytica
HM1: IMSS sheared DNA library
Unpublished (2000)

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2560 accgataacgatgcccttgttaacgccaaagacatcgccgaaaatctaaacaccctagcc
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No. 0.0058;
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High quality sequence stop: 860.
Location/Qualifiers
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Direct Submission

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Submistated (02-210N-1999) Genoscope - Centre National de Sequencage :
Web : www.genoscope.cns.fr)

Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila The BDGP is constructing a physical map of the Drosophila please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster BAC library was prepared by the BDGP Drosophila NV. The library is named RECI-99 and was constructed by partial EcorI digestion of Drosophila DNA provided by the BDGP from the Isogenic strain v2: on bw sp, the same strain used for the BDGP's pland EST library is named RECI-99 and was constructed by larany pland EST library is nore detailed description of the library and how to order individual BAC clones, the entire library, or filters for hypridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster genome survey sequence T7 end of BAC # BACR14N11 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                        1759 gitaaaattaccaaagacagiggcaltaaigcaggigatcaaaagaicagiaaigitaaa 1818
                                                                                                                                                                        1639 aatgeegeaaaatteggeactaetegtattaeegaaggaaattggetttgetgatget 1698
                                                                                                                                                                                                                                                                                                                                                   218 AATGATGATGATAATGATGATGACAATAATGATGATGACAATGATGATAATGATGAA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                338 AATTCAGTAACTAATTCTAGTAATATAAATACAGCACGAAATAATAATAATACATATATA 397
                                                                                                                                                                                                                278 GATTCCAATCTTCATGGTAGTTCTTCTAATATGCTAAATATTATAAACAGCGGTGATAAT
1459 aataaagctggtacagttgatgaaaacaaaccttatcttgataaagacaagctaaaagtt
                                                                                                                         ggcaacagcacctaaacaacggtggcttgactgttaataacaccattggtggtagcaat
                       Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins.
Pteryota; Metazoa; Arthropoda; Tracheata; Brachycera;
Pteryota; Bootera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:722"
/clone_lib="RECI-98"
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Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
'S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library Gene 200 (1:2), 149-156 (1997).
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1. (bases 1 to 500)

Watanabe,J. Sasaki,M., Suzuki,Y. and Sugano,S.
FULL-malaria: a database for a full-length enriched cDNA library from human malaria parasite, Plasmodium falciparum
Nucleic Acids Res. 29 (1), 70-71 (2001)
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AUG88119 Sugano Malaria CDNA library Plasmodium falciparum CDNA
clone XPFn6549, mRNA sequence.
AUG88119
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                                                                                                                                                                                                                                                                                                         1682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1743 acttcaagtgggtggtgttaaaattaccaaagacagtggcattaatgcaggtgatcaaaa 1802
                                                                                                                              1506 caagetaaaagttgggaacagcacctaaacaacggtggettgactgttaataacaccat 1565
                                          tggtggtagcaataaacaaatccaagtcggtgctgatggcattaaatttg---ccgatgt 1622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            589 AGCTCGAGCTGATGGAAATGAAAAAAAAATTGAGGATATTACTCAGGAACAGAATGGATG 648
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                                                                                  529 IGAATIGGCIGATGTTAAAATTAAAATTAGACACAACTCAACAAGAACTGGTIGCTACTCA
                                                                                                                                                                                                                                                             TGCTGGATTACAACAAGAATTAAAAAATAAAGAAGAAGAAATCATAACTGAAACAGATAA
                                                                                                                                                                                                                                                                                                            1623 gaatgttaatgtatcaaatgccgcaaaattcggcactactcgtattaccgaagaggaaat
                                                                                                                                                                                                                                                                                                                                                   349 AAATAAAAAAGATGACATTCTTGAATTACAAGCAATGGTATCAAATCTTAAACAAAATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Institute of Medical Science
The University of Tokyo, Department of Parasitology
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Tel: 81.3-5449-5378
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/dlone="xPEn6549"
/clone=lib="sugano Malaria cDNA library"
/dev_stage="erythrocytic stage"
17. c 86 g 163 t
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46.0%; Pred. No. 0.0052;
tive 0; Mismatches 211; 1
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    214;
    Mismatches
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Plasmodium falciparum
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Best Local Similarity 46.0
Matches 180; Conservative
         Conservative
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           Matches 195;
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Eukaryota: Entamoebidae; Entamoeba.

E (bases 1 to 905)
S Loftus, B., Van Aken,S. and Fraser,C.
Determination of clone end sequences from Entamoeba histolytica
HM1:MSS sheared DNA library
L Unpublished (2000)
Contact: Brendan J Loftus
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 cools
Email: bloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
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/clone_lib="Entanceba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barall, Oxford University Press, 1999)."
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ENTEV58TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
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                                                                                                                                                            Length 849;
                                                                                                                                                                                                       Indels
                                                                                                                                                            DB 245;
                                                                                                                                                          0.8%; Score 53.2; DB 245;
50.4%; Pred. No. 0.0073;
Ive 0; Mismatches 128;
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High quality sequence start: 100
High quality sequence stop: 872.
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                                                                                                                                                                             ilarity 50.4%;
Conservative
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nes 130;
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Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ546009 849 bp DNA GSS 14-NOV-2000
ENTFW53TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
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/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
                                                                  DB 219; Length 884;
                                                                                                             Indels
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                0.8%; Score 53.4; DB 219;
ilarity 17.6%; Pred. No. 0.0066;
Conservative 114; Mismatches 101;
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Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 849)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences free that IMSS sheared DNA library
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High quality sequence stop: 796.
Location/Qualifiers
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Contact: Brendan J Loftus
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Seq primer: M13-Forward
Class: shotgun
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615 CMAMAAMAAAMCCMCMCCC 595
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Dictyostellum discoideum.
Dictyostellum discoideum.
Dictyostellum discoideum
Eukaryota, Mycetozoa; Dictyostellida; Dictyostellum.

[ (bases 1 to 537)

Morio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M., Yoshino, R., Matra, B.N., Pi, M., Satto, T., Takemoto, K., Yasukawa, H., Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.
The Dictyostellum developmental conn. project: generation and analysis of expressed sequence tags from the first-finger stage of
77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + 1 method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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university of Taukuba
3-3-10 Ten-nodal, Tsukuba, Ibaraki 305, Japan
Bmail: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoideum cDNA project in Japan',
Iccation/Qualifiers
1. 537
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/db_xref="taxon:44689"
/clone="SLE877"
/clone_lib="Dictyoste1
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ORIGIN

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Dictyostellum discoideum.
Dictyostellum discoideum.
Dictyostellum discoideum
Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
1 (bases 1 to 540)
Morio, T., Urushihara, H., Salto, T., Ugawa, Y., Mizuno, H., Yoshida, M., Yoshino, R., Mitra, B.N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H., Williams, J., Maeda, M., Takeuchi, I., Ochial, H. and Tanaka, Y.
The Dictyostellum developmental cDNA project: generation analysis of expressed sequence tags from the first-finger stage of development.
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AU034415 Dictyostellum discoideum SL (H.Urushihara) Dictyostellum
discoideum cDNA clone SLCB43, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Dictyostellum discoideum SL (H.Urushihara)"
/dev_stage="slug"
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                                                                            gataaagacaagctaaaagttggcaacagcaccctaaacaacggtg-----gcttgact 1551
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                                           Gaps
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University of Tsukuba
3.3.10 Pen-nodai, Tsukuba, Ibaraki 305, Japan
Email: G402huGaskura.cc.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoldeum cDNA project in Japan'
                                       9
    537;
  Length
                                         Indels

    . 540
    /organism="Dictyostelium discoideum"

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  Score 52.6; DB 107;
Pred. No. 0.0088;
                                         0; Mismatches 239;
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/clone="SLC843"
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99156227
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0.8%;
nilarity 46.4%;
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Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information plaase see http://www.fruitfly.org The BDGP prosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the lisogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library
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Pterzygota: Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 861)
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                                                                                              Score 52.6; DB 107; Length 540;
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0; Mismatches 239; Indels 6;
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and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 861;
                                                                                                                                                                               others
                                                                                                                                                                                                                                                                                 Indels
                                                                                  /organism="Drosophila melanogaster"
/db.xref="Laxon:7227"
/clone_lib="RPCI-98"
/clone="BACRI4D11"
                                                                                                                                                                             175
                                                                                                                                                                                                                                                 DB 219;
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32.4%; Pred. No. 0.018;
vative 63; Mismatches 1
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AAW56322 AAW56319 AAB23858 AAR99392 AAR99394

AAW30292 AAY75097 AAW30291

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AAR63505 AAB01846 AAR41724 AAB15945 AAR63506

AAW30294

Non-typeable Haemo High molecular wei

Haemophilus influe

H. pylori GHPO 148 Helicobacter polyp

faeca

Enterococcus Enterococcus Enterococcus

AAR41728 AAB01848 AAW98828 AAY00136 AAY00136 AAY00140 AAY10142 AAR41731 AAR41731 AAR41731

Protein sequence t H. pylori HPN165 p Haemophilus influe

AAB46351

AAB01844

ALIGNMENTS

Klein MH

Υ, Yang

Bordetella pertuss Filamentous haemag

High molecular wei

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New nucleic acid encoding Moraxella catarrhalis outer membrane protein, useful in protective vaccines and for diagnosis
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200kDa outer membrane protein; antibacterial; immunogenic; infection;
otitis media; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            catarrhalis les1 200kDa protein SEQ ID NO:11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moraxella catarrhalis.
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N-PSDB; AAF59105.
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AAB69136;
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    RESULT
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M. catarrhalis str
M. catarrhalis str
Moraxella 200 kDa
M. catarrhalis M56
Haemophilus adhesi
Haemophilus influe
Haemophilus influe
Haemophilus influe
Haemophilus influe
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(without alignments)
1781.835 Million cell updates/sec
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                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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The present invention describes an isolated and purified nucleic acid (I) that encodes a 200 kDa outer membrane protein of Moraxella catarrhalis. The 200 kDa outer membrane protein (I) has antibacterial activity and can be used in vaccines. (II), and its truncated versions, are used as can be used in vaccines. (II), and its truncated versions, are used as infections, particularly otitis media in humans. (II) is also used as antiection in particularly office media in humans. (II) is also used as a netion in immunoasays for detecting specific antibodies (Ab), and to artical as probes for recombinant production of (II) and its generate Ab. (I) are used as probes for identifying/Choining 200 kDa protein fragments are used as probes for identifying/Choining 200 kDa protein (I) makes possible production of large amount of recombinant immunogens. (I) makes possible production of large amount of recombinant immunogens. (I) makes possible production of large amount of recombinant immunogens. Characts the Escherichia coll host. The present sequence represents the containing and the present invention. English 5A-Y; 247pp; Claim

2314 AA Sequence

ö 480 480 420 360 300 180 180 Gaps 9 VNVNVSNAAKFGTTRITEEEIGFADADGKVDKKSPYLDKKQLQVGGVKITKDSGINAGDQ TASEKVTVGSGUNTAELQSGGLTFTPTTNASTDKTVYGTDGLKFTDNSNTALEDTTRITK DKIGFSNKAGTVDENKPYLDKDKLKVGNSTLNNGGLTVNNTIGGSNKQIQVGADGIKFAD SNIKSSKATGNGLFSIGSSTIKRKIINVGAGYEDTDAVNVAQLKAVENLAKRQITFKGDD NGTGVKKKLGETLTIKGGETQADKLTDNNNIGVVTDNNTGLKVKLAKNLSGLETVSTKNL EKGYTIAIGSNAQAINYGALALGADTRVDLDYGIALGYGSQILNNNNNNKAYVPEGNG MNHIYKVIFNKATGTFNAVAECAKSHSGGSSSSTAGQVGSSPVIRLTRVATLAILVIGAT Length 2314; .. O 0; Indels DB Score 11694; Pred. No. 0; ; Mismatches .; 100.0%; ilarity 100.0%; Conservative 0, Best\_Local Similarity Matches 2314; Conserv Match 481 541 601 501 661 361 421 121 481 301 361 181 241 301 \_ 181 Н 61 121 121 Query g δy Ob ò Db οy S G οŽ do Oy Ob g ô QQ ò ga ŏ õ g ö q à

1080 960 NPNAGKGSTGDAVALNNLSKAVFKSKDGTTTTTVSSDGISIQGKDNSSITLSKDGLNVGG TFAGDTGTTAKKLGETLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAG PITDADKLANLAAHGKPLDAGHQVVASLGGNSDAITLTNIKSTLPQIDTPNTGNANAGQA KGASQASSSASYVDADGNKVIYDSTDKKYYQVNDKGQVDKNKEVAKDKLVAQAQTPDGTL RAASIGDVLNAGENLQGNGEAVDEVSTYDTVDFIDGNATTAKVTYDDTSKTSKVVYDVNV DNKTIEVTSDKKLGVKTTTLTKTSANGNATKFSAADGDALVKASDIATHLNTLAGDIQTA KDKLKVGEVEITNTGINAGGKKITNIQSGDITONSNDAVTGGRVYDLKTELESKINSAAK TAQNSLHEFSVADEQGNHFTVSNPYSSYDTSKTSDVITFAGENGITTKVNKGVVRVGIDQ 1141 TKGLTTPKLTVGNNNCKGIVIDSKDGQNTITGLSNTLANVTNDGAGHALSQGLANDTDKT SIKNPASNEQIQVGADGVKFAKVDKGNSSTGIDGTSRITKDQIGFTGANGSLDTTKPHLT ETITVGKDGTQNGKTVNTLKLKGENGLTVATNKDGTVTFGINTQSGLKAGDSTTLNKDGL NIIRGLSPTLPSITNAGGVRTTEQGNTITSDEDKSKAASIGDILNTGFNLKNNSNSVGFV 1741 1741 1801 1561 1621 1621 1681 1681 1561 1441 1441 1501 1261 1321 1321 1381 1381 1501 1141 1201 1201 1261 1081 961 961 1021 841 901 781 781 901 721 721 9 ò g g à q οy q οy Dp QY qq ç ò Dp οý οχ Q ΟŸ g g οy q ŏ g S Ωp ŏ QΩ ò oy oy

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                                                                                                                                                                                                                                                                                                                               Moraxella catarrhalis strain Q8; major outer membrane protein;
200kDa outer membrane protein; antibacterial; immunogenic; infection;
otitis media; detection.
GIANATNELDHRIHONENKANAGISSAMAMASMPQAYIPGRSMVTGGIATHNGOGAVAVG
                                                                                                                                   NSYSVGNNNQFIDATQTDVFGVGNNITVTESNSVALGSNSAISAGTHAGTQAKKSDGTAG
                                                                                                                                                                TTTTAGATGTVKGFAGQTAVGAVSVGASGAERRIQNVAAGEVSATSTDAVNGSQLYKATQ
                     KVISNVGKGTKDTDAANVQQLNEVRNLLGLGNAGNDNADGNQVNIADIKKDPNSGSSSNR
                                                                                                        KADGEAAVAIGRQTQAGNQSIAIGDNAQATGDQSIAIGTGNVVTGKHSGAIGDPSTVKAD
                                                                            AAGQTNYLTNNPAEAIDRINEQGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQA
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                                                                                                                                                                                                                                                                                                                   catarrhalis strain Q8 200kDa protein SEQ ID NO:9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid encoding Moraxella catarrhalis
useful in protective vaccines and for diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                  (CONN-) CONNAUGHT LAB
                                                                                                                                                                                                                                                                                                                                                            Moraxella catarrhalis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig
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38; that encodes a 200 kba outer membrane protein of Moraxella catarrhalis. The 200 kba outer membrane protein (II) has antibacterial activity and can be used in vaccines. (II), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarrhalis infections, particularly otitis media in humans. (II) is also used as antigen in immunoassays for detecting specific antibodies (Ab), and to generate Ab. (I) are used for recombinant production of (II) and its fragments are used for recombinant production of (II) and its genes from other strains, and for idagnostic detection of M. catarrhalis. (I) makes possible production of large amount of recombinant immunogens. Expression of truncated versions of (II) reduces toxicity of the protein M. catarrhalis strain Q8 200kDa protein, which is given in the exemplification of the present invention. 410 460 519 234 292 294 353 401 583 621 681 Gaps 61 LNGSAYAQN-NSKIAFGTTGNNDN----ASASNEASIAIGSLAKAHANQAIAIGGSKPD 114 9 ngdlvdssgnittptynisvkttklnsngtsgnnkfsvsnahdnnslvtakdladylnkv 1 mnhiykvifnkatgtfmavaeyakshstgggscatggvgsvrtlsfariaalavlvigat 344 KAVENLAKRQITFK--GDDNGTGVKKKLGETLTIKGGETQADKLTDNNNIGVVTDNNTGL KVKLAKNLSGLETVSTKNLTASEKVTV-GSGNNTAELQSGGLTFTPTTNASTDKTVYGTD GLKFTDNSNT-ALEDTTRITKDKIGFSNKAGTVDENKPYLDKDKLKVGNSTLNNGGLTVN NTIGGSNKQIQVGADGIKFADVNVNVSN-AAKFGTTRITEEEIGFADADGKVDKKSPYLD 1 MNHIYKVIFNKATGTFMAVAECAKSHSGGSSSSTAGQVGSSPVIRLTRVATLAILVIGAT 115 PRNQAANQKAGSHAKGKESIAIGGDVLAEGDASIAIGSDDLYLDRN-STNSKYPNGLLST 174 LIQNHTVLRQIRDS-NGSQKYRRTAAEGHASTAVGAMAYAKGHFANAFGTRSTAEGNYSL 233 AVGLTAKAEKGYTIAIGSNAQAINYGALALGADTRVDLDYGIALGYGSQILNNNNNNNK AYVPEGNGSNIKSSKATGNG----LFSIG-----SSTIKRKIINVGAGYEDTDAVNVAQL QQDADGALQSFSIR--DEKGQEFTISNLYSNGNTPNTFETITFAGENGISISNDIAKGKV DB 22; Length 2053; 250; Indels 481; KKQLQVGGVKITKDSGINAGDQKISNVKDATDDTDAVTYKQLK----Query Match
61.7%; Score 7219.5;
Best Local Similarity 64.1%; Pred. No. 0;
Matches 1553; Conservative 140; Mismatches 

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A X X X X X X X X X X X X X X X X X X X	27-JUL-1999; 99US-0361619. (CONN-) CONNAUGHT LAB LTD. Loosmore SM, Sasaki K, Yang Y, Klein MH;
XX DR XX TP	WPI; 2001-159722/16. N-PSDB; AAF59102, AAF59103. New nucleic acid encoding Moraxella catarrhalis outer membrane protein

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generate Ab. (1) are used for recombinant production of (11) and its fragments are used as probes for identifying/cloning 200 kba protein genes from other strains, and for diagnostic detection of M. catarrhalis. (1) makes possible production of large amount of recombinant immunogens. Expression of truncated versions of (11) reduces toxicity of the protein M. catarrhalis strain 4223 genomic 200kDa protein, which is given in the exemplification of the present invention. The present invention describes an isolated and purified nucleic acid (I that encodes a 200 kDa outer membrane protein of Moravatla catarrhalis. The 200 kDa outer membrane protein (II) has antibacterial activity and can be used in vaccines. (II), and its truncated versions, are used as immunosenic compositions and vaccines to protect against M. catarrhalis infections, particularly office media in humans. (II) is also used as antigen in immunoassays for detecting specific antibodies (Ab), and to diagnosis for in protective vaccines and Claim 1; Fig 3A-W; 247pp; English. useful 

2047 AA; Sequence

48; 643 357 407 464 LNGSAYAQ--NNSKIAFGTTG---NNDNASASNEASIAIGSLAKAHANQAIAIGGSKPDP 115 RNQAANQKAGSHAKGKESIAIGGDVLAEGDASIAIGSDDLYLDRNSTNSKYPNG-LLSTL 174 9 |:|||||| : || || | |sgsayaqkkdtkhiaigeqnqprrsgtakadgdraiaigenanaqggqaiaigssnktv 1 MNHIYKVIFNKATGTFMAVAECAKSHSGSSSSTAGQVGSSPVIRLTRVATLAILVIGAT inghavlkeirsskdndvkyrrttasghastavgamsyagghfsnafgtrataksaysla DEKGQEFTISNLYSNGNTPN - - TFETITFAGENGISISNDIAKGKVKVGIDPINGLTTPK IQNHTVLRQIRDSNGSQ-KYRRTAAEGHASTAVGAMAYAKGHFANAFGTRSTAEGNYSLA VGLTAKAEKGYTIAIGSNAQAINYGALALGADTRVDLDYGIALGYGSQILNNNNNNKA TDNS-NTALEDTTRITKDKIGFSNKAGTVDENK-PYLDKDKLKVGNSTLNNGGLTVNNTI GGSNKQIQVGADGIKFAD-VNVNVSNAAKFGTTRITEEEIGFADADGKVDKKSPYLDKKQ LQVGGVKITKDSGINAGDQKISNVKDATDDTDAVTYKQ----LKQVQQDADGALQSFSIR YVPEGNGSNIKSSKATGN---GLFSIGSSTIKRKIINVGAGYEDTDAVNVAQLKAVENLA NLSGLETVSTKNLTASEKVTVGSGNN-TAELQSGGLTFT-PTTNA-STDKTVYGTDGLKF dagnkkisnlakgssandavtieglkaak--ptlnagagisvtpteisvdaksgnvtapt 351 K-RQITFKGDDNGTGVKKKLGETLTIKGG-ETQADKLTDNNNIGVVTD-NNTGLKVKLAK Indels 471; DB 22; Query Match 56.4%; Score 6593.5; DB 22 Best Local Similarity 60.7%; Pred. No. 2.6e-283; Matches 1466; Conservative 149; Mismatches 330; 415 61 61 180 408 475 116 234 294 465 523 529 587 638 ŏ g à g q ŏ q ò g ò Q ò g ò a ογ g δ g ð ò à

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1221 1281 983 924 eeddddanaitv-akdttknagavsilklkgkngltvatk-kdgtvtfglsqdsgltigk 701 DKSKAASIGDILNTGFNLKNNSNSVGFVSTYNTVDFIDGNATTAKVTYDETNQTSKVTYD VNVDEKTIELTG-DNGKTNKIGVKTTTTTTNANGK-ATNF--STTDNDALVNAKDIAEN LNTLAKEIHTTKGTADTALQTFKVKK - - - - DGATDDETITVGKDGTQNGKTVNTLKLKGE DKGNSSTGIDGTSRITKDQIGFTGANGSLDTTKPHLTKDKLKVGEVEITNTGINAGGKKI VDFVSTYDTVDFIDGNATTAKVTYDDTSKTSKVVYDVNVDNKTIEVTSDKKLGVKTTTLT KTSANGNATKF --- SAADGDALVKASDIATHLNTLAGDIQTAKGASQASSSASYVDADGN KKQGINEDNAFIKGLENAAKDTKTKNAAVTVGDLNAVAQTPLTFAGDTGTTAKKLGETLT KANTPVLSANGLDLGGKRISNIGAAVDDNDAVNFKQFNEVAKTVNNLNNQSNSGASLPFV DAGHQVVASLGGNSDAITLTNIKSTLPQIDTPNTGNANAGQAQSLPSLSAAQQSNAASVK stlnndgltvkdtneg--iqvgangikftnvngsnpgtgiantaritrdkigfagsdgav --- IRGLSPILPSITNAGGVRTTEQGNTITSDE dtnkpyldqdklqvgnvkitntginaggkaitglsptlpsiadgss-rnielgnti-qdk NGLTVATNKDGTVTFGINTQSGLKAGDSTTLNKDGLSIKNPASNEQIQVGADGVKFAKV-1044 TNIQSGDITQNSNDAVTGGRVYDLKTELESKINSAAKTAQNSLHEFSVADEQGNHFTVSN PYSSYDTSKTSDVITFAGENGITTKVNKGVVRVGIDQTKGLTTPKLTVGNNNGKGIVIDS 1164 KDGQNTITGLSNTLANVTND-GAGHALSQG-LANDTDKTRAASIGDVLNAGFNLQGNGEA VTDANGKPINGTDGKPQKAIKGADGKYYHANANGVPVDKDGKPITDADKLANLAAHGKPL 813 936 1053 1104 1161 1221 1282 1340 1458 1518 1519 1578 1579 1639 702 094 869 1222 1399 1459 1592 723 925 ρp g ò g Db g οy D ŏ g δ 셤 qq ò qq ò g ŏ q ò δ 셤 δ g ŏ 9 QΥ g q à g ò ò ò Q Q

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                                                                                                                                                                           Moraxella catarrhalis strain 4223; major outer membrane protein; 200kpa outer membrane protein; antibacterial; immunogenic; infection; otitis media; detection.
                                                                         1611
                                                                                             GNVLIKAKDGKFYKADDLMPNGSLKAGKSASDAKTPTGLSLVNPNAGKGSTGDAVALNNL 1818
                                                                                                                                                                                                                                                                                                                                                                  M. catarrhalis strain 4223 lambdaEMBL3 clone 200kDa protein SEQ ID
                                                                                                                                                                                                                         1972 kanagissamamasmpqaylpgrsmvtgglathngqgavavglsklsdngggwvfkingsa
                                                                                                                                                                    QSIAIGDNAQATGDQSIAIGTGNVVTGKHSGAIGDPSTVKADNSYSVGNNNQFIDATQTD
                                                                                                                                                                                                                                                    KANAGISSAMAMASMPQAYIPGRSMVTGGIATHNGQGAVAVGLSKLSDNGQWVFKINGSA
                                                                                                                       QQLNEVRNLLGLGNAGNDNADGNQVNIADIKKDPNSGSSSNRTVIKAGTVLGGKGNNDTE
                                                                                                                 KLATGGVQVGVDKDGNANGDLSNVWVKTQKDGSKKALLATYNAAGQTNYLTNNPABALDR
                                                            1819 SKAVFKSKDGTTTTVSSDGISIQGKDNSSITLSKDGLNVGGKVISNVGKGTKDTDAANV
                                                                         .-----ggkvisnvgkgtkdtdaanv
      1699 DVLNVGFNLQTNHNQVDFVKAYDTVNFVNGTGADITSVRSADGTMSNITVNTALAATDDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klein MH;
                                                                                                                                                                                                                                                                                                                             AAB69133 standard; Protein; 1992 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUL-2000; 2000WO-CA00870.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CONN-) CONNAUGHT LAB LTD..
                                                                                                                                                                                                                                                                                  2299 DTQGHVGAAVGAGFHF 2314
                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                              Moraxella catarrhalis.
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The present invention describes an isolated and purified nucleic acid (I) that encodes a 200 kDa outer membrane protein of Moraxella catarrhalis. The 200 kDa outer membrane protein (II) has antibacterial activity and correct acid of the compositions and vaccines to protect against M. catarrhalis infections, particularly otilis medla in humans. (II) is also used as confections, particularly otilis medla in humans. (II) is also used as confections, particularly otilis medla in humans. (II) is also used as confections, particularly of the recombinant production of (II) and its generate Ab. (I) are used for recombinant production of (II) and its generate Ab. (I) are used as probes for identifying/cloning 200 kDa protein fragments are used as probes for identifying/cloning 200 kDa protein confers from other strains, and for diagnostic detection of M. catarrhalis. (I) makes possible production of large amount of recombinant immunogens. The present sequence represents the cowards the Escherichia coll host. The present sequence represents the consequence in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    460 DGLKFTDNS-NTALEDTTRITKDKIGFSNKACTVDENK-PYLDKDKLKVGNSTLNNGGLT 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding Moraxella catarrhalis outer membrane protein, useful in protective vaccines and for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNNKAYVPEGNGSNIKSSKATGN---GLESIGSSTIKRKIINVGAGYEDTDAVNVAQLKA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VKLAKNLSGLETVSTKNLTASEKVTVGSGNN-TAELQSGGLTFT-PTTNA-STDKTVYGT 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 471; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNNTIGGSNKQIQVGADGIKFAD-VNVNVSNAAKFGTTRITEEEIGFADADGKVDKKSPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLSTLIQNHTVLRQIRDSNGSQ-KYRRTAAEGHASTAVGAMAYAKGHFANAFGTRSTAEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 VIGATLNGSAYAQ--NNSKIAFGTTG---NNDNASASNEASIAIGSLAKAHANQAIAIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 8%; Score 6407.5; DB 22;
ilarity 60.5%; Pred. No. 4.2e-275;
Conservative 146; Mismatches 316; In
                                                                                                                                          Example 3; Fig 2A-W; 247pp; English.
WPI; 2001-159722/16.
N-PSDB; AAF59100, AAF59101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 1428; Conserv
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An approx. 200 kDa outer membrane protein (AAW04505) can be isolated from Moraxella catarhalis otitis media strain 4223 by electroelution, or expressed from a gene (see also AAT38740) obtd. from a strain 423 genomic library. Natural or recombinant outer membrane protein is useful as an immunogen to protect against infection by Moraxella, esp. M. catarhalis. It can also be used to detect antibodies, esp. for differential diagnosis between bacteria that cause similar symptoms, and also useful as a carrier for other antigens and used to raise antitumour antibodies for conjugation to therapeutic agents.
       Klein MH,
                                                                                         Moraxella outer membrane protein vaccine and for diagnosis
                                                                                                                                          Claim 14; Fig 6; 109pp; English.
          RE,
                                       WPI; 1996-506162/50.
N-PSDB; AAT38740.
                                                                                                                                                                                                                                                                                                                                                                 1992 AA;
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useful as immunogen in protective

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Sasaki

SM,

Loosmore

Gaps Query Match 54.8%; Score 6404.5; DB 17; Length 1992; Best Local Similarity 60.4%; Pred. No. 5.6e-275; Matches 1427; Conservative 147; Mismatches 316; Indels 471;

48;

690 641 468 459 517 288 345 297 402 354 228 518 VNNTIGGSNKQIQVGADGIKFAD-VNVNVSNAAKFGTTRITEEEIGFADADGKVDKKSPY vtaptyni-gvkttelnsdgtsdk--fsvkgsgtnnslvtaehlasylnevnrtadsalg SFSIRDEKGQEFTISNLYSNGNTPN--TFETITFAGENGISISNDIAKGKVKVGIDPING LDKKQLQVGGVKITKDSGINAGDQKISNVKDATDDTDAVTYKQ----LKQVQQDADGALQ NNNKAYVPEGNGSNIKSSKATGN---GLFSIGSSTIKRKIINVGAGYEDTDAVNVAQLKA VKLAKNLSGLETVSTKNLTASEKVTVGSGNN-TAELQSGGLTFT-PTTNA-STDKTVYGT 56 VIGATLNGSAYAQ--NNSKIAFGTTG---NNDNASASNEASIAIGSLAKAHANQAIAIGG SKPDPRNQAANQKAGSHAKGKESIAIGGDVLAEGDASIAIGSDDLYLDRNSTNSKYPNG-469 577 527 633 584 239 355 415 346 298 403 460 583 120 528 180 111 61 170 g ò g Ω ò d δ qq οy g οy δý qq g QΥ g δ à ð g δ

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1694 AASVKDVLNVGFNLQTNHNQVDFVKAYDTVNFVNGTGADITSVRSADGTMSNITVNTALA 1753 HGKPLDAGHQVVASLGGNSDALTLTNIKSTLPQIDTPNTGNANAGQAQSLPSLSAAQQSN 1693 VNDANKKQGINEDNAFIKGLENAAKDTKTKNAAVTVGDLNAVAQTPLTFAGDTGTTAKKL 1453 1158 GNGEAVDEVSTYDTVDFIDGNATTAKVTYDDTSKTSKVVTDVNVDNKTIEVTSDKKLGVK 1276 FAKV-DKGNSSTGIDGTSRITKDQIGFTGANGSLDTTKPHLIKDKLKVGEVEITNTGINA 1038 GGKKITNIQSGDITQNSNDAVTGGRVYDLKTELESKINSAAKTAQNSLHEFSVADEQGNH 1098 875 919 817 863 807 747 GETLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGTRIDEKGISFVD ANGQAKANTPVLSANGLDLGGKRISNIGAAVDDNDAVNFKQFNEVAKTVNNLNNQSNSGA SLPFVVTDANGKPINGTDGKPQKAIKGADGKYYHANANGVPVDKDGKPITDADKLANLAA TTTLTKTSANGNATKF---SAADGDALVKASDIATHLNTLAGDIQTAKGASQASSSASYV IVIDSKDGQNTITGLSNTLANVTND-GAGHALSQG-LANDTDKTRAASIGDVLNAGFNLQ sdgavdtnkpyldqdklqvgnvkitntginaggkaitgisptipsiadqss-rnlelgnt KUTYDVNVDEKTIELTG-DNCKTNKIGVKTTILTTNANGK-ATNF--STTDNDALVNAK DIAENLNTLAKEIHTTKGTADTALQTFKVKK----DGATDDETITVGKDGTQNCKTVNTL ITSDEDKSKAASIGDILNTGFNLKNNSNSVGFVSTYNTVDFIDGNATTAKVTYDETNQTS -- IRGLSPTLPSITNAGGVRTTEQGNT ssgqakantpvlsangldl------LTTPKLTVGSD----KDGKTQLVIEQVASGNDTKNI-1518 1574 1634 1458 1514 1537 1454 1537 11011 1161 1277 1280 1334 1338 1394 1398 1217 1221 1159 993 1041 1099 980 1039 200 864 876 642 723 748 759 808 q δy Ob g qq ò q ò OD ò òγ g qq ò ò qq δy qq ŏ Db ò Q Q g δy g δ QQ δ P δ g ŏ ò d

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                                                                                                                                                                                                                                                                                                                                                                                         Moraxella catarrhalis strain Q8; major outer membrane protein;
200kDa outer membrane protein; antibacterial; immunogenic; infection;
otitis media; detection.
                                                                                                              TQAGNQSIAIGDNAQATGDQSIAIGTGNVVTGKHSGAIGDPSTVKADNSYSVGNNNQFID
                                                                                                                                                                                                                        FAGQTAVGAVSVGASGAERRIQNVAAGEVSATSTDAVNGSQLYKATQGIANATNELDHRI
                                                                                                                                                                                                    1754 ATDDDGNVLIKAKDGKFYKADDLMPNGSLKAGKSASDAKTPTGLSLVNPNAGKGSTGDAV
                                               1814 ALNNLSKAVFKSKDGTTTTTVSSDGISIQGKDNSSITLSKDGLNVGGKVISNVGKGTKDT
                                                       NNDTEKLATGGVQVGVDKDGNANGDLSNVWVKTQKDGSKKALLATYNAAGQTNYLTNNPA
                                                                                                                                   EAIDRINEOGIRFFHVNDGNOEPVVOGRNGIDSSASGKHSVAIGFOAKADGEAAVAIGRO
                                                                                                                                                                                            ATQTDVFGVGNNITVTESNSVALGSNSAISAGTHAGTQAKKSDGTAGTTTTAGATGTVKG
                                                                                                                                                                                                                                                                                                                                                                          catarrhalis M56 200kDa protein in pKS348 SEQ ID NO:13.
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that encodes a 200 kbs outer membrane protein of Morakella catarrhalis.

The 200 kbs outer membrane protein of Morakella catarrhalis.

The 200 kbs outer membrane protein (II) has antibacterial activity and can be used in vaccines. (II), and its truncated versions, are used as immunogenic compositions and vaccines to protect against M. catarrhalis infections, particularly otitis media in humans. (II) is also used as infections, particularly otitis media in humans. (II) is also used as antigen in immunoassays for detecting specific antibodies (Ab), and to generate Ab. (I) are used for recombinant production of (II) and its fragments are used as probes for identifying/cloning 200 kbs protein genes from other strains, and for diagnostic detection of M. catarrhalis.

(I) makes possible production of large amount of recombinant immunogens. Expression of truncated versions of (II) reduces toxicity of the protein towards the Escherichia coll host. The present sequence represents the cempalification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48;
                                                                                                                                present invention describes an isolated and purified nucleic acid (I)
     outer membrane protein,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 54.8%; Score 6404.5; DB 22; Length 1992; Best Local Similarity 60.4%; Pred. No. 5.6e-275; Matches 1427; Conservative 147; Mismatches 316; Indels 471; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 VIGATLNGSAYAQ--NNSKIAFGTTG---NNDNASASNEASIAIGSLAKAHANQAIAIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNNKAYVPEGNGSNIKSSKATGN---GLFSIGSSTIKRKIINVGAGYEDTDAVNVAQLKA
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  New nucleic acid encoding Moraxella catarrhalis useful in protective vaccines and for diagnosis
                                                                              8A-V; 247pp; English
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nucleic acid
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Οy	691 I	VIEQVASGNDTKNI72	QQ	153.
Dp	642	69	Qy	175
Qy	723	4	qa	153
qq	700 \$		Oy	181
οy	748		qq	153
Dp	759	s 81.	Oy	187
Qy	808	KVTYDVNVDEKTIELIG-DNGKTNKIGVKTTTLTTTNANGK-ATNFSTTDNDALVNAK 863	Dp	155
qq	818	alvnak 87	Qy	193
ογ		91	qu	161
qq	876	93	Qy	199
٥y	920	KLKGENGLTVATNKDGTVTFGINTQSGLKAGDSTTLNKDGLSIKNPASNEQIQVGADGVK 979	QC	167
qq	934		Qy	205
δy	086	PAKV-DKGNSSTGIDGTSRITKDQIGFTGANGSLDTTKPHLTKDKLKVGEVEITNTGINA 1038	qa	173
Ор	993	* OT	δλ	211
ŏ		GGKKITNIQSGDITQNSNDAVTGGRVYDLKTELESKINSAAKTAONSLHEFSVADEQGNH 1098	qa	179
QQ	1041	ggkkitniqsgeiaqnshdavtggkiydlktelenkisstaktaqnsineisvaueqguu ii	δλ	217
Qy	1099	FTVSNPYSSYDTSKTSDVITFAGENGITTKVNKGVVRVGIDQTKGLTTPKLTVGNNNGKG 1158	qq	18
QQ	1101	ftvsnpyssydtsKtsdvitfagengittkvnkgvvrvgidqtkglttpkltvgnnngkg llb	Qy	22
ογ	1159	IVIDSKDGQNTITGLSNTLANVTND-GAGHALSQG-LANDTDKTRAASIGDVLNAGFNLQ 1216	qq	19.
ф	1161	<pre>lvidsqngqnt1tg1snt1anvtndkgsvrtteqgn11kdedktraas1vuv1saytn14</pre>	٥y	22
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QY	1634	HGKPLDAGHQVVASLGGNSDAITLINIKSTLPQIDTPNTGNANAGQAQSLPSLSAAQQSN 169	XX Id	Ä
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HONENKANAGISSAMAMASMPQAYIPGRSMVTGGIATHNCQGAVAVGLSKLSDNCGWVFK 2293
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                                                                                                                                                                                                                       1694 AASVKDVLNVGFNLQTNHNQVDFVKAYDTVNFVNGTGADITSVRSADGTMSNITVNTALA 1753
                                           4 ATDDDGNVLIKAKDGKFYKADDLMPNGSLKAGKSASDAKTPTGLSLVNPNAGKGSTGDAV 1813
                                                                                      4 ALNNLSKAVFKSKDGTTTTTVSSDGISIQGKDNSSITLSKDGLNVGGKVISNVGKGTKDT 1873
                                                                                                    emophilus adhesion protein; HA2; hsf protein; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                 Haemophilus adhesion protein HAZ (AAR99393) is associated with the formation of surface fibrils involved in adhesion to various host cells; it is also referred to hsf (Haemophilus surface fibrils). Its amino acid sequence was deduced from a genomic DNA clone (AAM44476) derived from Haemophilus influence type b strain C65. Large quantities of recombinant HAZ can be produced in transformed prokaryotic or eukaryotic host cells, for use in vaccines against
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vvr----tapvlsfhsdkegtgekevtensnwgiyfdnkgvlkagaitlkagdnlkikq
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4; Conservative 349; Mismatches 908; Indels 865; (
                                                nse
                                           Recombinant Haemophilus adhesion proteins HA1 and HA2 - for
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                 RRIQNVAAGEVSATSTDAVNGSQLYKATQGIAN---ATNELDHRIHQNENKANAGISSAM
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                                                                                                   NANGVPVDKDGKPITDADKLANLAAHGK---PLDAGHQVVASLGGNSDAITLTNIKSTLP
                                                                                                                                                    QIDTPNTGNANAGQAQSLPSLSAAQQSNAASVKDVLNVGFNLQTNHNQVDF-----VK
                                                                                                                                                                             ----agkegtgevd--pansaggevkagd-kvtfkagdnlkikgsgkdftyslkkelk
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                                                   1550 VNFKQFNEVAKTVNNLNNQSNSGASLPFVVTDANGKPINGTDGKPQKAIKGA-DGKYYHA
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AAB23860 standard; Protein; 2411 AA.

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The present sequence represents a Haemophilus influenzae adhesin

(Hia) protein from the type c Haemophilus influenzae strain API.

(Hia) protein from the type c Haemophilus influenzae strain API.

Hia genes and proteins have antiinflammatory, auditory and antibacterial activities, and can be used in the production of a vaccine. An activities, and can be used in the production of a vaccine from the production of a vaccine. An activities, and can disease caused by Hemophilus strains in a protection against disease caused by Hemophilus strains in a susceptible host, preferably a human. An Hia protein is useful as an antigen, in immunogenic preparations including vaccines, as a carrier of for other immunogenic acused by the infection of Haemophilus is useful for treating diseases caused by the infection of Haemophilus influenzae such as meningitis, epiglottitis, septicaemia and otitis media. Recombinant production of Hia favours high recovery of the protein compared to the low recovery of institute protein from Haemophilus influenzae species. A truncated protein has a significantly higher compared to the length protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127;
                                   Hia; adhesin; Haemophilus influenzae adhesin; NTH1; infection; vaccine, non-typeable Haemophilus influenzae; antiinflammatory; auditory; antibacterial; meningitis; epiglottitis; septicaemia; otitis media; diagnosis; immunogenic; antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 IGSDDLYLDRNSTNSKYPNGLLSTLIQNHTVLRQIRDSNGSQKYRRTAABGHASTAVGAM 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 KPD------PRNQAANQK----AGSHAKGKESIAIGGDVLAEGDASIA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 vvrtapvlsfhsdkegtgekevtensnwgiyfhnkgvlkagaitlkagdnlkikqstnas 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AYAQN------NSKIAFGTTGNN-DNASASNEASIAIGSLAKAHANQAIAIGGS 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.1%; Score 1175.5; DB 21; Length 2411;
11arity 23.5%; Pred. No. 5.8e-44;
Conservative 369; Mismatches 963; Indels 771; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acid encoding Hemophilus influenzae adhesin protein, fuse as antigens and vaccines and for treating Hemophilus influenzae infection –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 lpdavtntgvlssssftpndvektraatvkdvlnagwnikgakt--aggnv-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 VIRLTRVATL-----TLNGS
       Haemophilus influenzae adhesin (Hia) protein from type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MNHIYKVIFNKATGTFMAVAECAKSHSGGSSSSTAGQVGSS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 24; 275pp; English.
                                                                                                                                                                                                                                                                                                                                                                  MH;
                                                                                                                                                                                                                                                                                                                                                                  Klein
                                                                                                                                                                                                                                                                                        99US-0268347.
                                                                                                                                                                                                                                                      16-MAR-2000; 2000WO-CA00289.
                                                                                                                                                                                                                                                                                                                            (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                           Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAA92499
                                                                                                                                                                               WO200055191-A2.
                                                                                                                                                                                                                                                                                            16-MAR-1999;
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Matches 645;
                                                                                                                                                                                                                  21-SEP-2000
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279 261 339 309 305 366 444 409	455 563 623 553 606 606 663	704 828 761 821 939 939 929	974 108 985 1114 103 120 107
-esvalvsaynnvefitgdkntldvvltakengkttevkftpktsvikekdgkl AYAKGHFANAFGTRSTAEGNYSLAVGL-TAKAEKGYTI-AIGSNAQAINYGALA	SGLETVSTKNLTASEKVTVGSGNNTAELQSGGLTFTPTTNASTDKT	F-AGENGISISNDIAKG-KVKVGIDPINGLT-TPKLTVGSDKDG	ATNKDGTVTFGINTQSGLKAGDSTTLNKDGLSIKNPASNEQIQVG
227 210 262 262 340 310 396 367 445	410 505 456 564 504 624 684 607	664 769 705 829 882 882 940 875	930 1030 975 1090 986 1150 1033
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1 2	1364	
an	1264	lrgigwvisakktadetqdkeihaavknaneveivgkngatvsakt
Qy	1130	-NKGVVRVGIDQTKGLTTPKLTVGNNNGKGIV-IDSKDGQNTITGLSN 1175
Qy	1176	VIN-DGAGHALSQGLANDFDKTRAASIGDVLNAGFNLQGNGEAVDFVS 12
qq	1384	: :     : :    14.8
δλ	1227	TYDTVDFIDGNATTAKVTYDDTSKTSKVVYDVNVDNKTIEVTSDKKLGVKTTTLT 1281
qq	1429	:
Οy	1282	DALVKASDIATHL
qq	1477	rdgknitfalan-dlsvksatvsdkls
QY	1342	YDSTDKKYYQVNDKGQVDKNKEVAKDKLVAQAQTPDGTLAQMNVKSVINKEQVNDANKKQ 1401
DÞ	1512	itsdtkglnfakdsktgddanihlngjastltdtllnsgattnlggngitdnekkr 1567
Qy	1402	AKDTKTKNAAVTVGDLNAVAQTPLTFAGDTGTTAKKLGE
q	1568	aasvkdvlnagwnvrgvkpasannqvenidratydtvdfvsgdkdtts 1616
QY	1457	LTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGTRIDEKGIS 1510
qq	1617	tveskdngkrtevkigaktsvikdhngkl
δλ	1511	FVDANGQAKANTPVLSANGLDLGGRRISNIGAAVDDNDAVNFKQFNEVAKTVNNLNN 1567
qq	1662	vtetdgkdegnglvtakavidavnkagwrvkttgangqndd1711
δλ	1568	IANGVPV
qq	1712	vtfadgngttaevtkandgsitvkynvkvadglkidgd-kivadtt 1756
QY	1627	NSDAITLT
QQ	1757	vltvadgkvtapnngdgkkfvdasgladalnklswtatagkegtgevd 1804
δλ	1684	PSLSAAQQSNAASVKDVLNVGFNLQTNHNQVDFVKAYDTVNFVNGTGADI 1733
qq	1805	
ΟŸ	1734	TSVRSADGTMSNITVNTALAATDDDGNVLIKAKDGKFYKADDLMPNGSLKAGKSASD 1790
QQ	1864	tkitkdgltitpangagaagantantisvtkdgisagnka 1903
οy	1791	AKTPTGLSLVNPNAGKGSTGDAVALNNLSKAVFKSKDGTTTTTVSSDGISIQGK 1844
QQ	1904	lkkfgdghtlangtvadfekhydnay
QY	1845	SNVGKGTKDTDAANVQQLNE
QQ	1948	dkttgepnqeyn-aqv
οy	1896	KKDPNSGSSSNRTVIKAGTVLGGKGNNDTEKLAT
g	2007	ktlngtrvitfelakgevvksneftvknadgsetnlvkvgdmyyskedidpatskpmtg- 2065
Øγ	1945	VQVGVDKDGNANGDLSNVWVKTQKDGSKKALLATYNAAGQTNVLTNNPABAIDRINEQGI 2004
g	2066	ğğ
ΟY	2002	RFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGRQ 2053
qq	2112	elgladaaeaekafaesakdkqlskdkaetvnahdkvrfangln 2155

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The present sequence represents a Haemophilus influenzae adhesin (Hia)

protein from the non-typeable Haemophilus influenzae (NTH1) strain 29,

protein from the non-typeable Haemophilus influenzae (NTH1) strain 29,

Hia genes and proteins have antiinflammatory, auditory and antibacterial

cativities, and can be used in the production of a vaccine. An

cativities, and can be used in the production of a vaccine. An

composition composition comprising an Hia gene, a polypeptide encoded

protection against disease caused by Hemophilus strains in a

cativities host, preferably a human. An Hia protein is useful as an

cantigen, in immunogenic preparations including vaccines, as a carrier

antigen, in immunogenic preparations including vaccines, as a carrier

con other immunogenic preparations including vaccines, as a carrier

is useful for treating diseases caused by the infection of Haemophilus

in luenzae such as meningitis, epidlotitis, septicaemia and otitis

in including recombinant production of Hia favours high recovery of the

media. Recombinant production of Hia favours high recovery of the
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                                                                                                  2184 lpltgiyntdangnkivkkadgkwyelnadgtasnkevtlgnvdangkkvvkvtengadk 2243
                                                                                                                                                                                        2244 wyytnadgaadktkgevsndkvstdekhvvrldpnnqsngkgvvidnvangeisatstda 2303
                                                                                                                                                                                                                            2210 VNGSQLYKATQGIAN---ATNELDHRIHQNENKANAGISSAMAMASMPQAYIPGRSMVTG 2266
                                                                                                                                                                                                                                                   Novel nucleic acid encoding Hemophilus influenzae adhesin protein, f
use as antigens and vaccines and for treating Hemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 non-typeable, Haemophilus influenzae; antiinflammatory; auditory; antibacterial; meningilis; epiglottitis; septicaemia; otitis media; diagnosis; immunogenic; antigen.
TQAGNQSIAIGDNAQATGDQSIAIGTGNVVTGKHSGAIGDPSTVKADNSYSVGNNNQFID
                                                                                                                                                       -----ASGAERRIQNVAAGEVSATSTDA
                                      tkv---saatvestdangdk-----vtt-----tfvktd-----ve
                                                                           2114 ATQTDVFGV---GNNITVT-----ESNSVALGSNSAISAG---THAGTQAKKSDGTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           influenzae adhesin (Hia) protein from NTH1 strain 29.
                                                                                                                                                                                                                                                                                                          2267 GIATHNGQGAVAVGLSKLSDNGQWVFKINGSADTQGHVGAAVGAGFHF 2314
                                                                                                                                                                                                                                                                                                                                 ::: || :|:|| :|:||| : |::|| || || || :: 2364 agssyggmglaigvsrisdngkviirlsgttnsggktgvaagvgygw 2411
                                                                                                                                                             2162 TTTAGATGTVKGFAGQTAVGAVSVG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-618897/59.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1551 NFKQFNEVAKTVNNLNNQSNSGASLPFVVTDANGKPINGTDGKPQKAIKGADGKYYHANA 1610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1491 LTNLNSVNAGGTRIDEKGISFVDANGQAKANTPVLSANGLDLGGKRISNIGAAVDDNDAV 1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1431 DLNAVAQTPLTFAGDTGTTAKKLGETLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKD 1490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1257 DVNVDNKTIEVTSDKKLGVKTTTLTKTSANGNATKFSAADGDALVKASDIATHLNTLAGD 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1317 IQTAKGASQASSSASYVDADGNKVIYDSTDKKYYQVNDKGQVDKNKEVAKDKLVAQAQTP 1376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TDKTRAASIGDVLNAGFNLQGNGEAVDFVSTYDTVDFIDGNATTAKVTYDDTSKTSKVVY 1256
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1078 AAKTAQNSLHEFSVADEQGNHFTVSNPYSSYDTSKTSDVITFAGENGITTKVNKGVVRVG 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I-DQTKGLTTPKLTVGNNNGKGIVIDSKDGQNTITGLSNTLANVTNDGAGHALSQGLAND 1196
                                                                                                                                                                                                                                                                                                                               960 LSIKNPASNEQIQVGADGVKFAKVDKGNSSTGIDGTSRITKDQIGFTGANGSLDTTKPHL 1019
                                                                                                                                                                                                                                                                                                                                                                                          1020 TKDKLKVGEVEITNTGINAGGKKITNIQSGDITQNSNDAVTGGRVYDLKT--ELESKINS 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ngksv----tfalakd-----ldvtsakvsdkls-----igkdtnkvd 300
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                                                                                                                                                                                                                                                                                                                                                            -----qvnadrgkv----kaedengadvdkkvatvkdvakaindaatfvkves 226
                                                                                                                                                                             17 vvvseltrahtkcasatvavavlatalsataeannntsvtnglnaygd-tnfnttnnsla 75
                                                                                                                        Gaps
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n------dadggkatqtlnnglnfkfkstdgell---nikvendtvtftpk----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ::| :| || dlekhvqdaykgllnlnek-----dtnkssflv----adntaatvgnlrklgwvls
                                                                                                                                                                                                                                                                       907 -KDGTQNGKT-----VNTLKLKGENGLTV-ATNKDGTVTFGINTQSGLKAGDSTTLNKDG
                                                                                                                                                                                                                                                                                          influenzae species. A truncated protein has a significantly higher amount of recovery than a full-length protein.
                                                                                                                                                                                                             DALVNAKDIAENLNTLAKEIHTTKGTADTALQTFKVKKDGATDDETITVG------
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                                                                                                                      Indels 590;
                                                                                             Length 1104;
                                                                                         Query Match
Best Local Similarity 24.6%; Pred. No. 3.3e-35;
Matches 391; Conservative 168; Mismatches 441;
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                                                      1104 AA
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                                                         Sequence
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Hia; adhesin; Haemophilus influenzae adhesin; NTH1; infection; vaccine; non-typeable Haemophilus influenzae; antlinflammatory; auditory; antibacterial; meningitis; epiglottitis; septicaemia; otitis media; diagnosis; immunogenic; antligen
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                           640 deltgvks-----ngast 662
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The present sequence represents a Haemophilus influenzae adhesin (Hia) protein from the non-typeable Haemophilus influenzae (NTH1) strain K22. Hia genes and proteins have antiinflammatory, auditory and antibacterial activities, and can be used in the production of a vaccine. An immunogenic composition comprising an Hia gene, a polypeptide encoded by a recombinant Hia polypeptide is useful for inducing protection against disease caused by Haemophilus strains in a susceptible host, preferably a human. An Hia protein is useful as an antigen, in immunogenic preparations including vaccines, as a carrier for other immunogens, and in the generation of diagnostic reagents. Hia is useful for treating diseases caused by the infection of Haemophilus influenzae such as meningitis, epiglottitis, septicaemia and otitis media. Recombinant production of Hia favours high recovery of the protein compared to the low recovery of native protein from Haemophilus influenzae species. A truncated protein has a significantly higher amount of recovery than a full-length protein.
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                                                                                                    Novel nucleic acid encoding Hemophilus influenzae adhesin protein, fuse as antigens and vaccines and for treating Hemophilus influenzae infection
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8.3%; Score 968; DB 21; Length 1104;
Best Local Similarity 24.6%; Pred. No. 3.3e-35;
Matches 391; Conservative 168; Mismatches 441; Indels 590;
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  Klein MH;
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AAB23857 standard; Protein; 1004

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                                                                               DLNAVAQTPLTFAGDTGTTAKKLGETLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKD 1490
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The present sequence represents a Haemophilus influenzae adhesin (Hia)

C protein from the non-typeable Haemophilus influenzae (NTH1) strain M407.

C Ha genes and proteins have antiinflammatory, additory and antibacterial

C Hia genes and can be used in the production of a vaccine. An

activities, and can be used in the production of a vaccine. An

c activities, and can be used in the propertied is useful for inducing

C munogenic composition comprising an Hia gene, a polypeptide encoded

immunogenic composition comprising an Hia polypeptide is useful for inducing

c protection against disease caused by Heemophilus strains in a

susceptible host, preferably a human. An Hia protein is useful as an

antigen, in immunogenic preparations including vaccines, as a carrier

c for other immunogenic preparations including vaccines, as a carrier

influenzae such as meningitis, epiglottitis, septicaenia and ottlis

media. Recombinant production of Hia davours high recovery of the

mount of recovery than a full-length protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QVGADGVKFAKVDKGNSSTGIDGTSRITKDQIGFTGANGSLDTTKPHLTKDKLKVGEVEI 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : : :|::|:|| : : |||| :::|
hadevlfegkdgvtvtsksengkhtvtf------tlekd-lnvknatvsdkl 185
                                                                                                            Hia; adhesin; Haemophilus influenzae adhesin; NTH1; infection; vaccine; non-typeable Haemophilus influenzae; antlinflammatory; auditory; antibacterial; meningitis; epiglottitis; septicaemia; otitis media; diagnosis; immunogenic; antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 697; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acid encoding Hemophilus influenzae adhesin protein, i
use as antigens and vaccines and for treating Hemophilus influenzae
infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     871 TLAKEIHTTKGTADTALQTFKVKKDGATDDETITVG------KDGTQNGKT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                916 -VNTLKLKGENGLTVATNKDG---TVTFGINTQSGLKAGDSTTLNKDGLSIKNPASNEQI
                                                                                 Haemophilus influenzae adhesin (Hia) protein from NTH1 strain M407.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.2%; Score 959.5; DB 21;
larity 23.7%; Pred. No. 7.1e-35;
Conservative 168; Mismatches 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          819 TIELTGDNGKTNKIGVKTTTLTTTNANGKATNFSTTD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 21; 275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                            Klein MH;
                                                                                                                                                                                                                                                                                                          16-MAR-2000; 2000WO-CA00289.
                                                                                                                                                                                                                                                                                                                                              99US-0268347
                                                                                                                                                                                                                                                                                                                                                                            (CONN-) CONNAUGHT LAB LTD.
                                                        (first entry)
                                                                                                                                                                                                              Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                Loosmore SM, Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-618897/59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1004 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 373; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAA92496
                                                                                                                                                                                                                                              WO200055191-A2.
                                                                                                                                                                                                                                                                                                                                                16-MAR-1999;
                                                                                                                                                                                                                                                                                21-SEP-2000
                                                                17-JAN-2001
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RESULT 11 AAB23857

----iafgsgskalrdntvalgtgnvvnaeksgafg 753

Db 708 treitfelak	Qy 2093 DPSTVKADN     :       Db 754 dpnyjedkag	2135	Db 811 tkvtvpgalge	Qy 2181 GAVSVGASGAE	2241	927	Qy 2301 QGHVGAAVGAC	Db 987 qgktgvaagvo	RESULT 12	ID AAB23854 standar	AC AAB23854;	DT 17-JAN-2001 (fi	DE Haemophilus infl		KW antibacterial; m KW 'diagnosis; immur	OS Haemophilus infl	XX PN WO200055191-A2.	PD 21-SEP-2000.	PF 16-MAR-2000; 200	PR 16-MAR-1999; 9	PA (CONN-) CONNAUGE XX	PI Loosmore SM, Ya	DR WPI; 2000-618897 DR N-PSDB; AAA92493		PT use as antigens PT infection -	XX PS Claim 1; Fig 18;		CC Hia genes and pr				CC is useful for tr
	1032 INTGINAGGKKITNIQSGDITONSNDAVTGGRVYDLKTELESKINSAAKTAQNSLHEFSV	207	240gvd	1152 GNNNGKGIVIDSKDGQNTITGLSNTLANVTNDGAGHALSQGLAN	244	1212 GFNLQGNGEAVDFVSTYDTVDFIDGNATTAKVTYDDTSKTSKVYYDVNVDNKTIEVTSDK   - - - - - - - - - - - - - - - - - -	1272 KLGVKTTTLTKTSANGNATKESAADGDALVKASDIATHLWTLAGDIOTA	295 ahnkkttvrvdvtglpvqyvtedgetvvkv	1332 YVDADGMKVIYDSTDKKYYQVNDKGQVDKNKEVAKDKLVAQAQTPDGTLAQMNVKSVINK 1391	325gneyyeakqdgsadm	1392 EQVNDANKKQGINEDNAFIKGLENAAKDTKTKNAAVTVGDLNAVAQTPLTFAGDTGTTAK 1451	349 352	1452 KLGETLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGTRIDEKGISF 1511	353vkl 355	1512 VDANGQAKANTPVLSANGLDLGGKRISNIGAAVDDNDAVNFKQFNEVAKTVNNLNNQ 1568	רבומים אינויטאני אינויטאני אינויסאני אינויסאני אינויסט איניט אינויסט אינויסט אינויסט אינויסט אינויסט א	1009 SNSGASLERVYICHNGREINGIDGREYNARMIGNEYVDRUGKEIIDA 1025 	1626 DKLANLAAHGKPLDAGHOVVASLGGNSDATTLTNIKSTLPOTDTPNTGNANGAGGLBS		1686 LSAAOOSNAASVKDVLNVGFNLOTNBNOVDFVKAXDTVNFVNGTGADITSVRSADGT			::   :   :   :     :	1803 NAGKGSTGDAVALNNLSKAV	:  :  :  :  :	1863 ISNVGKGTKDTDAANVQQLNEVRNLLGLGUAGN	597 vknvvsglkkfgdanfdpltssadnltkqydnaykgltnidekskgkqtptv 648	1918 SNRTVIKAGTVLGGKGNNDTEKLATGGVQVGVDKDGNANGDLSNV-WVKTQKDGSKKALL 1976	649 adntaatv	1977 AT	677 keyna	2033 SVAIGFQAKADGEAAVAIGRQTQAGNQSIAIGDNAQATGDQSIAIGTGNVVTGKHSGAIG 2092
đ	λō	ga 2	7 A	οy	qa	δ t	8 8	: A	οy	qq	Οy	qq	ΟÝ	qq	δ <del>ά</del>	i i	à é	ò	7 A	ò	: <u>a</u>	δ	qa	Oy	QΩ	οy	QQ	Oy	qq	οy	q <sub>Q</sub>	ò

sequence represents a Haemophilus influenzae adhesin (Hia) the non-typeable Haemophilus influenzae (NTH1) strain 33 d proteins have antiinflammatory, auditory and antibacterial and can be used in the production of a vaccine. An composition comprising an Hia gene, a polypeptide encoded nee, or a recombinant Hia polypeptide is useful for inducing gainst disease caused by Haemophilus strains in a host, preferably a human. An Hia protein is useful as an immunogenic preparations including vaccines, as a carrier munogenis, and in the generation of diagnostic reagents. Hia retaring diseases caused by the infection of Haemophilus r treating diseases caused by the infection of Haemophilus aemophilus influenzae adhesin; NTHi; infection; vaccine; emophilus influenzae; antiinflammatory; auditory; meningitis; epiglottitis; septicaemia; otitis media; cid encoding Hemophilus influenzae adhesin protein, for and vaccines and for treating Hemophilus influenzae --SNSAISAGTHAGTQAK----KSDGTAGTTTTAGATGTVKGFAGQTAV 2180 SRRIQNVAAGEVSATSTDAVNGSQLYKATQGIANATNELDHRIHQNENKA 2240 NSYSVGNNNQFIDATQTDVFGVGNNI-----TVTESNSV---luenzae adhesin (Hia) protein from NTHi strain 33. d; Protein; 1002 AA. nogenic; antigen. ang Y, Klein MH; 275pp; English. 00WO-CA00289. 99US-0268347. .rst entry) IT LAB LTD. |: : gygw 1000 **SFHF 2314** .uenzae. /59.

qa O	Qy Dy Oy	oy Ob	Qy	Qy	Qy Db	δλ Dp	RESU AAWS ID	XX XX DIX	X X D XX	XX XX XX XX XX XX XX XX XX XX XX XX XX	FH FT FT	FT XX PV XX	PD XX PP XX XX	PR XX PA	XX PI DR PI	z X
of the m Haemophilus Y higher	1002; 527; Gaps 53; NSAAKTA 1082 :	tdksk 103 IITTKV 1129 : :  vtvtsks 157		GNGEAVDF 1224   :     iggtvdnvdf 276	FTLTKTS 1284	NKVIYDS 1344	NKKQGIN 1404	ГІКGGQT 1464°	AKANTPV 1524     tnpv 367	JPFVVTD 1581 :  :sd 409	3KPLDAG 1641	ASVKDVL 1701  :::  htiqd 465	AATDDD 1758	GSTGDA 1812  -   : Igangas 559	GKGTKD 1872 	VIKAGT 1927
media. Recombinant production of Hia favours high recovery of the protein compared to the low recovery of native protein from Haemophilus influenzae species. A truncated protein has a significantly higher amount of recovery than a full-length protein.	tch  31 Similarity 24.9%; Pred. No. 4.7e-32; 345; Conservative 159; Mismatches 352; Indels 527; GageveithTGINAGGKKITNIGSGDITQNSNDAVIGGRVYDLKTELESKINSAAKTA	<pre>gsttgtns-invygknnsninsannsladinkqndsvydgllnlnekgtdksk QNSLHEFSVADEQGNHFTVSNPYSSYDTSKTSDVITFAGENGITTKV</pre>	NKGVVRVGIDQTKGLTTPKLTYGNNNGKGIVIDSKDGQNTI 	TGLSNTLANVTNDGAGHALSGGLANDTDKTRAASIGDVLNAGFNLQGNGEAVDF  :::	VSTYDTVDFIDGNATTAKVTYDDTSKTSKVVYDVNVDNKTIEVTSDKKLGVKTTLTKTS	ANGNATKFSAADGDALVKASDIATHLNTLAGDIQTAKGASQASSSASYVDADGNKVIYDS   :-	TDKKYYQVNDKGQVDKNKEVAKDKLVAQAQTPDGTLAQMNVKSVINKEQVNDANKKQGIN 	EDNAFIKGLENAAKDTKTKNAAVTVGDLNAVAQTPLTFAGDTGTTAKKLGETLTIKGGQT       aktkaktk	DTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGTRIDEKGISFVDANGQAKANTPV :	LSANGLDLGGKRISNIGAAVDDNDAVNFKQFNEVAKTVNNLNNQSNSGASLPFVVTD	ANGKPINGTDGKPQKAIKGADGKYYHANANGVPVDKDGKPITDADKLANLAAHGKPLDAG  :	IKSTLPQIDTPNTGNANAGQAQSLPSLSAAQQSNA/            tpkkgsvqvgddgk	NVGFNLQTNHNQVDEVKAYDTVNFVNGTGADITSVRSADGTMSNITVNTALAATDDD :	GNVLIKAKDGKFYKADDLMPNGSLKAGKSASDAKTPTGLSLVN-PNAGKGSTGDA :  : :	VALNNLSKAVFKSKDGTTTTTVSSDGISIQGKDNSSITLSKDGLNVGGKVISNVGKGTKD :	TDAANVQQLNEVRNLLGLGNAGNDNADGNQVNIADIKKDPNSGSSSNRTVIKAGT
media. Recombinant pro protein compared to th influenzae species. A amount of recovery tha Sequence 1002 AA;	10 O	gsttgtns-invygkn QNSLHEFSVADEQ             flvadettat	NKGVV   engkh													
CC medi CC prot CC infl CC amou XX Sequ	Query Best 1 Matche 102	Oy 1083 Db 104	Oy 1130 Db 158	Oy 1171 Db 218	Oy 1225 Db 277	Qy 1285 Db 309	Oy 1345 Db 330	Qy 1405 Db 352	Qy 1465 Db 356	Qy 1525 Db 368	Qy 1582 Db 410	Oy 1642 Db 442	Qy 1702 Db 466	Qy 1759 Db 506		Qy 1873

2045 EAAVAIGRQTQAGNQSIAIGDNAQATGDQSIAIGTGNVVTGKHSGAIGDPSTV--KADNS 2102 1928 VLGGKGNNDTEKLATGGVQVGVDKDGNANGDLSNV-WV--KTQKDGSKKALLATYNAAGQ 1984 1985 TNYLTNNPAEAIDRINEQGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADG 2044 2132 NSVALGSNSAISAGTHAGTQAKKSDGTAGTTTTAGATGTVKGFAGQTAVGAVSVGASGAE 2191 .-----ITV-----TES 2131 Haemophilus paragallinarum; antigenic protein; HI antibody; diagnosis; vaccine; chicken infectious coryza; CIC; fowl. 610 fgdanfnplt----ssadnltkgydnaykgltnldekskgkgtptvadnt---aat 658 ----eitfelakde 721 659 v------gdlrglgwvisadkttgeskeysaqvrnane ä Tokunaga Sakaguchi M, Tokiyoshi S, Haemophilus paragallinarum antigenic protein #2. Location/Qualifiers
1.70
/lable signal
71..2039
/note= "antigenic protein" (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO. (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST. 691 vkfksgnginvsgktldngtr------AAW56322 standard; Protein; 2039 AA. 2103 YSVGNNNQFIDATQTDVFGVGNN-----96JP-0271408. 97WO-JP03222 Haemophilus paragallinarum, 19-AUG-1998 (first entry) Hamada F, Matsuo K, WPI; 1998-230318/20. N-PSDB; AAV22837. 1000 ygw 1002 2312 FHF 2314 12-SEP-1997; 19-SEP-1996; WO9812331-A1 26-MAR-1998. AAW56322; Key Peptide Protein

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110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 AYAQNNSKIAFGTTGNNDNASASNEASIAIGSLAKAHANQAIAIGGSKPDPRNQAANQKA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 tytqldpr-----rapesrqgsvvigenaksagnqsvslg------qna 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217 wskt---nsisigagtfaegkstiaigtdkilgtnyndklpapswdgrtgkaptnsiwdi 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 --DLYLDRNSTNSKY-----PNGLLSTLIQNHTVLRQIRDSNGSQKY----- 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 RRTAAEGHASTAVGAMAYAKGHFANAFGTRS------TAEGNY-----SLAVGLT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 AKAEKGYTIAIGSNAQAINYGALALG----------ADTRV 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLDYGIALGYGSQILNN-----NNNNNNKAYVPEGNGSNIKSSKATGNG---LFSIGSS 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIKRKIINVGAG-YEDTDAVNVAQL---KAVENLAKRQITFKGDDNGTGVKKKLGETLTI 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGGETQADKLTDNNNIGVVTDNNTGLKVKLAKNLSGLETVSTKNLTASEKVTVGSGNNTA 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              563 -----snsfvggswvstlsartvvlgysasissdshdslamgvnafigngsnss 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        436 ELQSGGLTFTPTTNASTDKTVYGTDG----LKFTDN----SNTALEDTTRITKDKIGFSNK 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              612 lalgtgstiaknak-spdslaigkdsridakdtdngvlytpqvydettrafr----- 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               542 NVNVSNAAKFGTTRITEEEIGFADADGKVDKKSPYLDKKQL-----QVGGVKITKDSGI 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 596 NAGDQKISNVKDATDDTDAVTYKQLKQVQQDADGALQSFSIRDEKGQEFTISNLYSNGNT 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   656 PN--TFETITFAGENCISISNDIAKGK----VKVGIDPINCLTTPKLTVGSDKDGKTQL 708
                                                                                                                            The present sequence represents an antigenic protein derived from Haemophilus paragallinarum strain C-53-47. The antigenic protein stimulates the production of HI antibodies in fowl. The protein and DNA coding for it can be used in the preparation of vaccines for the prevention of chicken infectious coryza (CIC). The protein and its antibodies can be used in the diagnosis and treatment of CIC.
Antigenic polypeptide from Haemophilus paragallinarum induces HI antibody production - and is useful for diagnosis of and preparation of vaccines for chicken infectious coryza
                                                                                                                                                                                                                                                                                                                                                                                                                              12 ATGTFMAVAECAKSHSGGSSSSTAGQVGSSPVIRLTRVA-TLAI-----LVIGATLNGS 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        489 AGTVDENKPYLDK-----DKLKVGNSTLNNGGLTVNNTIGGSNKOIQVGADGIKFADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            514 tfaskansvalgsyalasaqnafalgsyslvsplaantivigvggyatg-----
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                                                                                                                                                                                                                                                                                                                                        Ouery Match 7.2%; Score 840.5; DB 19; Length 2039; Best Local Similarity 20.9%; Pred. No. 3e-29; Matches 533; Conservative 324; Mismatches 816; Indels 873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSHAKGKESIAIGGDVLAEGDASIAIGSD------
                                                                                    Claim 5; Page 71-87; 108pp; Japanese
                                                                                                                                                                                                                                                                              2039 AA;
                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394
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qq	:         :::     : o 797 vqylsvektningeag-rvasqirkgesykryvkl	 
δy	y 709 VIEQVASGNDTKNIIRGLSPTLPSIINAGGVRTTEQGNTITSDEDKSKAASIGDILNTGF	GF 768
qq	b 835 i	835
Qγ	y 769 NLKNNSNSVGFVSTYNTVDFIDGNATTAKVTYDETNQTSKVTYDVNVDEKTIELTGDNGK	IGK 828
qq	5 836yildarkklngekfdqtsldkiskavqeleaeysgelk	kt 873
δλ	y 829 TNKIGVKTTTLTTANGKATNFSTTDNDALVNAKDIAENLNTLAKEIHTTKGTAD	AD 884
QQ	874 taseln	nn 931
δλ	885 TALQIFKVKKDGAIDDEIIIGKDGIQNGKIVNILKI	VA 930
<b>q</b> 0	932 nylndgakgqdsiafgwqaktseannglagkqalaigfqan	ig 982
ΟŊ	y 931 THKDGTVTFGINTQSGLKAGDSTTLNKDGLSIKNPASNEQ1QVGADGVKFAKVDKGNSST	ST . 990
qa	983 tnsdtsmtgavaigkgatvtaggkpsialggdstv	ans 1020
ΟŻ	Y 991 GIDGTSRITKDQIGFTGANGSLDTTKPHLTKDKLKVGEVEITNTGINAGGKKITNIQSGD	GD 1050
qq	1021 aisrtssvmingltfnnfagsp	.gd 1066
Qy	y 1051 ITQNSNDAVTGGRVYDLKTELESKINSAAKTAQNSLHE	E- 1088
q	1067	ida 1126
Oy	1089FSVADEQGNHFTVSNPYSSYDTSKTSDVITFAGENGITTKVNKG	GI 1138
qa	b 1127 innvltklislsateeeevvsgeavydalkgakptvsaeankgitgl	-v 1174
Qy	1139 DQTKGLTTP	GL 1193
qa	b 1175 dvvkkansp-itvepstdnnkkktftvglmkdiegvnsitfdksgqdln	qvt 1225
δλ	y 1194 ANDTDKTRAASIGDVLNAGFNLQGNGBAVDFVSTYDTVDFIDGNATTAKVTYD	1246
qq	b 1226 grmssagltfkkgdttngstttfaedgltidsttnsagtnlvkvsrdgf	svk 1277
0y	1247 DTSKTSKVVYDVNVDN-KTIEVTSDKKLGVKTTTLTKTS	ANGN 1288
qq	b 1278 ngsdesklastklsigaenaehvevtksgialkadntsdkssitlagdaitla-gnatgt	gt 1336
Qγ	1289	ST 1345
qa	b 1337 aikitgvadgnitvnskdavnggqirtilgvdsgakiggtekttiseaisdvkqaltdat	it 1396
Qy	1346	NE 1405
qa	b 1397 -laykadnkngktvkldglnftsttnidasv	-e 1428
Qy	y 1406 DNAFIKGLENAAKDTKTKNAAVTVGDLNAVAQTPLTFAGDTGTTAKKLGETLIKGGQTD	TD 1465
q	1429 dngvvkftlkdkltglktiateslna-sqniiaggtvt	te 1471
Ωy	y 1466 TWKLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGTRIDEKGISFVDANGQAKANTPVL	VL 1525
qq	b 1472 givltksgsgndrt-lslsgagnaatd	1497
Qy	1526 SANGLDLGGKRISNIGAAVDDNDAVNFKQFN	IG- 1584
QQ	b 1498gikvsgvkagtadtdavnkgqldklfkaindalgttdlavtknpnqt	qt 1544
ΟŊ	y 1585rpingtdgkpgkaikgadgkyyhanangvpydkdgkpitdabklanlaahg	нс 1635
qa	1545 sifn	gi 1584
ΟŻ	y 1636 KPLDAGHQVVASLGGNSDAITLFNIKSTLPQIDTPNTGNANAGOAQSLPSLSAAQQSNAA	IAA 1695

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19-SEP-1996;
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                                                                                                                                                                                                                                   2049 AIGRQTQAGNQSIAIGDNAQATGDQSIAIGTGNVVTGKHSGAIGDPSTVKADNSYSVGNN 2108
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                                                                                                                          1873 TDAANVQQLNEVRNLLGLGNACN-DNADGNQVNIADIKKDPNS---GSSSNRTVIKAGTV 1928
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                                                                                                                                                                          SVKDVLNVGFNLQTNHNQVDFVKAYDTVNFVNGTGADITSVRSADGTMSNITVNTALAAT 1755
                                                                     -----vapagnvatgdia----ptqpal--pemktalvgdhlav 1690
                                                                                       1816 NNLSKAVFKSKDGTTTTVSSD---GISIQGKDNSSITLSKDGLNVGGKVISNVGKGTKD 1872
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                                                                                                                                                                                                1989 TINIPAEAIDRINEQGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAV
                                                                                                                                                                                                                                                                                                         2169 GTVKGFAGQTAVGAVSVGASGAERRIQNVAAGEVSATSTDAVNGSQLYKATQGIANATNE
                                                                                                   2109 NQFIDATQTDVFGVGNNITVTESNSVALGSNSAISAGTHAGTQAKKSDGTAGTTTTAGAT
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                                                    DDDGNVLIKAKDGKFYKADDLMPNGSLKAGKSASDAKTPTGLSLVNPNAGKGSTGDAVAL
 -isptsgdvvtgr----qlyalmgk·
                                    -----girvygdevsptktqttaptasstqggattantagg-
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71. 2042
/note= "antigenic protein"
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   dgidagnkkisnvadgd-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tevaagakfnshqtgnllqdnnayatlknadksddtktgnaltvftqsfdnmltnglplv 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -NNKAYVPEGNGSNIK----SSKATGNGLFSIGSSTIKRKIINVG-AGYEDTDAVNVAQ 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---DPRNQAANQKAGSHAKGK---------ESIAIGGDVLAEGDASIAI 150
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-satgaialgygvknetlakdslalgygaknestapssvtigkqalnrfekslvmglnay 179
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|aslfpqlanakwlevysssvklstvsaqsnsvnlnpsgaesvgtnspqgvalgygatndr 120
                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents an antigenic protein derived from Haemophilus paragallinarum strain A-221. The antigenic protein stimulates the production of HI antibodies in fowl. The protein and DNA coding for it can be used in the preparation of vaccines for the prevention of chicken infectious coryza (CIC). The protein and its antibodies can be used in the diagnosis and treatment of CIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                              Antigenic polypeptide from Haemophilus paragallinarum induces HI antibody production - and is useful for diagnosis of and preparation of vaccines for chicken infectious coryza
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                                                                                                                Tokunaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.8%; Score 796; DB 19; ilarity 20.9%; Pred. No. 2.7e-27; Conservative 322; Mismatches 816;
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                                                                                                                Tokiyoshi
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                                        (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
(KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 51-69; 108pp; Japanese.
                                                                                                                  Sakaguchi M,
96JP-0271408
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N-PSDB; AAV22834.
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632 510 681 725 623 680 680	736 852 796 891 856 920 916 970	1036 1054 1076 11111 11111 1170 1214 1230	1290 1269 1349 1323 1409 1343 1391
GLKFTDNSNsqnalai-gvnvfigndsasslalgmgstiaksakspdslaig GLKFTDNSNTALEDTTRITKDKIGFSNRAGTVDENKPYLDKDKLKVG-NST	VKVGIDPINGLTTPKLTVGSDKDGKTQLVIEQVASGNDTKNIIRGLSPTLPSITNA 7   1   1   1   1   1   1   1   1   1		VDFIGNATTAKVTYDDTSKTSKVVYDVNVDNKTIEVTSDKKLGVKTTLTKTSANGNAT 129G vtfskggagtkls
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1439 nfstdillsdg-----rsgnattandgvgkrrlsd-gftiksenftlgskgyngsd 1488
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                                                                                                                                                                                                 1645 asstggwattantaggvapagnvatgdiaptgptlpemntalvddhlavplggslki--- 1701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1882 NEVRNLLGLGNAGNDNA-----DGNQVNIADIKKDPN---SGSSSNRTVIKAGTVLGGK 1932
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                                                          1519 KANTPVLSANGLDLGGKRISNIGAAVDDNDAVNFKQFNEVAKTVNNLN-----NQSNSGA 1573
                                                                                                                    1574 SLPFVVTDANGKPINGTDGKPQKAIKGADGKYYHANANGVPVDKDGKPITDADKLANLAA 1633
                                                                                                                                                                                                                                                                                                       1754 ATDDDGNVLIKAKD---GKFYKADDLMPNGSLKAGKSASDAKT-PTGLSLVNPN----- 1803
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                 1694 AASVKDVLNVGFNLQTNHNQVDFVKAYDTVNFVNGTGADITSVRSADGTMSNITVNTALA
                                                                                                                                                                                                                                                                                                                                                                                                                                              1993 AEAIDRINEQGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGR
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The present sequence represents a Haemophilus influenzae adhesin (Hia)

protein from the non-typeable Haemophilus influenzae (NTH1) strain K9.

Ha genes and proteins have antiinflammatory, auditory and antibacterial
activities, and can be used in the production of a vaccine. An
activities, and can be used in the production of a vaccine. An
immunogenic composition comprising an Hia gene, a polypeptide encoded
by an Hia gene, or a recombinant Hia polypeptide is useful for inducing
by an Hia gene, or a recombinant Hia polypeptide is useful for inducing
protection against disease caused by Heemophilus strains in a
susceptible host, preferably a human. An Hia protein is useful as an
antigen, in immunogenic preparations including vaccines, as a carrier
antigen, in immunogenic preparations including vaccines, as a carrier
for other immunogenic preparations including vaccines, as a carrier
antigen, in immunogenic preparations including vaccines, as a carrier
for other immunogenic preparations including vaccines, as a carrier
antigen, in production of Hia favours high recovers of the
media. Recombinant production of Hia favours high recovery of the
protein compared to the low recovery of neative protein from Haemophilus
influenzae species. A truncated protein has a significantly higher
amount of recovery than a full-length protein.
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                                          Hia; adhesin; Haemophilus influenzae adhesin; NTHi; infection; vaccine; non-typeable Haemophilus influenzae; antiinflammatory; auditory; antibacterial; meningitis; epiglottitis; septicaemia; otitis media; diagnosis; immunogenic; antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acid encoding Hemophilus influenzae adhesin protein, for use as antigens and vaccines and for treating Hemophilus influenzae infection .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --qvtstsengkhai 164
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      Haemophilus influenzae adhesin (Hia) protein from NTHi strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
6.1%; Score 70%; DB 21;
Best Local Similarity 23.0%; Pred. No. 1e-23;
Matches 345; Conservative 186; Mismatches 430;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Klein MH;
                                                                                                                                                                                                                                                                                      16-MAR-2000; 2000WO-CA00289.
                                                                                                                                                                                                                                                                                                                                   99US-0268347
                                                                                                                                                             Haemophilus influenzae
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us-09-361-619-11.rai

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APPLICANT: TUCKER, KENNETH
APPLICANT: PLOSILA, LAURA
TITLE OF INVENTION: MORAXELLA CATARRHALIS OUTER MEMBRANE
TITLE OF INVENTION: PROTEIN-106 POLYPEPTIDE, GENE SEQUENCE AND USES THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE SS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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MEDIUW TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATIOS SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968 685A

FILING DATE: No. 621498lember 12, 1997

CLASSIFICATION:
ATTONREY/AGENT INFORMATION:
NAME: Baldwin, Geraldine F.
REGISTRATION NUMBER: 31,232

REGISTRATION NUMBER: 31,232

REGISTRATION NUMBER: 31,232

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (212) 790-9090
TELEFRAX: (212) 790-9090
TELEFRAX: (212) 780-9090
TELEFRAX: G121 PENNIE

INFORMATION FOR SEQ ID NO: 10:
                      US-08-728-470-9
US-08-169-927-2
US-09-377-155-13
US-09-377-155-15
US-09-377-155-15
US-09-377-155-15
US-09-377-155-15
US-09-377-155-15
US-09-377-155-12
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US-09-377-155-12
US-08-447-031A-2
US-08-685-467-5
US-08-685-467-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/08968685A Patent No. 6214981 GENERAL INFORMATION:
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; MOLECULE TYPE: peptide
US-08-968-685A-10
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STATE: New York
COUNTRY: USA
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Sequence 2, A
Sequence 15,
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                                                    Compugen Ltd
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US-08-913-942-4
US-08-408-467-4
US-08-685-467-4
US-08-685-467-4
US-08-913-32
US-08-913-942-2
US-08-913-942-1
US-08-913-942-1
US-08-617-697-9
US-08-719-641-10
US-08-719-641-10
US-08-718-641-10
US-08-302-832-2
US-08-302-832-2
US-08-302-832-2
US-08-302-832-2
US-08-302-832-2
US-08-310-832-2
US-08-310-832-2
US-08-530-198-2
US-08-530-198-2
US-08-718-641-10
US-08-718-641-10
US-08-108-108-2
US-08-108-108-2
US-08-108-108-2
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                   GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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ъ .a	61	LNGSAYAQNNSKIAFGTTGNNDNASASNEASIAIGSLAKAHANQAIAIGGSKPDPRNQAA 120 	
. > 4	121	NOKAGSHAKGKESIAIGGDVLAEGDASIAIGSDDLYLDRNSTNSKYPNGLLSTLIQNHTV 180 	
2 2 Q	181	LROIRDSNGSRYRRTAAEGHASTAVGAMAYAKGHFANAFGTRSTAEGNYSLAVGLT 237  :  :	
<u>≯</u> 4	238	AKAEKGYTIAIGSNAQAINYGALALGADTRVDLDYGIALGYGSQILNNNNNNKAY 294 	
λί Q	295	VPEGNGSNIKSSKAT-GNGLFSIGSSTIKRKIINVGAGYEDTDAVNVAQLKAV 346  :	
≿ q	347	ENLAKRQITFKGDDNGTGVKKKLGETLTIKGGETQADKLTDNNNIGVYTDNNTGLKVKLA 406 	
. ¥	407	KNLSGLETVSTKNLTASEKVTVGSGNNTAELQSGGLTFTPTTNASTDKTVYGTDGLKFTD 466 	
À.	467	NSNTALEDITRITKDKIGFSNKAGTVDENKPYLDKD502	
g è	434	50	
, e	485	YGQLKKVNQTAESALQTFTVKKVDKNGN	
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i d	545		
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70 4	629	FETITEAGENGISI	
a ko	702	KDGKTQLVIEQVASGNDTKNI	
qq	751	::           EDAVNIKTLTASDKVTVDSGNNTAKLQNGDLTFSKONTGATPATNSKTIYGVDGLKFTDN 810	
Qγ	723		
qq	811	NGIALDGTTYITKDKVGFAKQDGSLDKSKPYLDKDKLKVGEVEITTNGINAGGKALTGLS	
Oy Db	728	<pre>9 PTLPSITNAGCVRTTEQGNTITSDEDKSKAASIGDILNTGFNLKNNSNSVGFVSTYNTVD 787 11</pre>	
QY	788		
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λλ	006	ETITVGKDGTQNGI	104
o O	1047	TTVGKDAKTNQVNTLKLKGKNGLDIQINKDGIVIFGINIQSGLANGINITITITIC I	, ,
ζζ O	960	LSIKNPASNEOIQVGADGYKFAKVDKGNSSTGIDGTSRITKDQIGFTGANGSLDTTKPLH 10 	164
لام و	20	KLKVGEVEITNTGINAGGKKITNIQSGDITQNSNDAVTGGRVYDLKTELESKINSAA 1.	079
3 6	80	DNSLHEFSVADEQGNHFTVSNPYSSXDTSKTSDVIFFAGENGITTKVNKGVVRVGID 1	Ċ.
Db	1213	TTKVNKGVVRVGID 1	^
Qy	1140	OFKGLTFFKLTVGNNNGKGIVIDSKDGONTITGLSNTLANVIND-GAGHALSQG-LANDT 11 	197 332
a :	۰ ٥	FREI VORMINGENINGEN GENERALINGEN  257	
S 6	33	DATRASIVDVLSAGFNLQGNGEAVDFVSTYDTVNFADGNATTAKVTYDDTSKTSKVYXD 13 DKTRAASIVDVLSAGFNLQGNGEAVDFVSTYDTVNFADGNATTAKVTYDDTSKTSKVYXD 13	392
δy	1258	IEVTSDKKLGVKTTLLKTSANGNATKFSAADGDALVKASDIATHLNTLA 1	314
QΩ	1393	LS 1	449
ογ	1315	DIQTAKGASQASSSASYVDADGNKVIYDSTDKKYYQVNDKGQVDKNKEVAKDKLVAQAQ 1	~
qq	1450	SAGYVDADGNKVIYDSTDNKYYQAKNDGTVDKTKEVAKDKLVAQAQ 1	509
Qγ	-	TPDGTLAQMNVKSVINKEQVNDANKKQGINEDNAPIKGLENAAKDTKTKNAAVTVGDLNA 1/	434
Вр	1510	PDGTLAQMNVKSVINKEQVNDANKKQGINEDNAFVKGLEKAASDNKINNAAVIVGDENA I	٠,
Qy	1435		49
qq	1570	AQTPLIFAGDIGTTAKKLGETLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNL 1	ف
Οy	1495	SVNAGGTRIDEKGISFVDANGQAKANTPVLSANGLDLGGKRISNIGAAVDDNDAVNFK(	io.
q	1630	GTKIDDKGVSFVDSSGQAKANTPVLSANGLDL	1667
Qy	1555	GASLPFVVTDANGKPINGTDGKPQK	1614
qq	1668		1667
Οý	1615	VDKDGKPITDADKLANLAAHGKPLDAGHQVVASLGGNSDAITLINIKSTLPQIDTPNTGN	1674
qq	1668		1667
δ	1675	ANAGGAQSLPSLSAAQQSNAASVKDVLNVGFNLQTNHNQVDFVKAY	1734
QQ	1668	1	1667
δy	1735	SVRSADGTMSNITVNTALAATDDDGNVLIKAKDGKFYKADDLMPNGSLKAGKSASDAKTP	1794
qq	1668		1667
Qy	1795	TGLSLVNPNAGKGSTGDAVALNNLSKAVFKSKDGTTTTTVSSDGISIQGKDNSSITLSKD	1854
qq	1668		1667
οy	1855	ISNVGKGTKDTDAANVQQLNEVRNLLGLGNAGNDNADGNQVNIADIKKDPNS	6
qq	1668	GKVISNVGKGTKDTDAANVQQLNEVRNLLGLGNAGNDNADGNQVNIADIKKDPNS	
ΟŊ	-	5 GSSSNRTVIKAGTVLGGKGNNDTEKLATGGVQVGVDKDGNANGDLSNVWVKTQKDGSKKA [	1974
2	1727	SSSNRTVIKAGIVLGGRGNNDIENLATGGVQVGVDNDGMANGDESMVMVILENEGEN	

Qy 251 NAQAINYGALALGADTRVDLDYGIALGYGS    Db 270 TPKTSVIKEKDGK   Qy 310GNGLFSIGSSTIKRKIINVGAGYEDT   Db 303 NTDEGNGIVTAKAVI	. Qy 354 . Db 348 Qy 379	4	Qy         503 KLKVGNSTLNNGGLTVNNTIGG           b         587 PLVTDSTAATVGDLRKLGWVSTKNGTKEE           Qy         529IQVGADGIKFADVNVNV           b         647 ITVSVAETKADCGLEKDGDTKLKVDNONT           Qy         568 GKVDKKSPYLDKRQLQVGGVKITKDSGINA	Db 707 GKVTVKDATAND  Qy 627 ADGALQSFSIRDEKGGEFIISNLYSNGN  Db 749 IDE		Oy 783 YNTVDFIDGNATTAKVTYDETNQTSKVTYD	т г	Qy       986
QY 1975 LLATYNAAGGTNYLTNNPAEAIDRINEQGIRFFHVNDGNQEPVYQGRNGIDSSASGKHSV 2034	Qy         2095 STVKADNSYSVGNNNQFIDATQTDVFGVGNNITVTESNSVALGSNSAISAGTHAGTQAKK 2154           D	Oy 2215 LYKATOGIANATNELDHRIHQNENKANAGISSAWAMASMPOAYIPGRSMYTGGIATHNGQ 2274  DD 2024 LYKATOGIANATNELDHRIHQINENKANAGISSAMAMASMPOAYIPGRSMYTGGIATHNGQ 2083  QY 2275 GAVAVGLSKLSDNGQWVFKINGSADTOGHVGAAVGAGFHF 2314  DD 2084 GAVAVGLSKLSDNGQWVFKINGSADTQGHVGAAVGAFFF 2123	US-09-377-155-33 US-09-377-155-33 Sequence 33, Application US/09377155 Patent No. 6197312 GENERAL INFORMATION: APPLICANT: PEAK, Ian Richard Anselm APPLICANT: JENNINGS, Michard APPLICANT: MOXON, E. Richard APPLICANT: MOVEL SURFACE ANTIGEN FITTLE OF INVENTON: NOVEL SURFACE ANTIGEN FITTLE DEFERENCE IN CONTROL FOR THE PERFERENCE ANTIGEN		of o	Query Match         10.1%; Score 1177.5; DB 4; Length 2353;           Best Local Similarity 23.3%; Pred. No. 4.6e-57;           Matches 644; Conservative 349; Mismatches 908; Indels 865; Gaps           Qy         1 MNHYKVIFKNATGTFMAVACAKSHSGGSSSTAGQVGSS	43 VIRLTRVATLAILVIGATLNGSAYAQNNSKIAFGTTGNNDNASASNEASIAIGSLAKAHA	QY         152 SDDLYLDRNSTNSKYPNGLLSTLIQNHTVL

2	NAQAINYGALALGADTRVDLDYGIALGYGSQILNNNNNNNKAYVPEGNGSNIKSSKATTI
303	GNGLFSIGSSTIKRKIINVGAGYEDTDAVNVAQLKAVENLAKRQ353 
354 348	ITFKGBDNGTGV
379 408	-ETQADKLIDDNNIGVYTDNNTGLKVKLARNLSG-LETVS-TRNLTASEKVTVGSGNNTA 435
436	ELQSGGLTFTPTTNASTD-KTVYGTDGLKFTDNSNTALEDTTR 477
478	ITKDKIGFSNKAGTVDENKPYLDKD 502   1  1
503 587	KLKVGNSTLNNGGLTVNNTIGGSNKQ
529	
568	GKVDKKSPYLDKKQLQVGGVKITKDSGINAGDQKISNVKD-ATDDTDAVTYKQLKQVQQD 626
627 749	ADGALQSFSIRDEKGGEFTISNLYSNGNTPNTFETITF-AGENGISISNDIA 677
678 792	KG-KVKVGIDPINGLT-TPKLTVGSDKDGKTQLVIEQVASGNDTKNI-IR 724 
725 850	GLSPTLPSITNAGGVRTTEQGNTITSDEDKSKAASIGDILNTGFNLKNNSNSVGFVST 782
783 905	YNTVDFIDGNATTAKVTXDETNQTSKVTYDDNVDEKTIELTGDNGKTNKIGVKTTLTTT 842 
843 953	NANGKATNFSTTDND     :    KDLKDANNGATVSEDDGKD
896 1003	GATDDETITVGKDGTQNGKTVNTLKLKGENGLTVATNKDGTVTFGINTQSGL
948 1053	KAGDSTTLNKDGLSIKNPASNEQIQVGADGVKFAKVDK985 
986	997   1   1   1   1   1   1   1   1   1
1113	DGESEGETDQEVKAGDKYTFKAGKNLKVKQSEKDFTYSLQDTLTGLTSITLGGTANGRND 117.
1173	Ĭ,

Db 2080 KAETVNAHDENFRENGLNIKVSAATVESTDANGDKTT 2118  OY 2096 TVRADNSYSVGNNNGFIDATOTDVEGVGNNITVTESNSVALGSNSAISAG- 2145  OY 2196 TVRADNSYSVGNNNGFIDATOTDVEGVGNNITVTESNSVALGSNSAISAG- 2145  I	CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: COURTY: COUNTY:

1	MNHIYKVIFNKATGTFMAVAECAKSHSGGSSSSTAGQVGSS
43	VIRLTRVATLAILVIGATLNGSAYAQNNSKIAFGTTGNNDNASASNEASIAIGSLAKAHA 102  :
103 116	NQAIAIGGSKPDPRNQAANQKAGSHAKGKESIAIGGDVLAEGD-ASIAIG 151   :::   :::               NTDESTNASSFTYSLKKDLTDLTSVATEKLSFGANGDKVDITSD 159
152 160	SDDLYLDRNSTNSKYPNGLLSTLIQNHTVL
191 220	OKYRRTAAEGHASTAVGAMAYAKGHFANAFGTRSTAEGNYSLAVGLTAKAEKGYTIAIGS 250
251 270	NAQAINYGALALGADTRVDLDYGIALGYGSQILNNNNNNNKAYVPEGNGSNIKSSKAT- 309 
310	GNGLFSIGSSTIKRIINVGAGYEDTDAVNVAQLKAVENLAKRQ 353 
354	ITFKG
379	-ETQADKLIDNNNIGVYTDNNTGLKVKLAKNLSG-LETVS-TKNLTASEKVTVGSGNNTA 435 
436	ELQSGGLTFTPTTNASTD-KTVYGTDGLKFTDNSNTALEDTTR 477
478 527	ITKDKIGFSNKAGTVDENKPYLDKD 502
503 587	KLKVGNSTLNNGGL TVNNTIGGSNKQ
529	IQVGADGIKFADVNVNSNAAKFGTTRITEEEIGFADAD- 567 :
568	GKVDKKSPYLDKKQLQVGGVKITKDSGINAGDQKISNVKD-ATDJTDAVTYKQLKQVQQD 626 
627 749	ADGALQSFSIRDEKGQEFTISNLYSNGNTPNTFETITF-AGENGISISNDIA 677
678 792	KG-KVKVGIDPINGLT-TPKLTVGSDKDGKTQLVIEQVASGNDTKNI-IR 724   :   :   :
725 850	GLSPTLPSITNAGGVRTTEQGNTITSDEDKSKAASIGDILNTGFNLKNNSNSVGFVST 782  ::         :::
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ΩD	905	YDTVNFTDDSTGTTTVTVTQKADGKGADVKIGAKTSVIKDHNGKLFTG 952
Qy	843	NANGKATNFSTTDNDALVNAKDIAENLNTLAKEIHTTKGTADTALQTFKVKKD 895
qa	953	KDLKDANNGATVSEDDGKDTGTGLVTAKTVLDAVNKSGWRVTGEGATAET 1002
δŏ.	896	GATDDETITVGKDGTQNGKFVNTLKLKGENGLTVATNKDGTVTFGINTQSGL 947
αn	1003	SGISVNFKNGNATTAIVSKDNGNINVKYDVNVGDGL
y d	948	KAGDSTTLNKDGLSIKNPASNEQIQVGADGVKFAKVDK 985
QY	986	997
qq	1113	:  :   :   DGESEGETDQEVKAGDKVTFKAGKNLKVKQSEKDFTYSLQDTLTGLTSITLGGTANGRND 1172
Qy	866	ITKDQIGFTGANGSLDTTKPHLTKDKLKVGEVEITNTGINAGGKKITNIQSGDITQ 1053
QQ	1173	TGTVINKDGLTITLANGAAAGTDASNGNTISVTKDGISAGNKEITNVKSA 1222
Qy	1054	SKIN
qa	1223	
Qγ	1114	SDVITFAGENGITTKVNKGVVRVGIDQTKGLTTPKLTVGNNNGKGIV 1160
QQ	1248	ANEVEFVCKNGATVSAKTDNNGKHTVTIDVAEAKVGDGLEKDTDGKIKLKVDNTDGNNLL 1307
Qy	1161	-IDSKDGQNTITGLSNTLANVTN-DGAGHALSQGLANDTDKTRAASIGDV 1208
Dp	1308	VTTDATTAQGTNANERGKVVVKGSNG
Οy	1209	LNAGFNLQGNGEAVDFVSTYDTVDFIDGNATTAKVTYDDTSKTSKVVYDVNVDNK 1263
qq	1368	AKAINDAATFVKVENDDSATIDDSPTDDGANDALKAGD 1405
ΟŊ	1264	TTLTK
q	1406	TLTLKAGKNLKVKRDGKNITFALAN-DLSVKSATVSDKLS1444
QΣ	1324	SQASSSASYVDADGNKVIYDSTDKKYYQVNDKGQVDKNKEVAKDKLVAQAQTPDGTLAQM 1383
QQ	1445	
Oy	1384	
Dβ	1492	GATTNIGGNGITDNEKKRAASVKDVLNAGWNVRGVKPASANNQVENIDFVATYDT 1546
Qy	1439	PLTFAGDTGTTAKKLGETLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLT 1492
qq	1547	SKDNGKRT
Qy	1493	NLNSVNAGGTRIDEKGISFVDANGQAKANTPVLSANGLDLGGKRISNIGAAVDDNDA 1549
QQ	1599	NNGVTVTETDGKDEGNGLVTAKAVIDAVNKAGWRVKTTGANGQNDD- 1644
Qy	1550	VNFKQFNEVAKTVNNLNNQSNSGASLPFVVTDANGKPINGTDGKPQKAIKGA-DGKYYHA 1608
q	1645	FATVASGTNVTFADGNGTTAEVTKANDGSITVKXNVK 1681
Qy	1609	NANGVPVDKDGKPITDADKLANLAAHGKPLDAGHQVVASLGGNSDAITLTNIKSTLP 1665
qa	1682	
Qy	1666	QIDTPNTGNANAGQAQSLPSLSAAQQSNAASVKDVLNVGFNLQTNHNQVDFVK 1718
οp	1737	NSAGQEVKAGD-KVTFKAGDNL)
ΟY	1719	AYDTVNEVNGTGADITSVRSADGTMSNITVNTALAATDDDGNVLIKAKDGKFYK 1772
q	1788	DLTSVEFKDANGTGSESTKITKDGLTITPANGAGAAGANTANTISVTKDG 1838

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                                                                                                                                                                                                                                                                                                                                               ----ADGEAAVAIGRQTQAGNQSIAIGDNAQATGDQSIAIGTGNVVTGKHSGAIGDPS 2095
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2119 FVKTD------VELPLTQIYNTDANGNKIVKKADGKWYELNADGTASNKEVTLGN 2167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2146 --THAGTQAKKSDGTAGTTTTAGATGTVKGFAGQTAVGAVSVG------ASGAE 2191
                                                                                                                                                                                                                                                                              2041
                                                                   1878
                                                                                                                                    QOLNEVRNLLGLG-NAGNDNADGNQVNIADIKKDP------NSGSSSNRTVIKAGTV 1928
                                                                                                                                                                                                                                        1991 YYSKEDIDPATSKPMTG----KTEKYKVENGKV-----VSANGSKTEVTLINKGSG--- 2037
                        VDANGKKVVKVTENGADKWYYTNADGAADKTKGEVSNDKVSTDEKHVVRLDPNNQSNGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMASMPQAYIPGRSMVTGGIATHNGQGAVAVGLSKLSDNGQWVFKINGSADTQGHVGAAV
                                                                                                                                                                                                         LGGKGNND--TEKLATGGVQVGVDKDGNANGDLSNVWVKTQKDGSKKALLATYNAAGQTN
                                                                                                                                                                                                                                                                                                                                                                               2080 KAETVNAHDKVRFANGLNTKV---SAATVESTDANGDK------VTT-----T
                                                                                                                                                                   RNANEVKFKSGNGINVSGKTLNGTRVITFELAKGEVVKSNEFTVKNADGSETNLVKVGDM
                                                                                                                                                                                                                                                                              YLTNNPAEAIDRINEQGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAK----
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                                                                 DGTTTTTVSSDGISIQGKDNSSITLSKDGLNVG-----GKVIS---NVGKGTKDTDAANV
                                                                                                DLT------NLDEKGADNNPTVADNTAATVGDLRGLGWVISADKTTGEPNOEYN-AOV
1773 ADDLMPNGSLKAGKSASDAKTPTGLSLVNPNAGKGSTGDAVALNNLSKAVFKS---
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: Four Embarcadero Center, Suite 3400
San Francisco
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APPLICANT: St. Geme III, Joseph W.
TITLE OF INVENTION: Haemophilus Adhesion Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UMBER: US/08/409,995
24-MAR-1995
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Patent No. 5646259
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MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Silva, Robin M.
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CORRESPONDENCE ADDRESS:
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COUNTRY: USA
ZIP: 94111-4187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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2348 GVGYQW 2353
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495 NKPYLDKDKL---KVGNSTL----NNGGLTVNNTIGGSNKQIQVGADG--IKFADVNVNV 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       616 SNOVKQADEVLETGAGAATVTSKSENGKHTITVSVAETKADGGLEKDGDTIKLKVDNQNT 675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNAAKFGT--TRITE----EEIGFADAD-GKVDKKSPYLDKKQLQVGGVKITKDSGINA 597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       497 NDAKTVINKDGLTITPAGNGGTTGTNTISVT-KDGIKAGNKAITNVASGLRAYDDANFDV 555
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                                                                                                                                                                                                                                                                                                                                                                                                                                             NGSAYAQN------NSKIAFGTTGNN-DNASASNEASIAIGSLAKAHANQAIAI
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                                                                                                                                                                                                                                                                                                                                Query Match
7.2%; Score 841; DB 1; Length 1912;
Best Local Similarity 23.0%; Pred. No. 1.6e-38;
Matches 475; Conservative 255; Mismatches 657; Indels 676;
                                                                                                                                                                                                                                                                                                                                                                            44 IRLTRVATL------AILVIGA-----
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                                                                                                                                                                                                                                                                                                                  1 MNHIYKVIFNKATGTFMAVAECAKSHSGG-----
                 A-61053/RFT
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-6
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 781-1989
TELERAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1912 amino acids
     38,304
                                                                                                                                                                   double
                                                                                                                                                                                   TOPOLOGY: unknown
                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: dou
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QY         1448         TTAKKLGETLTIKGGQTDTNKLTDNNIGVVZ           : :	RESULT 5 US-08-685-467-4 ; Sequence 4, Application US/08685467 ; Patent No. 6060059 ; GENERAL INFORMATION: APPLICANT: St. Geme III, Joseph W. TITLE OF INVENTION: HAEMOPHILUS ADI NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS: ADDRESSER: Flehr, Hohbach, Test,	NATE STATE	FILING DATE: 22-UUL-1996 CLASSIFICATION: 424 FRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/409,999 FILING DATE: 24-MAR-1995 ATTORNEY/AGENT INFORMATION: NAME: Silva, Robin M. RECISTRENCE/DOCKET NUMBER: A 61053: TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989 TELEPHONE: (415) 781-1989 TELEFAX: (415) 398-3249	INFORMATION FOR SEQ ID NO: 4:   SEQUENCE CHARACTERISTICS:   IENGTH: 1912 amino acids   TYPE: amino acid   STRANDEDNESS: unknown   TOPOLOGY: unknown   MOLECULE TYPE: protein   US-08-685-467-4   Query Match   7.2%; Score   8     Best Local Similarity 23.0%: Pred   9	2 X . F   F   D
718 ADKKVATVKDVATAINSAATEVKTENLTTSIDEDNPTDNGKDD 760 655 TPNTFETITE-AGENGISINDIAKG-KVKVGIDPINGLT-TPK 695	### ### ##############################	967 -SNEQIQVGADGVK	NGATVSAKTDNNGKHTVTIDVAEAKVGDGLEKETESKINSAAKTAO	1145TPREATVORNINGKGIVIDSEDGONTTREISNINGKGHA 1188	1288 NATKFSAADGDALVKASDIATHLNTLAGDIQTAKGASQASSSASYVDADG 1337   1
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VAGTDGFTVKLAKDLTNLNSV ----NAG-- 1500
                                             PPVLSANGLDLGGKRISNI-----GAAV 1544
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No. 1.6e-38;
.Smatches 657; Indels 676; Gaps
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YFDNKGVLKAGAITLKAGDNLKXKQXTDEXT 120
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;, Suite 3400
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οy	259 /	ALALGADTRVDLDYGIALGYGSQILNNNNNN-NNKAYVPEGNGSNIKSSK 307	S G	
QQ	340	340 TVASGTNVTFESGDGTTASVTKDTNGNGITVKYDAKVGDGLKFDSDKKIVADTTAL 395	Ø	
δý	308	-ATGNGLFSIGSSTIKRKIINVGAGYEDTDAVNVAQLKAVENLAKRQ	qa	1376 FV
QQ	396	TVTGGKVAEIAKEDDKKKLVNAGDLVTALGNLSWKAKAEADTDGALEGISKDQ	Qy	1145
à á	354	354 ITFKGDDNGTGVKKKLGETLTIKGGETQADKLTDNNNIGVYDNNTG 400	qq	1436 AT
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QQ	616	SNOVKQADEVLFTGAGAATVTSKSENGKHTITVSVAETKADCGLEKDGDTIKLKVDNQNT 675	ò	1338 NK
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qq	919	DNVLTVGNNGTAVTKGGFETVKTGATDADRGKVTVKDATAND	ò	1388 VJ
Qy		GDQKISNVKD-ATDDTDAVTYKQLKQVQQDADGALQSFSIRDEKGQEFTISNLYSNGN	QO	1711
Ор		ADKKVATVKDVATAINSAATFVKTENLTTSIDEDNPTDNGKDD	οy	1448 TJ
δy		TPNTFETITF-AGENGISISNDIAKG-KVKVGIDPINGLT-TPK : :     :	qq	1753
qq		ALKAGDILIFKAGKNLKVKRDGKNITFDLAKNLEVKTAKVSDTLTIGGNTPTGGTTATPK	QY	1501
δλ		LTVGSDKDGKTQLVIEQVASGNDTKNI-IRGLSPTLPSITNAGGVRTTEQGNTITSDE	qa	1802 SI
g		VNITSTADGLNFARETADASGSRNVYLKGIATTLIEPSAGARSSHVDLNVDAIR	Qy	1545 DI
Qy Dp	753 875	DKSKARASIGDILURGFRILKNSNSVGFFYTVATVDFIDGNATTAKVTYDETNTSKYTYD B12	DD	1862 A
ογ	813	VNVDEKTIELTGDNGKTNKIGVKTTLTTTNANGKATNFSTTDNDALVNAKDI	RESULT US-08-	RESULT 6 US-08-409-99
QQ	932	VKIGAKTSVIKDHNGKLFTGKDLKDANNGATVSEDDGKDTGTGLVTAKTV 981		Sequence : Patent No
Qy	9866	AENLNTLAKEIHTTKGTADTALQTFKVKKDGATDDETITVGKDGTQNGKTVNTLK 920   :		GENERAL APPLICA APPLICA
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Qy	196	- SNEQIQVGADGVK PAKVDK 985		STRE CITY STAT

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TTPKLTVGNNNGK------GIVIDSKDGQNT---ITGLSNTLAN-VTNDGAGHA 1188
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                                                                                                                                                                                                                                                                            LHEFSV-----TSDVIT 1118
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NNKKLVNAEGLATALNNLSWTAKADKYADGESEGETDQEVKAGDKVTFKAGKNLKVKQ 1141
                                     -----GNSSTGIDGTSR-----ITKDQIGFTGANGSLDTTKPHLTKDK 1023
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ce 2, Application US/08409995

AL INCRAMITON:

LICANT: Barenkamp, Stephen I.

LICANT: St. Geme III. Joseph W.

LE OF INVENTION: Haemophilus Adhesion Proteins
BBER OF SEQUENCES:

GESCONDENCE ADDRESS:

DDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
DDRESSEE: Flehr, Hobbach Test, Suite 3400

ITY: San Francisco
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	QY         1953 GNANCDLSNVWVKTOKDGSKKALLATYNAAGQTNYLTNNPAEAIDRINBQGIRFEHVNDG           DD         807 ADA	RESULT 7 US-08-68-67-2   Sequence 2, Application US/08685467   Sequence 2, Application US/08685467   Patent No. 6060059   GENERAL INFORMATION:   APPLICANT: St. Geme III, Joseph W. APPLICANT: Barenkamp, Stephen J. TITLE OF INVENTION: HAEMOPHILUS ADDESION PROTEINS   NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS: 6 CORRESPONDENCE ADDRESS: 6 CORRESPONDENCE Flahr, Hohbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400 (ITY: San Francisco) STATE: California (CUNTX: United States)   STATE: 94111-4187
COUNTRY: USA ZIP: 94111-4187 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/409,995 FILING DATE: 24-MAR-1995 CLASSIFICATION: APTICATION NUMBER: 08/304 FILING DATE: 24-MAR-1995 TILING DATE: 24-MAR-1995 TILING DATE: 34-MAR-1995 TILING DATE: 1989 TELEPHONE: (415) 781-1989 TELEPHONE: (415) 781-1989 TELER: 910 277299 TELEPHONE: (415) 781-1989 TELER: 910 277299 TRECHONE CHARACTERISTICS: LENGTH: 1098 amino acids TYPE: amino acids TYPE: amino acid STRANDEDNESS: double TOPOLOGY: unknown US-08-409-995-2	Query Ma Best Loc 1008 1008 1055 103 1114 1170 220 220 279 279 339	QY         1327         SSSASYVDADGNKVIYDSTDKKYYQVNDKGQVDKNKEVAKDKLVAQAQTPDGTL         1380           BD         398         FASGNGTTATVTNGTDGTTVKYDAKVGDGLKLDGDKIAADTTA         440           QY         1381         AQMNVKSVINKEQVNDANKKQGINEDNAFIKGLENAARDTKTKNAAVTVGDLNAVQ         1437           BD         441         LTVNDGKNANNEKGGKVADVASTDEKKLYTALNSLSW         482           QY         1438         TPLTFAGDTGTTAKKLGTLTTKGGOTDTNKLTDNNIGVVAGTDGFTVKLAKD         1490           BD         483         TTTAAABAGGTCLDCNASEQEVKAGDKVTFKAGC

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,467
FILING DATE: 22-JUL-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                               A-61053-2/RFT/RMS
                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,995
FILING DATE: 24-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: S11va, RObin M.
                                                                                                                                                                                                                                          38,304
                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: DNA (genomic) US-08-685-467-2
                                                                                                                                                                                                                                                                                                                               TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                        1098 amino acids
                                                                                                                                                                                                                         NAME: Silva, Robin M. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS LENGTH: 1098 amino aci
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1543 AVDDNDAVNFKQFNEVAKTVNNLNNQSNSGASLPFVVTDANGKPINGTDGKPQKAIKGAD 1602
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CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
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                                     CLKKFGDAN---FDPLTSSADNLTKONDD--
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; Patent No. 6197312
; GENERAL INFORMATION:
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COUNTRY: United States ZIP: 94111-4187
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CITY: San Francisco
STATE: California
COUNTRY: United State
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                                                                                                                                                                                     Length 1098;
                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                 1008 ANGSLDTTKPHLTKDKLKV---GEVELTNTGINAGGKKITNIQSGDITQN-
                                                                                                                                                                                Query Match 5.6%; Score 659.5; DB 4; Best Local Similarity 22.9%; Pred. No. 8.5e-29; Matches 323; Conservative 168; Mismatches 457;
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594 GLKKFGDAN---FDPLTSSADNLTKQNDD-----
                                                                                                    ; ORGANISM: Haemophilus influenzae US-09-377-155-32
NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin V
                                        SEQ ID NO 32
LENGTH: 1098
                                                                                   TYPE: PRT
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ADDRESSEE: Flehr Hohbach Test Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
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PPLICANT: Barenkamp, Stephen J.
TITLE OF INVENTION: HAEMOPHILUS ADHESION PROTEINS
NUMBER OF SRQUENCES: 19
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APPLICATION NUMBER: US 08/409,995
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/4031
FILING DATE: 22-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Vance, Dolly A.
REGISTRATION NUMBER: 39,054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/913,942
FILING DATE: 29-DEC-1997
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
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                                                                                                                                                                                                                       Query Match 5.6%; Score 659.5; DB 4; Length 3 Best Local Similarity 22.9%; Pred. No. 8.5e-29; Matches 323; Conservative 168; Mismatches 457; Indels
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            TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1098 amino acids
(415) 781-1989
                                                                                                                 STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-913-942-2
                                                                                                    amino acid
TELEPHONE:
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1773 ADDLMPNGSLKAGKSASDAKTPTGLSLVNPNAGKGSTGDAVALNNLSKAVFKSKDGTTTT 1832
                                                                                                     1833 TVSSDGISIQGKDNSSITLSKDGLNVGGKVISNVGKGTKDTDAANVQQLNEVRNLLGLGN 1892
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STREET: Four Embarcadero Center, Suite 3400
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APPLICANT: St. Geme, Joseph
APPLICANT: Barenkamp, Stephen J.
APPLICANT: Barenkamp, Stephen J.
NUMBER OF SEQUENCES: 19
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CLASSIFICATION
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-913-942-15
'Sequence 15, Application US/08913942
'Patent No. 6200578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy dis
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CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1772 KADDIMPNGSIKAGKSASDAKTPTGLSLVNPNAGKGSTGDAVALNNLSKAVFKSKDGTTT 1831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1832 TTVSSDGISIQGKDNSSITLSKDGLNVGGKVISNVGKGTKDTDAANVQQLNEVRNLLGLG 1891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1892 NAGNDNADGNQVNIADIKKDPNSGSSSNRTVIKAGTVLGGKGNNDTEKLATGGVQVGVDK 1951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 ASELVESLNKLGWKVGVEKVGSGELDGTSKETLVKSGDKVTLKAGDNLKVKQEGTN--FT 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 -----DDEEELEPVQRSVLRWSFK--SAKEGTGEQEGTTEVINLN-TDSSGNAVGSST 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----NGQNSNVH 177
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.1%; Score 592; DB 4; Length 679; Best Local Similarity 23.9%; Pred. No. 2.4e-25; Matches 221; Conservative 121; Mismatches 285; Indels 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 NVVTQTWVVVSELTRTHTKCASATVAVAVLATLLSATVQANATDENE-----
NAME: Vance, Dolly A.
REGISTRATION NUMBER: 39,054
REFERENCE/DOCKET NUMBER: A-61053-1/RFT/RMS/DAV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELERA: (415) 398-3249
TELEX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SDANGLKLAKTGNG-------
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                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-913-942-15
                                                                                                                                                                                                                                                                         TOPOLOGY:
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2173 GFAGQTAVGAVSVGASGAERRIQNVAAGEVSATSTDAVNGSQLYKATQGIAN---ATNEL 2229
                                                                                                  2230 DHRIHQNENKANAGISSAMAMASMPQAYIPGRSMVTGGIATHNGQGAVAVGLSKLSDNGQ 2289
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                                                                                                                               1 MNHIYKVIFNKATGTFMAVAECAKSHSGGSSSSTAGQVGSSPVIRLTRVATLAILVIGAT
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                                                  --- DADKIKVASDGISAGNKAVKNVAAGEISATSTDAINGSQLYAVAKGVTNLAGQVNNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5977336-Typeable Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 4.8%; Score 565.5; DB 2; Best Local Similarity 22.1%; Pred. No. 2.3e-23; Matches 413; Conservative 242; Mismatches 709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 05-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/02166
FILING DATE: 16-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22.651
REFERENCE/DOCKET NUMBER: 1038-557
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,697
FILING DATE: 01-APR-1996
CLASSIFICATION: 424
                                                                                                                                                                                                    2290 WVFKINGSADTQGHVGAAVGAGFHF 2314
                                                                                                                                                                                                                                         655 VIIRLSGTTNSQGKTGVAAGVGYQW 679
                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/08617697
Patent No. 5977336
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (703) 415-0810
TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLSLGMASIPQSVLASGLQG---
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COUNTRY: U.S.A.
ZIP: 22202-0286
COMPUTER REAGABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1600 amino acids
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TOPOLOGY: linear
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY:
US-08-617-697-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
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ANQKAGSHAKGKESIAIGGDVLAEGDASIAIGSDDLYLDRNSTNSKYPNGLL 171	SELAGORITEDINGTANDANGANISANDON   1   1   1   1   1   1   1   1   1	IINVGAGYEDTDAVNVAQLKAVENLAKRQITFKGDDNGTGVKKKLGETLTI 375	VTVGSCNNTAELQSGGLTFTPTINASTDKTVYGTDGLKFTDNSNTALEDTT- 476    :		DDTDA	EQVASGNDTKNIIRGLSPTLPSITNAGGVRTTEQGNTITSDEDKSKAASIG 761	GNINITNKANVTLQADTSNSN-TGLKKRTLTLGNISVBGNLSLTGANANIVGNLSIAED- 907  NTLAKEIHTTKGTADTALQTFKVKKDGATDDETITVGKDGTQNGKTVNTLKLKGENG 926	
ANQKAGSE STLIQNHT STLIQNHT SDQISQ	ISE-AVGI ::   ENIKARNF ALGYGSQ] :    :  SLLAGQKI	VSKDKSGN VSKDKSGN VSKDKGET	VTVC :: VWGDIALJ V-RITKDF RITKDF GRNNTGER	IGGSNKQ:         INLSNGS: IGFADADC :   : :  VAF-EREC	DDTDA HKFDGEINISGNTPNTET :::	EQVASGNI  :   NITATGNE DIL KDLTINAT	GUINITHI NTLAKETI LTVATNKI       LNITTNAKI	: NISOK-E
120		325 291 376 344	426 392 477 452		610 627 654 687	711 740 762 795 811	850 870 908 927 949	990
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1316 ---TVGSTINGT-----NSVTTSQSGD------IEGTISG----NTVNVTA 1349 1253 KVVYDVNVDNKTIEVTSDKKLGVKTT----TLTKTSANGNATKFSAADGDALVKASDIAT 1308 1368 KLVAQAQTPDGTLAQMNVKSVINKEQVNDANKKQGINEDNAFIKGLENAAKDTKTKNAAV 1427 1488 AKDLTNLNSVNAGGTRIDEKGISFVDANGQAKANTPVLSANGLDLGGKRISNIGAAVDDN 1547 1548 DAVNEKQENEVAKTVNNLNNQSNSGASLPFVVTDANGKPINGTDGKPQKAIKG--ADGKY 1605 1606 YHANANGVPVDKDGKPITDADKLANLAAHGKPLDAGHQVVASLG------GNSDAIT 1656 SGFNKAEITAKNGSDLTIGNASGGNADAKKVTFDKVKDSKISTDGHNVTLNSEVKTSNG 1106 1085 SLHEFSVADEQGN-----HFTVSNPYSSYDTSKTSDVITFAGENGITTKVNKGV 1133 1134 VRVGIDQTKGLTTPKLTVGNNNGKGIVIDSKDGQN-TITGLSNTLANVTNDGAGHALSQG 1192 1193 LANDIDKTRAASIGDVLNAGFNLQGNGEAVDFVSTYDTVDFIDGNATTAKVTYDDTSKTS 1252 1309 HLNTLAGDIQ-TAKGASQASSSASYVDADGNKVIYDSTDKKYYQVNDKGQVDKNKEVAKD 1367 1428 TVGDLNAVAQTPLTFAGDTGTTAKKLGETLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKL 1487 Sequence 9, Application US/08617697

Patent No. 5977336

GENERAL INFORMATION:
APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5977336-Typeable Haemophilus
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1 CITY: Arington
STATE: Virginia
CONTRY: U.S.A.
Z1D: 2202-0286
Z2D: 2202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,697
FILING DATE: 01-APR-1996 1560 TQNEFTTKP 1568 1657 LTNIKSTLP 1665 RESULT 12 US-08-617-697-9 1048 1107 qq g Db δý Dρ δ g οy g δ q δ qq ŏ QQ δ q Qγ QQ οy ΟŸ δ

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962 IKNPASNEQIQVGADGVKFAKVDKGNSSTGIDGTSRITKDQIGFT------GANG 1010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1109 DTSKTSDVITFAGENGITTKVNKGVVRVGIDQTKGLTTPKLTVGNNNGKGIVIDSKDGQN 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1169 -TITGLSNTLANVTNDGAGHALSQGLANDTDKTRAASIGDVLNAGFNLQGNGEAVDFVST 1227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   902 TITVGKDGTQNGKTVNTLKLKGENGLTVATNKDGTVTFGINTQSGLKAGDSTTLNKDGLS 961
                                                                                                                                              674 NDIA-----KGKVKVGIDPINGLTTPKLTVGSDKDGKTQLVIEQVASGNDTKNIIRGLS 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                             854 TDNDALVN-AKDIAENLN-----TLAKEIHTTKGTADTALQTFKVKKDGATDD---E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --NNLTITAQGTITSGNSNGFRFNNVS-----
                                                       VTYKQLKQVQQDADGALQSFSIRDEKGQEFTISNLYSNGNTPNTFE-TITFAGENGISIS
                                                                                    -----LNSLGCKLSFTDSREDRGRR-----TKGNISNKFDGTLNISGTVDISMK
                                                                                                                                                                                                                                                                                      692 -TGPSIRNAELNGITFNKATFNIAQGSTANFSIKASIMPFKSNANYALFNEDISVSGGGS
                                                                                                                                                                                                                                                                                                                                    758 -----ASIGDILNTGFNLKNNSNSVGFVSTYN-------TVDFIDGNAT
                                                                                                                                                                                                                                                                                                                                                               1228 YDTVDFIDGNATTAKVTYDDTSKTSKVVYDVNVDNKTIEVTSDKKLGVKTT----TLTKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1343 DSTDKKYYQVNDKGQVDKNKEVAKDKLVAQAQTPDGTLAQMNVKSVINKEQVNDANKKQG
                                                                                                                                                                                            652 APKVSWFYRDKGRTYWNV-----TTLNVTSGS----KFNLSIDSTGSGS-----
                                                                                                                                                                                                                                          728 PTLPSITNA--GGVRTTE-----QGNTIT------SDEDKSKA---
                                                                                                                                                                                                                                                                                                                                                                                                                              795 TAKVTYDETNQTSKVTYDVNVDEKTIELT-GDNGKTNKIGVKTTTLTTNANGKATNFST
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         571 EGDIAFEDKSGR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALGYGSQILNNNNNNNKAY ---VPEGNGSNIKSSKATGNGLFSIGSSTIKRK----- 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 SLLAGOKITISDIINPTITYSIAAPENEAINLGDIFAKG-GNINVRAATIRNKGKLSADS 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---KGGETQ--ADKLTDNNNIGVVTDNNTGLKVKLAKNLSGLETVSTKNLTASEK---- 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MNKIYRLKFSKRLNALVAVSELTR----GCDHST--EKGSEKPVR-TKVRHLALKPLSAI 53
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Best Local Similarity 21.4%; Pred. No. 6.7e-21;
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 05-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/02166
FILING DATE: 16-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BETKSTESSET, JETTY W
                                                                                                                                                                                   NAME: BEFKRIESSET, JESTY W
REGISTRATION NUMBER: 22,651
REGISTRACCOMUNICATION NUMBER: 1038-557
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEFAN: (703) 415-0813
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1599 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: Single
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TOPOLOGY: linear
US-08-617-697-9
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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87;
1583 NGKPINGTDGKPQKAIKG--ADGKYYHANANGVPVDKDGKPITDADKLANLAAHGKPLDA 1640
                       97 LAKAHANQAIAIGGSKPDPRNQAANQKAGSHAKGKESIAIGGDVLAEGDASIAIGSDDLY 156
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                                                                                                                                                                                                                                                                                                        APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: Of No. 5928651-Typeable Haemophilus
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
STREET: Arlington
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYVHGTATMQVDGNKTTIRN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,470
                                                                                                                               1534 ERETLAKLGVSAVRFVEPNNAITVNTQNEFTTKP 1567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US PCT/US93/02166 FILING DATE: 16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BERKSTLESSER, JGTTY W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 1038-633
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEFACK: (703) 415-0813
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 16-WAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/03
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APPLICATION NUMBER: GB 9205704.1
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                         Sequence 10, Application US/08728470 Patent No. 5928651 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 21.9%; Pr
Matches 389; Conservative 232;
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LENGTH: 1529 amino acids
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                                                                                          1641 GHQVVASLG-
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                                                                                                                                                                                                                         US-08-728-470-10
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Best Local 9
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1106 SSYDTSKTSDVITFAGENGITTKVNKGVVRVGIDQTKGLTTPKLTVGNNNGKGIVIDSKD 1165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        760 ILGGN-----VTLGGENSSSSITGNINITNKANVTLQADTSNSN-TGLKKRTLTLGNISV 813
                                                                                                                                                                                                                                                                                                                 TVYGTDGLKFTDNSNTALEDTT---RITKDKIGFSNKAGTVDE-----NKPYLDKDKLK 505
                                                                                                                                                                                                                                                                                                                                                                                                  -----SGINAGDQKISNVKDATDDTDA------VTYKQLKQVQQDADGALQSF 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIRDEKGQEFTISNLYSNG-----NTPNTFETITFAGENGISISNDIAKGKVKVGIDP 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          688 INGLTTPKLTVGSDKDGKTQLVIEQVASGNDTKNII------RGLSPTLPSITNAGG 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              652 -NAATDPK-----KELPITFNANITATGNSDSSVMFDIHANLTSRAAGINMDSINITGG 704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KATNESTIDNDALVNAKDIAENLNTLAKEIHTTKGTADTALQTFKVKKDGATDDETITVG 906
                                                                                                                                                                                                                                                                         QITFKGDDNGTGVKKKLGETLTI---KGGETQ--ADKLTDNNNIGVVTDNNTGLKVKLAK 407
                                                                                                                                                                                                                     MIT-----GDKVTLKTGAVIDLSGKEGGETYLGGDERGEGKN------GIQLAK 297
                                                                                                                                                                                                                                                   408 NLSGLETVSTKNLTASEK-----VTVGSGNNTAE----LQSGGLTFTPTTNASTDK 454
209 MAYAKGHFANAFG-TRSTAE-GNYSL-AVGLTAKAEKGYTIAIGSNAQAINYGALALGAD 265
                                                                                 ---IINVGAGYEDTDAVNVAQLKAVENLAKR 352
                                                                                                                                            814 EGNLSLTGANANIVGNLSIAED-----STFKGEASDNLNI----TGTFT
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                   ---IALGYGSQILNNNNNNNKAY---VPEGNGSNIKSSKA
                                                                                                                                                                                                                                                                                                                                    -----VGNSTLNNGGLTVNNTIGGSNKQIQVGA--DGIK-----
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                                                                   266 TRVDLDYG-----
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1234 VTITA------DSGKLTS-----TVGSTINGT----NSVTTSSQSGD--- 1265
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                                                                                                                                   1225 VSTYDTVDFIDGNATTAKVTYDDTSKTSKVVYDVNVDNKTIEVTSDKKLGVKTT----TL 1280
                                                                                                                                                             1281 TKTSANGNATKFSAADGDALVKASDIATHLNTLAGDIQ-TAKGASQASSSASYVDADGNK 1339
                                                                                                                                                                                                                                         1340 VIYDSTDKKYYQVNDKGQVDKNKEVAKDKLVAQAQTPDGTLAQMNVKSVINKEQVNDANK 1399
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                                                       1166 GQN-TITGLSNTLANVTNDGAGHALSQGLANDTDKTRAASIGDVLNAGFNLQGNGEAVDF
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Patent No. 6218141
GENERAL INCPRARTION:
APPLICANT: Barenhamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 6218141-Typeable Haemophilus
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shoemaker and Mattare, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
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APPLICATION NUMBER: US 08/302,832
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/02166
FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/719,64
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ZIP: 22202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STATE: Virginia
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4.4%; Score 518; DB 4;
Best Local Similarity 21.9%; Pred. No. 9.2e-21;
Matches 389; Conservative 232; Mismatches 668
                                                                                                                                              REFERENCE/DOCKET NUMBER: 1038-625
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1529 amino acids
GB 9205704.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 MSVVHGTATMQVDGNKTTIRN------
                   FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
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   APPLICATION NUMBER:
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US-08-719-641-10
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1410 NTINGLNIISENGRNIVRERGKEIDVKYIQPGVASVEEVIEAKRV--LEKVKDLS---- 1462
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                                                                                                                                                                                                                                 KDGTQNGKTVN----TLKLKGE----NGLTVATNKDGTVTFGINTQSGLKAGDSTTLNKD 958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1357 INA---TSGTLTINAKDAKLDGAASGDRTVVNATN----ASGSGNVTAKTSSSVNITGDL
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-- NSNSVGFVSTYNTVD
                        903 DENIKNIKADAEIQIG------GNISQK-EGNLTISSDKVNITNQITIKAGVEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      959 GLSIKNPASNEQIQVGADGVKFAKVDKGNSSTGIDGTSRITKDQIGFT-
                                                                                                                                                                                            EGNLSLTGANANIVGNLSIAED-----STFKGEASDNLNI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1638 LDAGHQVVASLG-----GNSDAITLTNIKSTLP 1665
  VRTTEQGNTITSDEDKSKAASIGDIL-----NTGFNLKN-
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Sequence 2, Application US/08038682

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------DA--IINWKQFNIDQNEMVQFLQENNNSAVFNRVTS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 TLIQNHTVLRQIRDSNGSQKYRRTAAEGHASTAVGAMAYAKGHFANAFG-TRSTAE-GNY 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SL-AVGLTAKAEKGYTIAIGSNAQAINYGALALGADTRVDLDYG------IA 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKDKSGNIVLSAKEGEAEIGGVISAQNQQAKG-GKLMIT-----GDKVTLKTGAVIDLS 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LNGSAYAQNNSKIAFGTTGNNDNASASNEASIAIGSLAKAHANQAIAIGGSKPDPRNQAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 NOKAGSHAKGKESIAIGGDVLAEGDASIAIGSDDLYLDRN------STNSKYPNGLLS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 NQISQ---LKGILDSNG-QVFLINP-----NGITIGKDAIINTNGFTASTLDISNE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MNHIYKVIENKATGTEMAVAECAKSHSGGSSSSTAGQVGSSPVIRLTRVATLAILVIGAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MNKIYRLKFSKRLNALVAVSELAR----GCDHST--EKGSEKPARM-KVRHLALKPLSAM 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGYGSQILNNNNNNNKAY - - - VPEGNGSNIKSSKATGNGLFSIGSSTIKRK - - - - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 572;
GENERAL INFORMATION:
APPLICANT: BARENKAMP, STEPHEN J
APPLICANT: ST. GEME III, JOSEPH W
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
TITLE OF INVENTION: OF NON-TYPEABLE HAEMOPHILUS
                                                                                                                                     ADDRESSEE: Shoemaker and Mattare, Ltd
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 482; DB 1; L
Pred. No. 9.2e-19;
7; Mismatches 649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: BERKSTRESSER, JERRY W
REGISTATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 1038-293
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 415-0810
TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/038,682 FILING DATE: 16-MAR-1993 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative 257;
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Similarity 21.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1536 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                   NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 22202-0286
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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                                                                                                                                                                                                   CITY: Arlington
STATE: Virginia
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COMPUTER: IB
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Best Local Simi
Matches 394;
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US-08-038-682-2
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> 0	376	KGGETQADKLTDNNNIGVVTDNNTGLKVKLAKNLSGLETVSTKNLTASEK 4	25
۵ 🗻 ۵	426	LOSGCLTFTPTTNASTDKTVYGTDGLKFTDNSNTA ::	2 7
s- Ω	472		511
۵ ۔<	512		547 563
<b>λ</b> Ω	548	AAKFGTTRIT-EEEIGFADADGKVDKKSPYLDKKQLQVGGVKITKDSGINAGDQK1S  :	603 60 <b>4</b>
<u>م</u>	604	NVKDATDDTDAVTYKQLKQVQQDADGALQSFSIRDEKGQEFTISNLYSNGNTPNTFETIT 6	.63 .36
۵ م	664	FAGENGISISNDIARGKVKVGIDPINGLTTPRLT-VGSDKDGKTQLVIEQVASGNDTKNI 7 :   :   :   :   :   :   :   :   :   :	722 687
<b>م</b> ج	723	IRGLSPTLPSITNAGGVRTTEQGNTITSDEDKSKAASIGDILNTGFNLKNNSNSVGF	779
۵ م	780	VSTYNTVDFIDGNATTAKVTYDETNQTSKVTYDVNVDEKT	819 799
ъ д	820	IELTGDNGKTNKIGVKTTTLTTTNANGKA 8 :	.48 .59
λ Q	849	TNFSTTDNDALVNAKDIAENLNTLAKEIHTTKGTADTALQTFKVKKDG	896 919
α .«	897 920	ATDDETITVGKDGTQNGKTVNTLKLKGENGLTVATNKDGTVTFGINTQSGLKAGDST 9	.53 166
۵ ہ	954	TLNKDGLSIKNPASNEQIQVGADGVKFAKVDKGNSSTGIDGTSRITKDQIGFTGANG 1	1010 1020
× 0	1011	SLD-TTKPHLTKDKLKVGEVEITNTGINAGGKKITNIQSGDIT-QNSNDA1	058
ъ o	1059	VTGGRVYDLKTELESKINSAAKTAONSLHEFSVADEQGNHFTVSNPYS 1	106
» Ω	1107	- N	1154 1189
<b>م</b> ح	1155	NGKGIVIDSKDGONTITGLSNTLANVTNDGAGHALSQGLANDTDKTRAASIGDVLNAGFN 1 : : :	214
>-	1215	QGNGEAVDEVSTYDTVDF1DGNATTAKVTYDDTSKTSKVVYDVNVDNKTIEVTSDKKLG	1274
0 5	1241	VKTTTTTR-TSANGNATKESAADGDALVKASDIAPHINTIAGDIOTAKGAS-DASSSSY	1251
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1333 VDADGNKVIYDSTDKKYYQVNDKGQVDKNKEVAKDKLVAQAQTPDGTLAQMNVKSVINKE 1392
                                                     1393 QVNDANKKQGINEDNAFIKGLENAAKDTKTKNAAVTV---GDLNAVAQTPLTFAGDTGTT 1449
                                                                                                     1450 AKKLGETLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGTRIDEKGI 1509
                                                                                                                                                                                1569 -SNSGASLPFVVTDANGKPI---NGTDGKPQKAIKGADGKYYHANANGVPVDKDGKPITD 1624
                                                                                                                                                                                                                                               : | | : | : | : | 1477 LAKLGVSAVRFIEPNNTITVDTQNEFATRPLSRIVISEGRACFSNSDGATV------ 1527
                                                                                                                                                                                                                                                                               1625 ADKLANLAAHGK 1636
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1528 ---CVNIADNGR 1536
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Search completed: September 13, 2001, 12:39:11 Job time: 48267 sec

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; Search time 76.31 Seconds (without alignments) 2309.893 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                  September 13, 2001, 12:41:04
                                                                                                OM protein - protein search, using sw model
                                                                                                                                                     Run on:
```

1 MNHIYKVIFNKATGTFMAVA...........NGSADTQGHVGAAVGAGFHF 2314 US-09-361-619-11 11694 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB : Maximum DB :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

probable adhesin z surface protein XF probable RTX famil 190K surface antig cell surface antig hypothetical prote ABC-type transport hypothetical prote hemagglutinin/hemo hypothetical prote mucin, submaxillar hypothetical prote probable invasin 2 probable membrane hypothetical prote extracellular matr toxin-like outer m high-molecular-wei outer membrane pro high-molecular-wei hemolysin A precur hypothetical prote hypothetical prote probable PPE prote outer membrane pro surface protein XF hemagglutinin/hemo filamentous hemagg filamentous hemagg Description SUMMARIES A86036 A82615 A81615 A417704 A417704 S76109 C76109 C76109 F81045 C83333 A83412 E85822 H81193 A43855 JC1340 B43855 D64962 S76412 T31110 A64556 A35140 T34434 S21010 D70575 D71630 D82671 Query Match Length DB 1222.5 953 743.5 463.5 462.5 459.5 450.5 448.6 448 446.5 445.5 Score 668.5 642.5 571.5 571.5 550 552.5 53.5 520.5 520.5 504.5 Result No. 

toxin-like outer m probable hemagalut	hypothetical prote	tac procein - syne crystalline surfac	toxin-like outer m	. toxin-like outer m	hypothetical prote	hemagglutinin-like	hemagglutinin-like	hypothetical prote	hypothetical prote	RTX toxin RtxA VC1	plasma membrane-as	toxin-like outer m	hemagglutinin/hemo
D71917 E83641	E85649	JN0896	H71879	C71953	877300	E82589	B82519	F83068	F82885	C82199	T17372	B64635	в81192
77	7 0	4 79	N	~	~	~	~	7	~	~	7	~	7
3194 3535	1270	1645	2399	2905	3016	3442	3455	2154	4688	4558	1403	2529	1975
e e.	3.8	3.7	3.7	3.7	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6
444	440.5	438.5	436.5	433.5	425.5	425.5	425.5	425	425	424.5	424	419	418
30	32	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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215 HFANAFGTRSTAEGNYSLAVGLTAKAEKG-YTIAIGSNAQAINYGALALGADTRVDL-DY 272

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qq	970 STA	STAVDOGWTLTASGANGSKVASGGTVDLKNTDGNLTISKSGDSNDVVFNLSKDFK 103	124
Ó	1260	-	309
QQ	1025 VDG	LTIANGPAVTASGIDAGSKVISH	375
δλ	1310 LNT		1369
qq	: 1076 V	AAGAVSETSTDAVNGSQLNAVQVQASQPVTFTGNE-GAVKRSLGQSVV 112.	133
Qy	1370 VAQ	H	122
QQ	1124 isG	SGESSTAGTYSGGNLKSVVDEAAGRIHLQLADSPKFGNVVINNGGKISGVTAGTEETD- 118	82
Qy	1423 KNA	OTPLIFAGDIGITAKKLGETLIIKGGOTDINKLIDNNI	174
qq	1183		227
ΟŸ	1475 GVV	GVVAGTDGFTVKLAKDLTNLNSVNAGGTRIDEKGISFVDANGQAKANTPVLSA 152'	527
QQ	1228 Tis		
Οy		NGLDLGGKRISNIGA-AVDDNDAVNFKOFNEVAKTVNNLNNGSNSGASLPFVVTDANG 158	584
<b>a</b> :	1287 SGI		632
S 8		GOSVVISGESSTAGTYSGGNLKSVVDEAAGTIHLOLADSPKFGNVV	387
Oy			1690
qq	1388	:  : :   TEETDAVNFSQLKSISTAVDQGWTL-TASGAN	1431
δ	1691 QSN	GTGADITSVRSADGTMSNITV 17	748
qq	1432 GSF		1476
QY	1749 -NJ	TIDDDGNVLIKAKDGKFYKADDLMPNGSLKAGKSASDAKT-PIGLSLVNPNAGK	1806
q	1477 GNJ		1526
Qγ	1807 G-	STGDAVALNNLSKAVFKSKDGTTTTVSSDGISIQGKDNSSITLSKDGLNVGGKVI 18	1863
qq	1527 GDC	-	563
δy	1864 SN	-	915
qq	1564 TN	VSGGTVDLKNTDGNLAISK	1623
Qy	1916 58	SSSNRTVIRAGTVLGGKGNNDTEKLATGGVQVGVDKDGNANGDLSNVWV 19	964
qq	1624 SGI		1678
Qy	1965 KT	KTQKDGSKKALLATYNAAGQTNYLTNNPABAIDRINEQGIRFFHVNDGNQEPVVQGR 20	2021
qq	1679 SG	LKQAVQSVTVKATRYYSTN	731
Qy	2022 NG		2080
qq	1732 NY	DGDCATGSKAIAAGVGTQASGEGAAAVGSGAAASGKGSTAIGRNAIASADGSVALGDG	1791
Qy	2081		2115
οp	1792 AK	GVQNNTVGTVSVGDAAKGETRSISNVADAKEAMDAVNLRQLDAV	1851
Qy	2116	QTDVEGVGNNITYTESNSVALGSNSAISACTHAGTQAK 21	2153
qq	1852 AQ		1910
Qy	2154 KS		2213
qq	: TN 1191	DTDAVNVS	1961

QY   518   VNNTIGGSNKQIQVGADGIKFADVNVNVSNAAKFGTTRITEEEIGFADADGKVDKKSP   575	670 ISNLTETVTNLGEDALKWDK 932 NKDGTVTFGINTQSGLKAGDSTTL
Oy 2214 OLYKATOGIANATNELDHRIHQNENKANAGISSAMAMASMPQAXIPGRSMYTGGIATHNG 2273  1	

4

QY 1734 TSVRSADGTMSNITVNTALAATDDDGNV	
558	A, Experimental source: strain 9a5c R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
1682	A; Residues: 1-1100 CSIM> A; Residues: 1-1100 CSIM> A; Cross-references: GB: AE004017; GB: AE003849; NID: g9107083; PIDN: AAF84783.1; GSPDB: GN001
Db 509NDVTFNLATALEADSLTTGNTAM	A)ACCESSION: A0.00.3 A)Status: preliminary A.Moleoule tope: DNA
Qy 1623 TDADKLANLAAHGKPLDAGHQVVASLGG	A; Reference number: A82515; MUID:20365717 A; Note: for a complete list of authors see reference number A59328 below
DD 470 SKGWILLASGTNSSNVAPGASVI	201
Db 410 GVTVGKRVTLDSTGLVIAEGPSVISSGII	C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 (C;Date: 18-Aug-2000 Established Comment of the Organization for National August
1508	surface protein XF1981 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa
Db 360 V-ALGESVDLKNSDGNLLITI	RESULT 3 A82615
QY 1450 AKKLGETLTIKGGQTDTNKLTDNNIGVV	1.1.4. 16661.1766557771645577777777777777777777777777
:	OY 2266 GGIATHNGGAVAVGLSKLSDNGQWVFKINGSADTGGHVGAAVGAGFHF 2314
Qy 1395 NDANKKQGINEDNAFIKGLENAAKDTKT	1480
280	2210 VNGSOLYKATQGIANATNELDHRIHQNENKANAGISSAMAMASMPQAYIPGRSMVT
DD 238ALGNGALISTANGIALGA	Db 1429 VAQLKSSEAGGVRYDTKADGSIDYSNITLGGGNGGTTRISNVSAGVNNNDV 1479
Qy 1275 VKTTTLTKTSANGNATKFSAADGDALVKA	2151 OAK-KSDGTAGTTTTAGATGTVKGFAGOTAVGAVSVGASGAERRIONVAAGEVSATSTDA
Db 218QSQDAISIGTGASTTGN	OY 2091 IGDPSTVKADNSYSVGNNNQFIDATQTDVFGVGNNITVTESNSVALGSNSAISAGTHAGT 2150
Qy 1215 LQGNGEAVDFVSTYDTVDFIDGNATTAKN	1372 KDSVAISVALGTGSVAT
Oy 1158 -GIVIDSKDGONTITGLSNTLANVTNDG- 	QY 2031 KHSVAIGFQAKADGEAAVAIGROTQAGNQSTAIGDNAQATGDQSIAIGTGNVVTGKHSGA 2090
123	
OY 1106 SSYDTSKTSDVITFAGENGITTKVNF	1971 SKKALLATYNAAGOTNYLTNNPAEAIDRINEOGIRFFHVNDGNOEPVVOGRNGIDSSASG
	Qy 1911 DPNSGSSSNRTVIKAGTVLGGKGNNDTEKLATGGVQVGVDKDGNANGDLSNVWVKTQKDG 1970
	Qy 1851 LSKDGLNVGGKVISNVGKGTKDTDAANVQQLNEVRNLLGLGNAGNDNADGNQVNIADIKK 1910   1
£ 5	DD 1265TNYTAYNWDAPQNSVGEFSVGSAD 1288
Query Match 6.4%; Score	Db 1258TTTRGAQ 1264
A; Reterence number: A59528 A; Contents: annotation C; Genetics:	:
A; Authors: da Silva, A.C.R.; da Silva, M.; Tsuhako, M.H.; Vallada, H.; Van Sl.	QY 1671 NTGNANAGQAQSLPSLSAAQQSNAASVKDVLNVGFNLQTNHNQVDFVKAYDTVNFVNGTG 1730
A; Authors: Martins, E.M.F.; Matsukuma, F.G.; Nunes, L.R.; Oliveira, M.A.; de Rodrigues, V.; Rosa, A.J. de M.; de Ros	Qy 1616 DKDGKPITDADKLANLAAHGKPLDAGHQVVA-SLGGNSDAITLTNIKSTLPQIDTP 1670
A;Authors: Ferreira, V.C.A.; Ferro, J.J.D.; Junqueira, M.L.; Kemper, B.L.; K. chado, M.A.; Madeira, A.M.B.N.; Madeira	Db 1171TVRQLQNAIGAVATTPTRYFHANS 1194
as-Neto, E.; Docena, C.; El-Dorry, H.; submitted to GenBank, June 2000	Qy 1556 NEVAKTVNNLNNQSNSGASLPFVVTDANGKPINGTDGKPQKAIKGADGKYYHANANGVPV 1615

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Kitajima, J.S.; Franca, S.C.; Franco, M.C.; Fr
Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
Lra, H.W.F.; Marino, C.L.; Marques, M.V.; Martins
J. A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
Osa Jr., V.E.; de Sa, R.C.; Santelli, R.V.; Sawa
J. F.K.; da Silva, A.M.; Silva Jr., W.A.; da Silva,
Silvys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NKGVVRVGIDQTKGLT-TPKL-TVGNNNGK--- 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TKNAAVTVGDLNAVAQT-----PLTFAGDTGTT 1449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDLGGKRISNIGAAVDDNDAVNFKQFNEVAKTV 1562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NLQTNHNQVDFVKAYDTVNF-----VNGTGADI 1733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLI----KAKDGKFYKADDLMPNGSLKAGKSAS 1789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NTGINAGGKKITNIQSGDITQNSNDAVTGGR-- 1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----QNSLHEFSVADEQGNHFTVSNPY 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G--AGHALSQGLANDTDKTRAASIGDVLNAGFN 1214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVTYDDTSKTSKVVYDVNVDNKTIEVTSDKKLG 1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEVAKDKLVAQAQTPDGTLAQMNVKSVINKEQV 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VAGTDG - - FTVKLAKDLTNLNSVNAGGTRIDEK 1507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TDGKPQKAIKGADGKYYHANANGVPVDKDGKPI 1622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNSDAITLTNIKSTLPQIDTPNTGNA-NAGQAQ 1681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KASDIATHLNTLAGDIQTAKGASQASSSASYVD 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----AVNVAQLKLLAESVGGGWNLTASGANSSN 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | :| | ; | | ; | VD------LKNTDGNLLITKAIGI------ 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HITDGVIVGS-----NVTLGSTGLVITDGPSV 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQVYVNSDSTENCVEILGDSSQTSFIHSASNDK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----TSTLSTSMWRSTLGAVSI 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -------DAVNFSQLQAVSTASKG 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NFAI----- 237
                                                                                                                                                                                                                                                                                                                                                                                                        re 743.5; DB 2; Length 1190;
d. No. 3.3e-21;
Mismatches 481; Indels 441; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | || || : ||:|:| || SA----ASSKK------GTQPRRSNNAMTAKRSA 62
; Facincani, A.P.; Ferreira, A.J.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :| : | : | ::|
ASSSVTTR----GGVALGQGSLAATASGI---
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QY         29 GSSSSTAGQVGSSPVIRLTRVATLAILVIG-ATLNGSAYAQNNSKIAFGTTGNNDNASAS 87           Db         283 GGKTYTATVAGDGSWTTTVPAADLSVLRDGDATVQASVSTINGNTASAT 331           QY         88 NEASIAIGSLAKAHANQAIAIGGSKPDPRNQAANQKAGSHAKGKESI 134           Db         332 HAYSVDATAPTLAINTIATDDILNAAEAGNPLTISGSSTAEAGGTVTVTLNGV 384           QY         135 AIGGDVLAEGDASIAIGSDLXLDRNSTNSKYPNGLLSTLIQNHTVLRQIRDSNGSQKYR 194           Db         385 TYSGSVQADGSMSVSLPTADLSNLTASQXTVSASYSDKAG 424           QY         195 RTAAEGHASTAVGAMAYAKCHFANAFGTNSTAGNYSLAVGLTAARAEKGYTIAIGSNAQA 254	Db 425	QY   QY   VKLAKNLEGLETVSTKNLTASEKVTVGSGN-NTAELQSGGLTFTPTTNASTDKTVYG   458	592 DSGINAGDQKISNVKDATDDTD	TÄQAĞQTLTVTLNNNTYQİTVLADĞTW  TYDETNQTSKVTYDVNVDEKTIELTGDNGKTNKI	OY 894 KDGATDD
1790 DAKTPTGLELVNPNGRGSTGDAVALNILSTRTDSNDVTFNLATALKVD-SLTTGNT 654   OY   1790 DAKTPTGLELVNPNGRGSTGDAVALNILSTRATDSNDVTFNLATALKVD-SLTTGNT 654   OY   1790 DAKTPTGLELVNPNGRGSTGDAVALNILSTRAVFKSRDGTTTTVSSDGISIOGKDNSSI 1849   O	1932 KGNNDTEKLATGGVQVGVDKDGNANGDLSNV-WVKTQKDGSKKALLATYNAAG  1932 KGNNDTEKLATGGVQVGVDKDGNANGDLSNV-WVKTQKDGSKKALLATYNAAG  1947 MGLVITDGPSYTSSGINAGSQKITNVAAGTADTDAVHSQLNTAMAGS  1984 QTNYLTNNPAEAIDRINEGGIRFFHVNDGNQENVQGRNGIDSSAGKHSVAIGFQAKAD  1984 QTNYLTNNPAEAIDRINEGGIRFFHVNDGNQENGIDSSAGKHSVAIGFQAKAD  1985		<pre>Qy 2293 KINGSADTGGHVGAAVGAGFHF 2314    !  !                                </pre>	oer: A85480; MUID:21074935; PMID:11206551 5547 innary : DNA : BNA : BNA : GB:AE005174; NID:912513368; PIDN:AAG54838.1; source: strain 0157:H7, substrain EDL933	Query Match 5.7%; Score 668.5; DB 2; Length 5188; Best Local Similarity 21.6%; Pred. No. 1.7e-17; Matches 606; Conservative 290; Mismatches 1017; Indels 895; Gaps 141;

Dp	1195	:      :      :
Qy Db	964	NPASNEQIQVGADGVKFAKVDKGNSSTGIDGTSRITKDQIGFTG-ANGSLDTTKP 1017   ::
Qy Db	1018	HLTKDKLKVGEVEITNTGINAGGKKITNIQSGDITQNSNDAVTGGRVYDLKTELESKINS 1077 
Qy Db	1078	AAKTAQNSLHEFSVADEQGNHFTVSNPYSSYDTSKTSDVITFAGENGITTKYNKGVVRVG 1137
Qy Db	1138	IDQTKGLTTPKLTVGNNNGKGIVIDSKDG-QNTITGLSNTLANVTNDGAGHALSQGLAND 1196
oy D	1197	1
Qy Db	1219	126
67 07	1266	EVTSDKKLGVKTTTLTKT-SANGNATKFSA-ADGDALVK 1302 ::
Qy	1303	ASDIATHLNTLAGDIQTA-KGASQASSSASYVDADGNK 1339 
Qy	1340	VIYDSTDKKYYQVND-KGQVDKNKEVAKDKLVAQAQTPDGTLAQMNVKSVINKEQVN 1395 
o o	1396	DANKKOGINEDNAFIKGLENAAKDTKTKNAAVTVGDLNAVAQT 1438 
Oy Db	1439	PLTFAGDTGTTA-KKLGE-TLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNS 1496  :::    :
Qy Db	1497	VNAGGTRIDEKGISFVDANGQAKANTPVLSANGLDLGGKRISNIGAAVDDNDAVNF 1552 
Qy Db	1553 1879	KQFNEVAKTVNNLANQSNSGASLPFVYTDANGKPINGTDGKPQKAIK-GADGKYYHA 1608 
Qy Dp	1609 1922	NANGVPVDKDGKPITDADKLANLAAHGKPLDAGHQVVASLGGN 1651 
Oy Dp	1652 1982	SDAITLINIKSTLPQIDTPNTGNANAGQAQSLPSLSAAQQSNAASVKDVLNVGFNLQT 1709  :
Oy Dp	1710 2026	NHNQVDEVKAYDTVNFVNGTGADITSVRSADGTMSNITVNTAL 1752 
ογ Db	1753 2086	AATDDDGNVLIKAKDGKFYKADDLMPNGSLKAGKSASDAKTPTGLSLVNPNAGKG 1807       :
ογ	1808	STGDAVALNNI.SKAVFKSKDGTTTTTVSSDGISIQGKDNSSITL.SKDGLNVGGKVIS 1864   : :

190K surface antigen precursor - Rickettsia rickettsil
C; Species: Rickettsia rickettsi
C; Species: Rickettsia rickettsi
C; Species: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change OB-Oct-1999
C; Accession: A41477
R; Anderson, B.E.; McDonald, G.A.; Jones, D.C.; Regnery, R.L.
Infect. Immun. 58, 276-2789, 1990
A; Title: A protective protein antigen of Rickettsia rickettsii has tandemly repeated, A; Reference number: A41477; MUID: 90354033
A; Rossion: A41477
A; Molecule type: DNA
A; Residues: 1-2249 < AND>
A; Residues: 1-2249 < COND
A; Residues: 1-2249 < COND
A; Residues: 1-2249 < COND
A; Residues: 1-2249 < COND
A; Residues: 1-2249 < COND
A; Residues: 1-2249 < COND
A; Residues: 1-2249 < COND
A; Residues: 1-2249 < COND
A; Residues: 1-2249 < COND
A; Residue 430 as Gly, and CAA for residue C; Reywords: Surface antigen; tandem repeat 114; 2174 FAGQTAVGAVSV------GASGAERRIQNVAAGEVSATSTDAVNGSQL 2215 AG-----TVLGGKGNNDTEK------LATGGVQVGVDKDG---NANGDLSNV 1962 2233 TGLPTITFNAISGDNILNADEKGQPLTISGGSTGLAT-GAQVTVTLNGHNYSATTDASGN 2291 2292 WTLTVPVSDLAAL-----GQANYTVSASATSAAGNTASSQANLLVDSGLPDVTINTVA 2344 2345 GDDIINAAEAGADQTISGVVTRAAAGDTVTVTLGGNTYTATVQSNLSWSVSVPTADLQAL 2404 2146 D--DVINATEHAQAQIISGSATGAATGSTVTVTI-GTNTFTTVLDASGNWSVGVPASVVS 2202 1865 NVGKGTKDTDAANVQQLNEVRNLLGLGNAGNDNADGNQVNIADIKKDPNSGSSSNRTVIK 1924 ------KHSVAI---GFQAK 2041 2042 ADGEAAVA----IGROTQAGNQSIAIGDNA-----QATGD---QSIAIGTGNVVTCKH 2087 -NNITVT----ESNSVALGSNSAIS----AGTHAGTQAKKSDGTAGTTTTAGATGTVKG 2173 2216 YKATQGIANATNELDHRIHQNENKANAGISSAMAMASMPQAYIPGRSMVTGGIATHNGQG 2275 2637 TLTINTIAS-----DDIL----NAAEAGSPLTISGTSTAE-----TGQTVTVTLNG 2678 Gaps 261 ALGADTRVDLDYGIALGYGSQILNNNNNNNNKAYVPEGNGSNIKSSKATGNGLFSIGSST 320 321 IKRKIINVGAGYEDTDAVNVA----QLKAVENLAKRQITFKGDDNGTGVKKKLGETLTI 375 1963 WVKTQKDGSKKALLATYNAAGQTNYLT-----NNPAEAIDRINEQGIRFFHVNDGN Ouery Match 5.5%; Score 642.5; DB 2; Length 2249; Best Local Similarity 23.6%; Pred. No. 5.6e-17; Matches 522; Conservative 210; Mismatches 776; Indels 707; 2276 AVAVGLSKLSDNGQWVFKINGSA-------DTQGHVGAA 2307 2679 ATYTG--TVQADGSWSVSVPTSALGALNASNYTVSATVNDKAGNPGSA 2724 ---AIGDPSTVKADNSYSVGNNNQFIDATQTDVFGVG------NASVTDAGG-----2014 QEPVVQGRN-GIDSSASG-------2203 ALANGTVTI----------S 1925 2405 2088 2124 q ò a δy qq δ g δ qq ò g ò q g g a δ QQ δλ ò à ð Dp ŏ q

ΟŊ	376	KGGETQADKLTDNNNIGVVTDNNTGL	
Д	145	NGNNAVAANHGFDAPADNYTGLGNIALGGANAALIIQSAAPSKITLAGNIDGGGII 200	
Qy	414	TVSTKNLTASEKVTVGSGNNTAELQSGGLTFTPTTNASTDKTVYGTDG 461	
δy	462	YLDKD	
qq	252		
ΟŊ	503	KLKVGNSTLNNGGLTVNNTIGGSNKQIQVGADGIKFADVNVNVSNAAKF 551	
Dp	297	SVGAGTATLGGAVIKATTTKLTDAASAVKFTNPVVVTGAIDNTGNANNGIVTFT 350	
οy	552	GTTRITEEEIGFADADGKVDKKSPYLDKKQLQVGGVKITKDSGINAGDQKISNVKDATDD 611	
qq	351	3GVVKANTINLTD	
οy	612	TDAVTYKQLKQVQQDADGALQSFSIRDEKGQEFTISNLYSNGNIPNIFETIIFAGEN 668	
QQ	393	ASAVTFTNPVVVTGAIDTGAIDTGAIDTGAIDVTFTGNSTVT 428	
οy	699	-GISISNDIAKGKVKVGIDPINGLTTPKLTVGSDKDGKTQLVIEQVASGNDTKNII 723	
qq	429	GDIGNTNALATVNVGAGTATLGGAVIKATTTKLINAA	
ΟŊ	724	DKSK	
qq	466	:: ::	
Qγ	784	NTVDFIDGNATTAKVIYDETNQTSKVTYDVNV 815	
QQ	513	ATISVGAGIATLGGAVIKATTTKLTDAASAVKFTNPVVVTGAIDNTGNANNGIVTFTGN- 571	
οy	816	DEKTIELTGDNGKTNKIGVKTTTLTTTNANGKATNFSTTDNDALVNAKDIAENLNTLAKE 875	
qq	572		
δÿ	876	IHTTKGTADTALQTFKVKKDGATDDETITVGKDGTQNGKTVNTLKLKGENGLTVAT 931	
qq	623	:	
δy	932	STTLN	
QQ	657	NSLATISVGAGTATLGGAVIKATTTKITNAVSAVKFTNPVVVTGAID 703	
δy	985	K-GNSSTGIDGTSRITKDQIGFTGANGSLDTTKPHLTKDKLKVGEVEITNTGINAGG 1040	
q	704	STGNANNGIVTFTGNSTVTGD-IGNTNALATVNVGAGTATLGGAVIKATT 752	
ΟŊ	1041	KKITNIQSGDITQNSNDAVIGGRVYDLKTELESKINSAAKTAQNSLHEFS 1090	
οqα	753	TKLTNAASVETETNANAVETGAIDNTTGGDNVGVENENGALSQVTGDIGNTNSLATIS 810	
Qy	1091	VADEQGNHFTVSNPYSSYDTSKTSDVITFAGENGITTKVNKGVVRVGIDQTKGLTTP 1147	
Ob	811	VGAGTATLGGAVIKATTTKLTNAASVLTLTNANAVLTGAVDNTTG 855	
οy	1148	KLTVGNNNGKGIVIDSKDGQNTITGLSNTLANVTNDGAGHALSQGLANDTDKTR 1201	
qq	856	GDNVGVLNLNGALSQVTGDIGNTNSLATI-SVGAGTATLGGAVIKATTTKLTN 907	
δλ	1202	AASIGDVLNAGFNLQGNGEAVDFVSTYDTVDFIDGNATTAKVTYDDTSKTSKVYYDVNVD 1261	
QQ	806	AASVLTLTNANAVLTGAIDNTTGGDNVGVLNLNGALSQYTGDIGNTNSLATISVGAG 964	
QY	1262	NKTIEVTSDKKLGVKTTTLTKTSANGNATKFSAADGDALVKASDIA-THL 1310	
QQ	965	TATLGGAVIKATT-TKLTDAASAVKFTNPVVVTGAIDNTGNANNGIVTFTGN 1015	

oy D	1311	TLAGGIQTAKGASQASSASYUDAGNKVIYDSTDKKYYQVNDKGYVKKEVAKKKIV 1370
δλ	1371	PDGTLAQMNVKSVINKEQVNDANKKQGINEDNAFIKGLENAAKDTKTKNAAVT 142 
g	1058	ANNGIVTFTGNSTVTGN 109
Qy Dp	1429	VGDLARVAQTPLIFAGDIGITAKKLGETLITKGGQTDINKLIDN 1472 
οy	1473	KLAKDLTULN SVNAGGTRIDEKGISFVDANGOAKAN
qq	1142	AIDNTGNANNGIVTFTGNSTVTGDIGNTNALATVNVGAGIT-LQAGGSLAAN 1192
δλ	1522	TPVLSANG-LDLGGKRISNIGAAVDDNDAVNFKQFNEVAKTVNNLNNQS 1569
Dp	1193	NIDFGARSTLEFNGPLDGGGRAIPYFKGAIANGNNAILNVNTKLLTASHLTIGTV-AEI 1251
δ δ	1570	NSGASLPFVVTDANGKPINGTDGKPQKAIKGADGKYYHANANGVPVDKDGKPI 1622
6	· ~	291 IFUS
g G	1300	IVVFNGGVNGLNVGSNVAGTARNIGDGGGNKFNTLLIYNAVTITDDV 135
Οy	1656	TLTNIKSTLPQIDTPNT
Dp	1360	NEGIQNVLINKNADFTSSTAFNAGAIQINDATYTIDANNG-NLNIPAGNIQ 1410
δy	1716	
ф	1411	FAHADAQLVLQNSSGNDRITILGANIDPDNDDEGIVIL1448
Qy	1776	LMPNGSLKAGKSASDAKTPTGLSLVNPNAGKGSTGDAVALNNLSKAVFKSKDGTTTT 1833
qq	1449	NSVTAGKKLTIAGGKTFGGAHKLQTILFKGA-GDCSTAGTTFNT 1491
δy	1834	VSSDGISIQGKDNSSITLSKDG-LNVGGKVISNVGKGTKDTDAANVQQLNEVRNLLGLGN 1892
qq	1492	TINIVEDITGOLELGATTANVVLFNDAVQLTQTGN 1525
δλ	1893	AGNDNADGNQVNIADIKKDPNSGSSSNRTVIKAGTVLGGKGNNDTEKLA 1941
g	1526	IGGFLDFNAKNGMVTLNNNVNVAGAVQNTGGTNNGTLIVLGASNLNRVNGIAML 1579
Qy	1942	-TGGVQVGVDKDCNAN-GDLSNVWVKTQKDGSKKALLATYNAAGQTNYLTNNPAEAIDRI 1999
QQ	1580	KVGAGNVTIAKGGKVKIGEIQGTGTNTLTLPAHFNLTGSINKT 1622
δλ	2000	NEGGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVALGRQAKADGEAAVAIGRQTQAGNQ 2059
Db	1623	GGQALKINFMNGGSVSGVVGTAANSVGDITTAGAT 1657
Qy	2060	SIAIGDNAQATGDQSIAIGTGNVVTGKHSGAIGDPSTVKADNSYSVGNNNQFIDATQTDV 2119
СD	1658	SFASSVNAKGTATLGGTTSFANTFTNTGAVTLAKGSITSFAKNVTATSF 1706
Oy	2120	SAISAGTHAGTQAKKSDGTA
pp	1707	VANSATINFSNSLAFNSNITGGGTTLTLGANQVTYTGT-GSF 1747
ō,	2175	NGSQLYKATQGIANATN:
qq	1748	TDTLTLNTTFDGAAKSGGNILIKSGSTLDLSGVSTLALVVTATN 1791

RESULT 6 B71704 cell surface antigen (sca3) RP451 - Rickettsia prowazekii C;Species: Rickettsia prowazekii

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	978 VKFAKVDKGNSSTGIDGTSRITKDQIGFTGANGSLDTTKPHLTKDKLKVGEVEIT-NTGI	OY 1147 PKLTYGNN- NGKGIVIDSKDGONTITGLSNTLANYTNDGAGHALSQCLANDTDKT RAA 1203  Db 949GNNTYNLNAIIVNGCNGILNAFTKLKASDDTIGTVKII 986  QY 1204 SIGDV-LNAGFNLQGNGEAVDFVSTD-TVDFIDGNA-TTAKVTYDDTSKTSK 1253  1	OY 1296 DGDALVKASDIATHLNTLAGDIQTA	1441 TFAGDTGTTAKKLGETLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLIN  1271 DFQGNAGVINLNDDIEIDGSVTSTGNVNGTLNFNGSGKVTGLINNIVMLQAGAGDVSL  1494 LNSVNAGGTRIDEKGISFVDANGOAKANTPVLSANGLDGGKRISNIGAAVD  1	QY         1546 DNDAVNFKQFNEVARTVNNLANDSNSGASLPFVYTDANGKPINGTDGKPQKA 1597           DD         1389 DIIINAGSVNFSNTLKSGATWONNNYTATDISGKANN
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000 C;Accession: B71704 R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U Nature 396, 133-140, 1998 A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499 A;Accession: B71704 A;Accession: B71704 A;Accession: B71704 A;Molecule type: DNA A;Residues: 1-2340 cAND> A;Cross-references: GB:AJ23571; GB:AJ235269; NID:g3868717; PIDN:CAA14908.1; PID:g38610C A;Experimental source: strain Madrid E C;Genetics: A;Gene: sca3; RP451	Query Match Best Local Similarity 21.7%; Pred. No. 3.1e-14; Matches 554; Conservative 295; Mismatches 935; Indels 773; Gaps 133; Qy 59 ATLINGSAYAQNISKIAFGT-TGNIDINAGASINESIIGSLAKAHANQAIAIGGSKPDPRN 117	Qy         174 LIQNHTVLRQIRDSNGSQKYRRTAABGHASTAVGAMAYAKGHFANAFGTRSTAEGNYSLA         233           b         118 ISNNVTST	350 AKROI-TFKGDDNGTGYKKKLGETLIKGGETQADKL-TDNNNIGVYTDNN	OY 493 DENKRYLDKDKLKVGNSTLNNGGLTVNNTIGGSNKQIQVGADGIKFADVNVNV 545  OY 493 DENKRYLDKDKLKVGNSTLNNGGLTVNNTIGGSNKQIQVGADGIKFADVNVNV 545	OY 599 DQKISNVKDATDDTDAVTYRQLKQVQQDADGALQSFSIRDEKGQEFTISNLYSNGNTPNT 658  Db 503VTADRTFTIYNNLNQSGNDEYGIVKIEAIK

| | | | | : : : : | | PISLNQFALTGIDVDGNSTTEREFYEVS---GYSNY 488

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960 -LSIKNPASNEOIOVGADGVKFAKV	ò	vat
909 GTQNGKTVNTLKLKGENGLTVATNK 	Qy Dp	<ul><li>\$; Score 560; DB 2; Length 3029;</li><li>\$; Pred. No. 1.2e-13;</li></ul>
:  :    VATVSDLAGNPATPATRNI	q <sub>Q</sub>	A:Cross-references: EMBL:D65999; GB:AB001339; NID:g1001396; PIDM:BAA10087.1; PID:d101073 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
	òò	A; Molecule type: DNA A; Residues: 1-3029 <kan></kan>
818KTIELTGDNGKTNKIG ::  ::  1215 VEAGSPVAVSGTTTGVEDGQVVTVT	QY Dp	A;Reference number: S74322; MUID:97061201 A;Accession: S76109 A;Status: preliminary
: : :     :       :       :         :	QQ	DNA Res: 3, 109-136, 1996 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
765 NTGENLKNNSNSVGEVSTYNTVDFI	QY	R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
707 QLVIEQVASGNDTKNIIRGLSPTLP :   :   :         1102 -VTINAIAV-DDIINAVEAGSPVAV	Qy GB	A;Variety: PCC 6803 C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999 C;Accession: S76109
1052 TANGAGEWILDYTGTLLADGDYELS	qq	hypothetical protein - Synechocystis sp. (strain PCC 6803) C:Species: Synechocystis sp.
650 YSNGNTPNTFETITFAGENGIS	ΟŽ	RESULT 7 876109
	· q	Db 2063 TGIWGMSFYGKIKQNSKNSASGYQSNTGGGI-IGFDY 2098
	Oy O	2287 NGQWVFKINGSADTQGHVGAAVGAGFHF
545 VSNAAKFGTTRITEEEIG-FADADG	ð á	2027 NGLNKTNTLLNNKINLKRLNTNNQAIIAAGDEDNIV
:   907 INAIAVDDIINAVEAGSPVAVSGTT	QQ	DD 19/1 DELSNRINVNGLNEGVVGLNGIEVENFILDIAINMDNFTAKEIGNRIEELSDANTV 2026 Ov 2007 NDFDHDANBWRANAGTEGANAMGENEGANTMCCTARHUNCCANANAT GRIEG 2006
	Oy	KGFAGQTAVGAVSVGASGAERRIQNVAAGEVSATSTDAVNGSQLYKATQGIANAT
448 TNASTDKTVYGTDGLKFTDNSNT: :   :         :	ð á	
: :: :: :: : :	qa	DD 18/b NIUNGCKUNCDYGNISNNSSNEAGGSSSDKNYGIT 1910 OV 2118 DVFGVGNNITVTESNSVALG-SNSAISAGTHAGTOAKKSDGTAGTTTTAGATGTV 2171
404 KLAKNLSGLETVSTKNLTASEKV	Qy	NQSIAIGDNAQATGDQSIAIGTGNVYTGKHSGAIGDFSTVKADNSYSVGNNNQFIDATQT
: LTVNDKTFTGAVGAGGLFSI	qq	1836 ASEEQNKFVKWVADANGLVLLTDTGGRDDT-GGRDDTRGRG
685 YTLDNTAPAASITLDANITADDIIN 375 IETOA	a ò	
325 IINVGAGYEDTDAVN	Qy	OY 1938 EXLATGGVOVGVDGNANGDLENWWKYQKDGGKKALLATYNAAGQTNYLTNNPAEAID 1997  DD 1789 SDLDNLIIKIKAHSDTNITSDTKHQIVKLETGAIYPPVPQTKVIID 1835
280SQILNNNNNN   : :         628 SGATISNVSGSGSVYTVTVTGIANN	, dd	Db 1729 NVEVNTNLANVEDIVLDLANYELKYTGNVȚHNGLLTIITYFDTALQKGGHILVSQGSNVDM 1788
569 GTFSNPQTIDTIAPIVTSILRNNPT	qq	Qy 1897 NADGN-QVNIADIKKDPNSGSSSNRTVIKAGTVLGGKGNN-DT 1937
	oy .	Qy 1844 KDNSSITLSKDGLNVGGKVISNVGKGTKDTDAANVQQLNEVRNLLGLGNAGND 1896 
161 STNSKYPNGLLSTLIQNHTVLRQIR           : :     :   S20 _mx_GTTANETmDVGGT_MVDACTT	oy G	Db 1630 IDLDVLPRSLSLFNYFTDIKADNLNFADDTATANFKDAVVIDAHIDNGGI-LKF 1682
	QQ ·	Qy 1792KTPTGLSLVNPNAGKGSTGDAVALNNLSKAVFKSKDGTTTTTVSSDGISIQG 1843
105 AIAIGGSKPDPRNQAANQKAGS	Oy	QY 1/69 KEYKDDLMPWGSLKAGKAS
:      : 432 LIDANATGGGYERVOFEFODTLGNP	qq	1513 TDFDTGNDGIIGDANNRLKSIELTGNGT

56 VIGATLNGSAYAQNN-----SKIAFGTTGNNDNASASNEASIAIGSLAKAHANQ 104

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TIDGNTYTAT-VTGNAWTENIPVADIANFEATE-EV 1272 STWWSLDGIE-----IGTV 1051 : || : | | : | || :| SLDG-IEIGTVTANG--AGEWTLDYTGTLLADGDYEL 1371 GK-----VDKKSPYLDKKQLQVGGVKITKDS 593 AVTYKQLKQVQQDADGALQSFSIRDEKGQEFTISNL 649 SISNDIAKGKVKVGIDPINGLTTPKLTVGSDKDGKT 706 PSITNAGGVETTEQGN--TITSDEDKSKAASIGDIL 764 AKEIHTTKGTADTALOTFKVKKDGATDDETITVGKD 908 KDGTVTFGINTQSGLKAGDST----TLNKDG---- 959 TLRVDGRPSVLTG------527 RDSNGSQKYRRTAAEGHASTAVGAMAYAKGHFANAF 220 :| : | : | SDLIVDADLTIAASIATTDAAGNLGSATDNQT---- 790 AAESGQAIPITGTVGGEFNVGDTVTLTVNGKPFTGT 850 STLNNGGLTVNNTIGGSNKQIQVGADGIKFADVNVN 544 Trgvedgovtvtldgntrtatvtgnamte---nip 963 IDGN----ATTAKVTYDETNQTSKVTYDVNVDE---- 817 GVKTTTLTTTNANGKA-----TNFSTTDNDA 858 -- HAKGKESIAIGGDVLAEGDASIAIGSDDLYLDRN 160 TIAIGSNAQAINYGALALGADTRVDLDYGIALGYG- 279 NNNKAYVPEGNGSNIKSSKATGNGLFSIGSSTIKRK 324 NVAQLKAVENLAKRQITFKGDDNGTGVKKKLGETLT 374 ADKLTDNN------NIGVVTDNNTGLKV 403 -----TVGSGNN---TAELQSGGLTFTPT 447 TALEDITRITRDKIG-----FSNKAGTVDENKPYLD 500 :| | | |:|| IWNNASNDVRQ-----FSFALGA-----PL ΟY

qq	1372	SVTATNPTVDTTAPT 1397	
Οy	1019	LTKDKLKVGEVEITNTGINAGGKKITNIQSGDITQNSNDAVTGGRVYD 1066	
qq	1398		
δy	1067	LKTELESKINSAAKTAQNSLHEFSVADEQGNHFTVSNPYSSYDTSKTSDVITFAGENGIT 1126	
qq	1453	FNIPVADIANFEATEEVVA	
Qy Db	1127	TKVNKGVVRGIDQTKGLTTPKLTVGNNNGKGIVIDSKDGQNTITGLSNTLANV 1180	
ζ	1181	TNDGAGHALSOGLANDTDKTRAASIG-DVLNAGFNLOGNGEAVDEVST 122	
qq	1560		
δλ	1228		
QΩ	1616	DDTLVF-NGTAEADSTVVVSLDGIEIGTVTANGAGEWTLDYTGTLLADGDYELSVTATNP 1674	
Qy Dp	1281 1675	TKTSANGNATKFSAADGDALVKASDIATHLNTLAGDIQTAKGASQASSSASYVDADGN 1338	
οÿ	1339	KVIYDSTDKKYYQVNDKGQVDKNKEVAKDKLVAQAQTPDGTLAQMNVKSVINKEQVNDAN 1398	
QQ	1727		
οy	1399	KKQGINEDNAFIKGLENAAKDTKTKNAAVTVGD-LNAV-AQTPLTFAGDTGTTAKKL 1453	
οqα	1767	ATVSDLAGNPATPATRNITVDTTAPTVTINAIAVDDIINAVEAGSPVAVSGTTIGVED 1824	
Qy	1454	GETLTIK-GGQTDTNKLTDNNIGVVAGTDGFT 1484	
Dp	1825	GOVVIVILIGINIYTATVIGNAWIFNIPVADIANFEATEEVVATVSDLAGNPATPATRII 1884	
οy		VKLAKDLTNLNSVNAGGTRIDEKGISFVDANGQAKA-NTPVLSANGLDLGG 1534	
Q Q	1885	VDTVAPAVTIDSISDDTGAQANDFIINDDTLVFNGTAEADSTVVVSLDGIEIGT 1938	
οy		KRISNIGAAVDDNDAVNFKQFNEVAKTVNNLNNQSNSGASLPFVVTDANGKP 1586	
g	1939	VTANGAGEWTLDYTGTLLAD-GDYELSVTATNPTGNSATATQTIVVDTTAPTVTINAIAV 1997	
οy		INGTDGKPQKAIKGA 1615	
qq	1998	DDIINAVEAGSPVAVSGTTTGVEDGQVVTVTIDGNTYTÄTVTGNAWTFNIPVADIANFEA 2057	
y a	1616	DKDGKPITDA1637	
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දු දු	2118	JAGGHQVARSLGGNSDAITLINIKSITLPQLIDTPNTGNANAGQAQ 1681   ::	
Οy	1682		
QQ	2178	:: :	
οy	1741	G-TMSNITVNTALAATDDDGNVLIKAKDGKFYKADDLMPNGSLKAGKSASDAKTPTGLSL 1799	
qq	2229	: :	
οy	1800	VNPNAGKGSTGDAVALNNLSKAVFKSKDGTTTTVSSDGISIQGKDNSSITLSKDG 1855	
Dp	2278	INAVEAGSPVAVSGTTTG	
δλ		GNAGNDNADGNQVNIADIKKDPNS :  : :  : :  : :	
Dp	2328	NIYTATVIGNAWIFNIPVADIANFEATEEVVATVSDLAGNPAT 2370	

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C. Species: Escherichia coli
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C. Species: I: Glaser, P.; Danchin, A.
B. Mootalia: Multiple IS insertion sequences near the replication terminus in Escherichia A; Reference number: A48399; MUID:92190338
A; Recession: C48399
A; Rocession: C48399
A; Rocession: DNA
A; Residues: A64-2020
A; Consorter consistent with the nucleotide translation
A; Rose, D. St.; Plunkert III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A; Rose, D. J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Roses, D. J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Reference number: A64720; MUID:97426617
A; Rocession: D64891
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A;Cross-references: GB:AE000237; GB:U00096; NID:g1787665; PIDN:AAC74483.1; PID:g17876
A;Experimental source: strain K-12, substrain MG1655
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 'M',915-2020 <BLA2>
A;Coss-references: GB:AE000237; GB:U00096; NID:g1787665; PIDN:AAC74487.1; PID:g17876
A;Experimental source: strain K-12, substrain MG1655
                              --IKAGTVLGGKGNNDTEKLATGGVQVG----VD 1950
                                                                                                     -----ANGDLSNVWVKTQKDGSKKALLATYNAAGQTNYLTN 1990
                                                                                                                                         2424 IDGNTYTATVTGNAWTFNIPVADIANFEATEEVVATVSD-----LAGNPATPATRNITV 2477
                                                                                                                                                                                                                                         |: |: | : | : | | | | | |: |: | AGSPVAVSGTTTGVEDGQVVTVTIDGNTYTATVTGNAMTFNIPVADIANFEATEEVVATV 2657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2031 KHSVAIGFQAKADGEAAVAIGRQTQAGN-----QSIAIGDNAQATGDQSIAI------ 2077
                                                                                                                                                                                                                                                                                                                                                                                                                      -GTGNVVTGKHSGA-IGDPSTVKAD-NSYS---VGNNNQF------IDATQ 2116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TDVFG-----VGNNITVTES------NSVALGSNSAISAGTHAGTQAKKSD 2156
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                                                                                                                                                                                                        1991 N.-.-PAEAIDRINEQ---GIRFFHVND-----GNQE---PVVQGRNGID----SSASG
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                                                                                                     KDGN-----
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A; Start codon: GTG
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.ch 4.8%; Score 558; DB 2; Length 2020; 1 Similarity 22.3%; Pred. No. 8.2e-14; 493; Conservative 244; Mismatches 780; Indels 690; Gaps 120;	NGTCVKKKLGETLTIKGGETQADKLTDNNNIGVVTDNNTGLKVKLAKNLSGLE 413	NDVILDKTEKTLIRDSVFTYTENADGTISLQDSNGRKATINLMQIDEANNTVALE 199	TVSTKNLTASEKVTVGSGNNTAELQSGGLTFTPTTNASTDKTVYGTDGLKFTDNSNTA 471	ADGATKWQYNHNGELVITGDNATVNNNGKTTVDGKDSTGTEINGNNGKV 251	TRITKDKIGESNKAGTVDENKPYLDKDKLKVGNSTLNN 513	IQDGDLDVSGGGHGIDITGDSATVDNK-GTMTVTDPESMGIQIDGDKAIVNNEGESTITN 310	IDVGADGIKFADVN 542	GGTGTQINGDDATANNNGKTTVDGKDSTGTEINGNNGKVIQDGDLDVSGGGHGIDITGDS 370	VNVSNAAKFGTTRITE-EEIGFADADGKVDKKSPYLDKKQLQVGGVKITKDSGI-N 596	NKGIMIVIDPESIGIQVDGDQAVVNNEGESAIIN 408	AGDQKISNVKDATDDTDAVTYKQLKQVQQDADGALQSFSIRDEKGQEFTISNLYSNGNTP 656	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	AKGKVKVGIDPING	QDGDLDVSGGGHGIDITGDSATVDNKGTMTVTDPE-SIGIQIDGDQ 493	VASGNDTKNIIRGLSPTLPSITNAGGVRTTEQGNTITSDEDKSKAASIGDILNTGFNLKN 772	TITN-GGTGTQINGNDAT	PYNTVI	IGIVNLDGSLTVTGGAHGVENIGDNGTVNNK 572	KIGVKTTTLTTTNANGKAINFSTIDNDALVN	GDIVVSDTGSIGVLINGEGATVSNTGDVNVSNEATGFSITTNSGKVSLAGSMQVGDFSTG 632	KDIAENLNTLAKEIHTTKGTADTALQTFKVKKDGATDDE 901	VDLNGNNNSVTLAAKDLKVVGQKATGINVSGDANTVNITGNVLVDKDKTADNAAEYFFDP 692	TITVGKDGTQNGKTVNTLKLKGENGLTVATNKDGTVTFGINTQSGLKA 949	DGKLTVVSDS	GDSTTLNKDGLSIKNP-ASNEQIQVGADGVKFAKVDKGNSSTGIDGTSKITKD- 1001	GDGNTVNMNGGLELIGEKNALADGSQVTSLRTGYSYTSVIVVSGESSVYLNGDTTISGEF 800	TGANGSLDTTKPHLTKDKLKVGEVEIT 1032	PLGFAGVIRVQDKALLEIGSGATLTMQDIDSFEHHGTRTPELTYADSGAKIVNKGTVEIQ 860	NTGIN-AGGKRITNIQSGDITQNSNDAVTGGRVYDLKTELESKINSAAK 1080	: : :	LVAQSNSTIINTDSGIIDLYGRGSVGMLA 972	-TTKVNKGVVRVGIDQTKGLTTPKLTVGNNNGKGIVIDSKDGQNTITGL 1173	KITLDSMW	SNTLANVTNDGAGHALSQGLANDTDKTRAASIGDVLNAG-FNLQGNGEAVDFVSTYD 1229
y Match Local Simi hes 493;	NGTGVKK	NNDVILL	TVSTKNI	GVS	LED	IQDGDLE	99	естстог	VNVSNAA	ATVDNK-	AGDQKIS 	GGTGTQI	NTFETIT	орсьгру	VASGNDT	AIVNNEGES	NSNSVGF	NIGIVN		GDIVVSE	KDIAENI	VDLNGNA	TITVGKE	SVGINVY	GDSTTLN	GDGNTVN	QIGFTG-	PLGFAGV	NTGIN-P	- TAOUNT	TEQUEST	TTKV	IADSTAE	SNTLANV
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qq		NYD 1071
Οy	1230 TVDFIDGNATTAKVTYDDTSKTSKVVYDVNVDNKTIEVTSDKKLGVKTTTLTKT	SAN-GN 1288
qq	Db 1072DSLAANTLVGMAVYEHGTAINDQTGVININVGTGQAFYNDGTGT	i IVNYGT 1121
δλ	1289 ATKFSAADGDALVKASDIATHLNTLAGDIQTAKGASQASSSASYVI   : : :           : : :	
QQ	Db 1122 ICTFGVCQSGNEYNNTDDFTSLIYTGGDTITRSGETVTLNKSAAV	-TDKL 1170
Qy Db	1349 YYQVNDKGQVDKNKEVAKDKLVAQAQTPDGTLAQMNVKSVINKEQVNDAN	KKQGINE 1405    :   N:   KNAGVMT 1219
Οy	1406 DNAFIKGLENAAKDTKTKNAAVTVGDLNAVAQTPLTFAGDTGT	145
qq	:  :         :	- 127
Qy	1456 TLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGTRIDEKGI	SFVDAN 1515
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Qy	1516 GQAKANTPVLSANGLD	SNSG 1572
qq	1319	SSHNG 1369
Οy	1573 ASLPFVVTDANGKPIN	кр 1621
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Qy	1676 NAGQAQSLPSLSAAQQSNAASVKDVLNVGFNLQTNHNQVDFVKAYDT	SADIT 1734
qq	Db 1465 NLGTAGTTDTGMIGMQLDANATADAVIENNGTINIFANDSFA	A 1506
ΟŸ	1735 SVRSADGTMSNITVN-TALAATDDDGNVLIKAKD	GKFYKAD 1774
qq	Db 1507FSVLGTVGHVVNNGTVVIADGVTGSGLIKQGDSINVEGMNGNNGNSSEVHYGDYTLPD	TLPD 1564
δλ	QY 1775 DLMPNGSLKAGKSASDAKTPTGLSLVNPNAGKGSTGDAVALNNLSKAVFK	CAVFK 1824
qa	1565 VPKPNTVSVTSGSDEAGGSMNNLNGYVVGTNVNG	rA 1621
Qy	Qy 1825 SKDGTTTTTVSSDGISIQGKDNSSITLSKDGLNVGGKVISNVGKGTKDTDA	KDTDA 1875
qq	Db . 1622GTADTTVSFDNV-VEGSNLTDADAITSTSVVWTAKGSTDASGNVDVTMSKNAY	r-TDV 1676
QY	1876 ANVQQLNEVRNLLGLGNAGNDNADGNQVNIADIKKDPN	SNRTV 1922
qq	1677 ATDASVNDIAKALDAGYTNNELFTSLNVGTTAELNSALKQV	SGSQAT-TV 1725
Qy	QY 1923 IKAGTVLGGKGNNDTEKLATGGVQVGVDKDGNANGDLSNVWVKTQKDGSKKALLATYNAA	FYNAA 1982
QQ	Db 1726 FREARVLSNRFSMLADAAPKVGNGLAFNVVAKGDPRAELG	1765
Øλ	QY 1983 GQTNYLTNNPAEAIDRINEQGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKA	FQAKA 2042
qq	Db 1766NNTEYDMLALRKTIDLSESQTMSLEGT	:   - ARL 1796
Οy	QY 2043 DGEAAVAIGRQTQAGNQSIAIGDNAQATGDQSIAIGTGNVVTGKHSGAIGDPSTVKADNS	KADNS 2102
qq	Db 1797 DGDGAQKAGDNGVIGGYSQFFGLKHQMSFDNG	SFDNG 1828
δλ	QY 2103 YSVGNNNQFIDATQTDVFGVGNNITVTESNSVALGSNSAISAGTHAGTQ	AKK 2154
QQ	Db 1829 MNNNNALRYDVHNLDSSRSIAFG-NINKTADTDVKQQYLEFRSEGAKT	SGAKT 1875
δλ	QY 2155 SDGTAGTTTAGATGTVKGFAGQTAVGAVSVGA-SGAERRIONVA	AGE 2201   :

707	F EFSECENTIFIEG VALRHILEGGIQENNAGDENENNAGSETAVDSIVGLALDIAGANG 1935		
0v 2202	VSATSTDAVNGSOLYKATOGIANATNELDHRIHONENKANAGISS 2246	ΟŊ	497 PYLDKI
	WSASATLEGGPNLSYAKSORTASLAGAGSOHENVDDGOKGGGTNS	qq	625 SELAAI
		Qy	538
RESULT	6	Qa	685 TIAGII
hypotheti	cal protein 2 - Haemophilus ducreyi	Qy	593 SGINAC
C; Date: 2	1. maemophirus duciey. 2-0ct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999 01. m2110s	qa	741 SDFTS
C, Access 1 R; Ward, C		QY	647 SNL
A; Title:	A.Title: Haemophilus ducreyi secretes a filamentous hemagglutinin-like protein. A:Reference number: 20084: WITD-94010126	Dp	781 NASGTI
A; Accessi	CON: 111105 - 2200047, MOIL 19000020	QY	698 VGSDKI
A; Molecul	Preliminally; translated from GB/EMBL/DDBJ e type: DNA	QQ	:  : 840 ISSEA
A; Cross-ref	A; RESIGUES: 1.4919 < WARK> C. CADASTALES CONTROL OF THE CONTROL O	Qy	749 TSDEDI
A;Gene: IspA2	s: .spA2	qa	897 ESGKNI
Ouerv	4 7% · COOTS 642 6 · DB 2.	ογ	797 KVTYDE
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	THEFT COOL WINNERCHIES NOT, THERE NOW, CO	QY	852 STTDNI
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		ογ	1015 TKPHL1
П	TIFNOVTGDOESKISGGLEVEGEKADLFIINDNGVTLNGVKTINTDREVASTREVVEPHT	QQ	1117 NKSNAC
	ANAMORA OF CHANCE OF A PARTY AND A PARTY A	Qy	1066 DLKTEI
Oy 118 Db 241	QAANQKASSHAKKESIAIGGDVLAEGDASIAIGSDDLY 156 	qa	:  ::: 1164 EAKSD
0v 157		QY	1105YSS
		qa	
Qy 208	AMAYAKG-HFANAFGTRSTAEGNYSLAVGLTAKAEKGYTIAIGSNAQAINYGALALGADT 266	δŏ	
Db 351		qa	
Qy 267	267 RVDLDYGIALGYGSQILNNNNNNNKAYVPEGNGSNIKSSKATGNGL-FSIGSSTIKRKI 325	Οy	
Db 406	:: :      :::    : : : :       ::  406 ILNATCHVKLNDGSSVISNNNLGISALNLTLENATVSANNLSFRVTNDTKLNNL 459	qq	1328 EDFKK
Qy 326	326 INVGAGYEDTDAVNVAQLKAVENLAKRQITFKGDDNGTGVKKKLGETLTIKG 377	δλ	
Db 460		qq	1384 EITVPC
Oy 378	378 GETQADKLTDNNNIGVVTDNNFGLKVKLAKNLSGLETVSTKNLTASEKVTVGSGNNTAEL 437	δλ	1328
Db 520	:	DP	
Qy 438	OSGGLIFTPITNAS-TDKTVYGTDGLKFTDNSNTALEDTTRITKDKIGFSNKAGTVDENK 496	δo d	
Db 565	565 AANNLTLINVTKNVTLNDASKLSANKLDLNVTDNVTLNSKSTLSAGELTFKKVKNVTLNND 624	gg	1478 LKGIKB

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KDKLKVGEVEITNTG-INAGGKKI-----TNIQSGDITQNSNDAVTGGRVY 1065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDTSKTSDVITFAGENGITTKVNKGVVRVGIDQTKGLTTPKLTVGNNNGKGIVID 1162
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IDKEALDNLYRTRLSYINQNNYLGAKYFFNQLDTE---------DDK 1477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3DQKISNVKDATDDTDAVTYKQLKQVQQDADGALQSFSIRDEKGQEFTI----- 646
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----GLTVNNTIGGSNKQIQVGADGIK---
                                                                                                                                                                                                                                          ADVNVNVSNAAKFGTTRITEEEIGFADADGKVDKKSPYLDKKQLQVGGVKITKD
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NELKVG - - - NSTENNG - - - - - -
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Qy Db	1529	VGDLNAVAQTPLTFAGDTGTTAKKLGETLT	
οy	1459	TDGFTV 1485	
qq	1572	LAKQTIEEVEKORGVGTGQIRAGIIDVKVDDVRNTGTIAGYAVGLEAKNKLKNTGDILSQ 1631	
λo	1486		
o O	1632	LESTGVTY VDETGATK VRKAR I KSEGH I Y LETDKDKNVDLTASELKGNTG	
οy	1524	VLSANGLDLGDAVNFKQFN	
g	1692	QIKAKDLNENDIYETSYKYKYEKLFGKNGGELGDRVTQTSQAKSVGTDASFDHLHLSLEG	
oy Ob	1557	VSKRYNNLNNCNGSASCASEPEYVADANGKPINGTDGKPOKAIKGADGKYYHANAMGVPVD 1616	
Qy	1617	KDGKPITDADKLANLAAHGKPLDAGHQVVASLGGNSDAITLTNIKSTLPQIDTPNT 1672	
QQ	1802	GGGSAGISLIDQGVETYINKTATAGANADVINEMKRIRETETSLIHRNS 1850	
٥y	1673	GNANAGQAQSLPSLSAAQQSNAASVKDVLNVGFNLQTNHN 1712	
qq	1851	EFNALSGELYVMGKADIGGVDINRDVEVIKTPEEIAAEQKAAEEAKKAEVKEN 1903	
οy	1713	QVDFVKAYDTVNFVNGTGADITSVRSADGTMSNITVNTALAATDDDGNVLIKAKDGK 1769	
qq	1904	EASETAAKETEEAENDNVAEKDKTKPKFKKLTDEEIAAAFETKGEDFFAA 1953	
οy	1770	FYKADDLMPNGSLKAGKSASDAKTPTGLSLVNPNA	
QQ	1954	-YKAREBEDRKKGFTLSAEQIESTKARDEK 1982	
οy	1830	TTTVS-SDGISIQGKDNSSITLSKDGLNVGGKVISNVGKGTKDTDAANVQQLNEVRLL 1888	
ОС	1983	ETTYYELKVGVGAEAEA	
0y	1889		
QQ	2039	ATGDLAGASAKLKFELSTIEK-KSRGASDGRSILGGRLNLAARG- 2081	
ò i	1946	OVGVDKDGNANGDLSNVWVKTOKDGSKKALLATYNAAGQTNYLTNNPAEAIDRINEOG	
Q C	2082	GDITLNNV	
Oy Db	2004	IRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGRQTQAGNQSIAI 2063 	
ΟŸ	2064	GDNAQATGDQSIAIG	
Db	2145		
ōλ	2122		
Q O	2199	DINVVSKQDSYSRKERGVNYSVSAGVGVSTAGGARPNGSV 2238	
οy	2179	AVGAVSVGASGAERRIQNVAAGEVSATSTDAVNGSQLYKATQGIANATNELDHRIHQNEN 2238	
QQ	2239	GLGVSAENENSKIVKQQAGISAKRITGEINNLNLTGGYIEN 2279	
yo 4	2239	KANAGISSAMAMASMPQAYIPGRSMVTGGIATHNGQGAVAVGLSKLSDNGQWVF 2292	
3 6		13110111111111111111111111111111111111	
참 점	2293	KINGSAITQGHVGA 2306   1	

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Figures 1. Neisseria meningitidis (C. Species: Neisseria meningitidis (C. Species: Neisseria meningitidis (C. Species: Neisseria meningitidis (C. Species: Neisseria meningitidis (C. Species: Neisseria meningitidis (C. Species: Neisseria meningitidis (C. Species: Neisseria meningitidis (C. Species: Neisseria meningitidis (C. Species: Salwar-2000 sequence_revision 31-Mar-2000 #Hext_change 19-Jan-2001 (C. Accession: F81045 (N. J. Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000 (A. Status: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A; Accession: F81045 (A. Status: Specialman A. Status: Specialman A. Status: Specialminary A; Moolecule type: DME (C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Special C. Spec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 QNH-----TVLRQIRDSNGSQKYRRTAAEGHASTAV----GAMAYAKGHFANAF-G 221
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ag	464	TATGTGTATVSI	515
Οy	673	SNDIAKGKVKVGIDPINGLTTPKLTVGSDKDGKTQLVIEQV-ASG	716
QQ	516	SNITAPTFADGTIRTHGALDNSGSIIANGQTDVSAQQGLNNAGQIDIHQLNAKGSAFD	573
δλ	717	DDKSKAASIGDIL	764
Q	574	NHNGTIISDAVHIQAGSLNNQNGNITTRQQLEIETDQLDNAHGKLLSAEIADLA	627
Oy Dp	765	NTGFNLKNNSNSVGFVSTYNTVDFIDGNATTAKYTYDETNQTSKVTYDVNVDEKTIELTG :	824 681
QY	825		874
QQ	682	TLAADNKLDIALQDDFYVERNIVAGNELSLSTRGSLKNSHTLQAGKRIRIKANNLDNAAQ	741
Ολ	875	EIHTTKGTADTALQTFKVKKDGATDDETITVGKDGTQNGKTVNTLKLKGENGLTVATNKD	934
QQ	742	GNIQSGGTTDIGTQ-HNLTNRGLIDGQQTKI-QAGQMNNIGTGRIYG	797
οy	935		994
д	798		849
δy	995	TSRITKDQIGFTGANGSLDTTKPHLTKDKLKVGEVEITNTGINAGGK	1041
qq	850	KAQRIHNAGATIEAAGKMRLGVEKLHNTNEHLKTQLVETGREHIVDYEAFGRHELL	905
οy	1042	ONSNKITNIQSGDIUTIX	1057
qq	906	REGTQHELGWSVYNDESDHLRTPDGAAHENWHKYDYEKVTQKTQVTQTAPAKIISGND	696
οy	1058		1109
QQ	964	LIDGKEVFNIDSQIIAGGNLIVQTEKDGLHNEQIFGEKKVFSENGKLHSYWREKHKGRD	1023
ΩŸ	1110		1147
QQ	1024	STCHSEQ-NYTLPEELTRNISLGSFAVESHRKALSHHAPSQGTELPQSNGISLPYTSNSF	1082
οy	1148		1170
Op	1083	TPLPSSSLYIINPVNKGYLVETDPRFANYRQWLGSDYMLDSLKLDPNNLHKRLGDGYYEQ	1142
οy	1171	TGLSNTLANVTNDG	1211
QQ	1143		1198
οy	1212	BNIOGN	1218
QQ	1199	TSDIVWLVQKEVKLPDGGTQTVLVPQVYVRVKNGDIDGKGALLSGSNTQINVSGSLKNSG	1258
Qy	1219		1275
qq	1259	TIAGRNALIINT-DTLDNIGGRIHAQKSAVTATQDINNIGGMLSAE-QTLLLNAGNNINS	1316
οy	1276		1325
QQ	1317	QSTTASSQNTQGSSTYLDRMAGIYITGKEKGVLAAQAGKDINIIAGQISNQSEQGQTRLQ	1376
ογ	1326		1370
QQ	1377	AGRDINLDTVQ	1432
ογ	1371	AQAQTPDGTLAQMNVKSVINKEQVNDANKKQGINEDNAFIKGLENAAKDTKTKNA	1425
QQ	1433		1492
οy	1426		1471
g	1493	STFECKQVVLQAGNDANILGSNVISDNGTQIQAGNHVRIGTTQTQSQSETYHQTQ	1547

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                                                                                                                                    LGGKRISNIGAAVDDNDAVN--FKQFNEVAKTVNNLNNQS----NSGASLPF--VVTDA 1582
                                                                                                                                                                                                        -- GKHYEQIGSTVSSPEGNNTIYAQSIDIQAAHNKLNSNTTQTYEQKGLTVAFSSPVTDL 1650
                                                                                                                                                                                                                                                                            1583 NGKPINGTDGKPQKAIKGADGKYYHANAN-GVPVDKDGKPITDADKLANLAAHGKPLDAG 1641
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hypothetical protein PA2462 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Species: 15-sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000
C;Accession: C8339
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

Db 944 QGVDITARQVDNSVGEIASOGVVALNLTEQLDNRGGKIV 982  Qy 824 GDNGKTNKICVKTTTLTTTNANGKATNFSTTDNDALVNAKDIAENLNTLAKEIHTTKGTA 883	99 99 FCHYROSGIKAGDSTTHANDGLESTRIPASHDOLOVA-DOWRADKORGHSSTG 991 1077 -ALANDGGGRLASDA	Db 1869 LGNQAGSLSSQGRLSVKSGRLDNQGGAVSSAGTLSLSSQGALNNQGGR 1916
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A; Reference number: A82950; MUID:20437337 A; Accession: C83339 A; Status: preliminary A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-527 <870> A; Cross-references: GB:AE004673; GB:AE004091; NID:g9948501; PIDN:AAG05850.1; GSPDB:GN001 A; Experimental source: strain PAO1 C; Genetics: A; Gene: PA2462	Queery Match  4.6%; Score 536.5; DB 2; Length 5627;  Best Local Similarity 20.4%; Pred. No. 2.16-13;  Matches 553; Conservative 375; Mismatches 1009; Indels 771; Gatches 1009;  54 IUVICATINGSARAONESIJEGTTGNDD.  197 LITREAKLINKLINIVO	OY /64 LNTGFNLKNNSNSVGFVSTYNTVDFIDGNATTAKVTYDENQTSKVTYDVNVDEKTIELT 823

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A; Reference number: A40009; MUID: 91236743
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mucin, submaxillary - pig
mucin, submaxillary - pig
mucin, submaxillary - pig
my.Alternate names: apomucin
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Jun-2000
C;Accession: T03099; A40009; A28528; B29789
R;Eckhardt, A.E.; Timpte, C.S.; DeLuca, A.W.; Hill, R.L.
J. Biol. Chem. 272, 33204-3310, 1997
A;Title: The complete cDNA sequence and structural polymorphism of the polypeptide chain
A;Reference number: 214839; MUID:98070526
A;Title: The complete cDNA sequence and structural polymorphism of the polypeptide chain
A;Reference number: 214839; MUID:98070526
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-13288 CECK>
A;Residues: 1-13288 CECK>
A;Cross-references: EMBL:AF005273; NID:92581864
B;Eckhardt, A.E.; Timpte, C.S.; Abernethy, J.L.; Zhao, Y.; Hill, R.L.
J. Biol. Chem. 266, 9678-9686, 1991
A;Title: Porcine submaxillary mucin contains a cystine-rich, carboxyl-terminal domain in
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                                                                                    KAVFKSKDGTTTTTVSSDGISIQGKDNSS----ITLSKDGLNVGGKVISNVGKGTKDTDA 1875
                                                                                                                                                                           NG-----DLSNVWVKTQK-----DGSKKALLATYNAAG----QTNYLTNNPAEAIDR
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A Molecule type: mRNA
A; Residues: 12139-12167, T',12169-13288 <EC3>
A; Residues: 12139-12167, T', 12169-13288 <EC3>
A; Residues: 12139-12167, T', 12169-13288 <EC3>
B; Timpte, C.S.; Eckhardt, A.E.; Abernethy, J.L.; Hill, R.L.
J. Biol. Chem. 263, 1081-1088, 1988
A; Title: Porcine submaxillary gland apomucin contains tandemly repeated, identical se
A; Reference number: A28528; MUID:88087170
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A; Residues: 12139-12167, 'T', 12169-12641 < TLM>
A; Residues: 12139-12167, 'T', 12169-12641 < TLM>
A; Cross-references: GB:M21174; GB:J03512; NID:g164321; PIDN:AAA30990.1; PID:g552360
A; Experimental source: submaxillary gland
B; Eckhardt, A.E.; Timpte, C.S.; Abernethy, J.L.; Toumadje, A.; Johnson Jr., W.C.; H11
J. Biol. Chem. 262, 11339-11344, 1987
A; Title: Structural properties of porcine submaxillary gland apomucin.
A; Reference number: A92606; MUID:87280230
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4.5%; Score 520.5; DB 2;
Best Local Similarity 20.9%; Pred. No. 2.8e-11;
Matches 547; Conservative 316; Mismatches 1143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2028 TVSGASG-----STGSSSGSPGATGASIG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Residues: 1572-1607 < EC22
C; Superfamily: pig submaxillary mucin
C; Keywords: tandem repeat
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٥y	589	ITKDSGINAGDQKISNVKDATDDTDAVTYKQLKQVQQDADGALQSFSIRDEKGQEFT	645
qq	2060		2117
ργ	646	ISNLYSNGNTPUTFETITFAGENGI-SISNDIAKGKVKUGIDPINGLTTPKLTV	698
ď	669	GSDKDCKTQLVIEQVASGNDTKNIIRGLSPTLPSITNAGGVRTTEQGNTITSDEDKSK	758
QQ	2173		2224
δy	759	SIG-DILNTGFNLKNNSNSVGFVSTYNTVDFIDGNATTAKVTYDETNQTSKVTYDVNVDE	817
qq	2225		2277
ž ć	818	KTIELTGDNGKTN-KIG-VKTTLTTTTNANGKATNFSTTDNDALVN	875
3 2	976	THTTKCTADTAL OTEKVKKDCATDDFTTTVRKDCTONK	931
G Q	2323	SGAGPGTTASSVGVTETARPSV	2374
٥y	932	NKDGTVIFGINTQSGLKAGDSTTLNKDGLSIKNPASNEQIQVGADGVKFAKVDKGNSSTG	991
QQ	2375	GOPETSRISVAGSSGAPAVSSGASQAAGTSGAGPGTTAS-SVGVTETARPSV-AGSGTTG	2432
οy	992	-IDGTSRITKDQIGFTGANGSLDTTKPHLTKDKLKVGEVEITNTGINAGGKKITNIQSG-	1049
QQ	2433		2478
٥y	1050	DITQNSNDAVTGGRVYDLKTELESKINSAAKTAQ	1083
QQ	2479		2538
δý	1084	NSLHEFSVADEQGNHFTVSNPYSSYDTSKTSDVITFAGENGITTKVNKGVVRVGIDQTKG	1143
QQ	2539	PETSRISVAGSSGAPAVSSGASQAAGTSGAGPGTT-ASSVGVTETARPSVAGSG	2591
οy	1144	LTTPKLTVGNNNGKGIVIDSKDGQNTITGLSNTLANVTNDGAGHALSQGLANDTD	1198
QQ	2592	TTGTVSGASGSTGSSGSPGATGASIGQPETSRISVAGSSGAPAVSSGASQAAG	2645
Oy	1199	KTRAASIGDVLNAGFNLOGNGEAVDF	1243
ρρ	2646	TSGAGPGTTASSVGVTETARPSVAGSGTTGTVSGASGSTGSSSGSPCATGASI	2698
οy	1244	TYDDTSKTSKV	1282
QQ	2699	GQPETSRISVAGSSGAPAVSSGASQAAGTSGAGPGTTASSVGVTETARPSVAGSGTTGTV	2758
οy	1283		1342
qq	2759		2812
οy	1343	AQMNVKSVINKE	1402
QQ	2813	PGTTASSVGVTVSGASGTTGTVSGASGSTG	2847
ογ	1403	INEDNAFIKGLENAAKDIKTKNAAVTVGDLNAVAQTPLIFAGDIGTTAKKLGETLII	1459
QQ	2848	SSSGSPGATGASIGQPETSRISVAGSSGAPAVSSGASQAAGTSGAGPGTTASSVGVTETA	2907
οy	1460	KGGQTDTNKLTD	1519
QQ	2908	RPSVAGSGTTGTVSGASGSTGSSSGSPGATGASIGQPETSRISVAGSSG	2956
οy	1520	ANTPVLSANGLDLGGKRISNIGAAVDDNDAVNFKQFNEVAKTVNNLNNQSNSG	1572
qq	2957	APAVSSGASQAAGTSGAGPGTTASSVGVTETARPSVAGSGTTGTVSGASGSTGSS	3011
δy	1573	ASLPFVVTDANGKPINGTDGKPQKAIKGADGKYYHANANGVPVDKDGKPITDAD	1626

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3176
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SGSPGATGADETSRISVAGSSGAP--AV--SSGASQAAGTSG-----AGPGTAS 3061
                                                   1627 KLANLAAHGKPLDAGHQVVASLGGNSDAITLTNIKSTLP----QIDTPNTGNANAGQAQ 1681
                                                                                                                                                                                                                              3177 PGATGASIGQPETSRISVAGSSGAPAVSSGASQAAGTSGAGPGTTASSVGVTETARPSVA 3236
                                                                                                                                                                                                                                                                                     3237 GSGITGTV-----SGASGSTGSSSGSPGATGASIGQPETSRISVAGSS 3279
                                                                                                                                                                                                                                                                                                                                       1810 GDAVALNNLSKAVFKSKDGTTTTTVSSDGI-----SIQGK------DNSSIT 1850
                                                                                                                                                                                                                                                                                                                                                                                                            1851 LSKDGLNVGGKVISNVG-KGTKDTDAANVQQLNEVRNLLGLGNAGNDNADGNQVNIADIK 1909
                                                                                                                                                                                                                                                                                                                                                                                                                                    1910 KDPNSGSSSNRTVIKAGTVLGGKGNNDTEKLATG--GVQVGVDKDGNANGDLSNVWVKTQ 1967
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                                                                                                                                                                                                                                                                                                                                                                         3280 GAPAVSSGASQAAGTSGAG-PGTTASSVGVTETARPSVAGSGTTGTVSGASGSTGSSSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1968 KDGSKKALLATYNAAGQTNYLTNNPAEAIDRINEQGIRFFHVNDGNQEPV--VQGRNGID
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                                                                             SY-GVTETARPSVAGSGTTGTVSGASGS---TGSSSGSPGATGASIGQPETSRISVAGSS
                                                                                                                                                                                              -----TMSNI----TVNTALA
                                                                                                                                                                                                                                                                   1754 ATDDDGNVLIKAKDGKFYKADDLMPNGSLKAGKSASDAKTPTGLSLVNPNAGK----GST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2137 GSNSAISAGTHAGTQAKKSDGTAGTTTTA-----GATGTVKGFAGQTAVGASG
                                                                                                                        1682 SLPSLS----AAQQSNAASVKDVLNVGFNLQTNHNQVDFVKAYDTVNFVNG-
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## 13

hypothetical protein PA1874 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Species: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000
C;Accession: A83412
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Adman, S.; Yaun, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A;Accession: A83412

A;Status: preliminary A;Molecule type: DNA A;Molecule type: 1-2468 cSTO> A;Cross-references: GB:AE004613; GB:AE004091; NID:g9947856; PIDN:AAG05263.1; GSPDB:GN001 A;Experimental source: strain PAO1 C;Genetics: A;Gene: PA1874 125; Query Match
4.4%; Score 511; DB 2; Lengtn 2400;
Best Local Similarity 20.9%; Pred. No. 6.8e-12;
Matches 573; Conservative 292; Mismatches 1027; Indels 848; Gaps GK----ESIAIGGDVLAEGDASIAIGSDDLYLDRNSTNSKYPNGLLSTLIQNHTVLRQIR 185 270 GKAEPGSTVGVDTDGDGQPDTTVVVGPGGSF--EVPLNPPLTNGETVTVIV----- 318 DSNGSQKYRRTAAEGHASTAVGAMAYAKGHFANAFGTRSTAEGNYSLAVGLTAKAEKGYT 245 AHAN------QAIAI-----GGSKPDPRNQAANQKA------GSHAK 129 246 IAIGSNAQAINYGALALGADTRVD--LDYGIALGYGSQI----LNNNNNNNKAYV----P 296 EGNGSNIKSSKATGNGLFSIGSSTIKRKIINVGAGYEDTDAVNVAQLKAVENLAKRQITF 356 399 TGLKVKLAKNLSGLETVSTKNLTASEKVTVGSGN---NTAELQSGGLTFTPTTNASTDKT 455 -----TDPAGNNSTPVTVEAPDTTAPAPATDVQVAPDGS----SVTGNAEPGAT 363 ----TDNN 398 507 547 ----AAKFGTTRITE---EEIGFADADGKVDKKSPYLDKKQLQVGGVKITKDSGINAGDQ 600 682 LSGTAEPGATVTLTDGNGNPIGOVTADGS------GNWSFTPTTPLPNGTV 726 561 622 QVTADGSGNWTFTPSTPLPNGTVVNATATDPSGNASSPASVTVDAVAPATPVVNPSNGTT 681 KISNVKDATDDTDA---VTYKQL---KQVQQDADGALQSFSIRDEKGQEFTISNLYSNGN 654 TPNTFETITFAGENGISISNDIAKGKVKVGIDPINGLTTPKLTVGSDKDGKTQLVIEQVA 714 -PIGOVTADGSGNWSFTPSTPLADGTV-----VNATAT------DPAGNTS-----G 822 SGNDTKNIIRGLSPTLPSITNAGGVRTTEQGNTITSDEDKSKAASIGDILNTGFNLKNNS 774 72 KIAFGTTGNN-----LAK 99 12 ATGTFMAVAECAKSHSGGSSSSTAGQVGSSPVIRLTRVATLAILVIGATLNGSAYAQNNS 71 VAPNAPVVEPSNGSELSGTAEPGSSVTLTDGNGNPIGQTTADANGNWSFTPST-PLPDGT 456 VYGTDGLKFTDNSNTALEDTTRI-----TKDKIGFSNKAGTVD--ENKPYLDKDKLKVG ----LTVNNTIGGSNKQIQVGADGIKFADVNVNVSN---357 K-GDDNGTGVKKKLGETLTIKGGE---TQADKLTDNNNIGVV---508 NSTLNNGG-----100 130 297 186 319 364 548 601 655 783 715 823 q ô q a ð δý ò q ŏ g ò <u>а</u>. ç Db δ 셤 ŏ q δ q ò ga ò QQ QΩ δ ò

Qy		NSVGFVSTYNTVDFIDGNATTAKVTYDET
qq	845	SLSGTAEPGSTVILTDGNGGN 876
δŽ	835	KTTTLTTINANGKATNFSTTDNDALVNAKDIAENLNTLAKEIHTIKGTADTALQTF 890
qq	877	WIYTPSTPIANGTVVNVVAQDAAGNSSPGASVTVDSQAPAAPVVNPSNGTTLSG
QY	891	KVKKDGATDDETITVGKDGTQNGKTVNTLKLKGENGLTV-ATNKDGTV 937
q	933	EPGATVTLTDG
Qy	938	TFGINTQSGLKAGDSTTLNK DGLSIKNPA
Dβ	982	
Qy	975	ADGVKFAKVDKGNSSTGIDGTSRITKDQIGFTGANGSLDTTKPHLT 1020
QQ	1035	ADGSGNWSFTPSTPLADGTVVNATAIDPAGNIGGGGSTTVDAIAPATPIVNLS 1087
Qy	1021	KDKLKVGEVEITHTGINAGGKKITHNIQSGDITQNSNDAVTGGRVYDLKTELESKI 1075
qq	1088	NGSSLSCTAEPCSTVILTDGNGNPIAEVTADGSGNWTYTPSTPIANGTVVNVVAQDASGN 1147
Qy	1076	NSAAKTAQNSLHEFSVADEQGNHFTVSNPYSSYDTSKTSDVITFAGENGI 1125
QQ	1148	SSPPATVTVDSSAPPAPVINPSNGVVISGTAEAGATVTLTDAGGNPIGQVTA 1199
δλ	1126	TTKVNKGVVRVGIDQTKGLTTPKLTVGNNNGKGIVIDSKDGQNTITG 1172
qq	1200	DGSGNWSFTPGTPLANGTVIVATATDPTGNTGPQAATTVDAVAPPAPVIDPSNG 1253
Qy	1173	ANVTNDGAGHALSQGLANDTDKTRAASIG
Ob	1254	TISGTAEAGAKVILTDGNGNPIGETTADGSGNWSFTPGTPLANGTVVNAVAQD 1307
οy	1233	FIDGNATTAKVIYDDTSKTSKVVYDVNVDNKTIEVTSDKKLGVKTTTLTKTSANGNAT 1290
qq	1308	PAGNTGPOGSTTVDAVAPNTPVVNPSNGNLLNGTAEPGSTVTLTDGNGNPI 1358
Οy	1291	KFSAADGDALVKASDIATHLNTLAGDIQTAKGASQASSSASYVDADGNK 1339
QΩ	1359	GQTTADGSGNWSFTPGSQLPNGTVVNVTASDAAGNTSLPATTTVDSSLPSTPQVDPSNGS 1418
Qy	1340	VIYDSTDKKYYQVNDKGQVDKNKEVAKDKLVAQAQTPDGTLAQMNVKSVINKEQV 1394
Dp	1419	VISGTADAGNTIIITDGNGNPIGQVTADGSGNWSFTPGIPLPDGTVVNVVARSPSNVDSA 1478
Qy	1395	
QO	1479	PAVITVDGVAPAAPVIDPSNGTEISGTAEAGATVILTDGGGNPIGQATADGSGNWTFTPS 1538
δλ	1425	LTFAGDTGTTAKKLGETLTIKGGQTDTNKLTDNNIGV
qq	1539	SGPAS
ΟŊ	1482	FVDANGQAKANTPVL
qq	1591	GATVILTDGNGNPIGQVTADGSG-NWSFTPGTPLANGSVINALAQDAAGNNSSPTS 1645
Qy	1542	AAVDDNDAVNFKQFNEVAKTVNNLNNQSNSGASLPFVVTDANGKPINGTDGKPQKAIKGA 1601
qq	1646	ATVD1669
Οy	1602	DGKYYHANANGVPVDKDGKPITDADKLANLA-AHGKPLDAGHQVVASLGGNSDAI 1655
qa	1670	AEAGATVILTDGNGNPIGQVTADGSGNWSFTPGTPLSNGTVVNAVAQDAAGNTSGP 1725
ΟŊ	1656	TITNIKSTLPQIDTPNTGNANAGQAQSLPSLSAAQQSNAASVKDVLNVGFNLQTNHNQ 1713
qa	1726	VSTTVDAVAPATPVIDPSNGVELSGTAEPGVRVILTDGNGNP 1767
Qy	1714	VDEVKAYDTVNFVNGTGADITSVRSADGTMSNITVNTALAATDDDG 1759

OUEFY MATCH  4.3%; SCOIE 504.5; DB 2; Length 2660; Best Local Similarity 20.2%; Pred. No. 1.3e-11; Matches 550; Conservative 329; Mismatches 979; Indels 869; Gaps 138;  83 NASASNEASIAIGSLARAHANQAIAIGGSKPDPRNOAANOKAGSHAKGKESI 134  1	OY 183OIRDSNGSQKYRRTAAEG	277 277 321 469 469 355 410		
	DUSSITIENCE   1   1   1   1   1   1   1   1   1	TEKLATGGVQVGVDKDGNANGDLSNVWVKTQKDGSKKALLATYNAAGQTNYLT 1989	GTTTAGATGT VKGFAGQTAVGAVSVGASGAERRIONVAAGE VSATSTDAV - 2210	RESULT 14 E85822 probable invasin 23135 [imported] - Escherichia coli (strain O157:H7) Cispecies: Becherichia coli Cispecies: Becherichia coli Cispecies: Becherichia coli Cispecies: Becherichia coli Cispecies: Date: 16 Feb-2001 #sequence_revision 16 Feb-2001 #text_change 31-Mar-2001 Cispecies: Date: 15 Feb-2001 #sequence_revision 16 Feb-2001 #text_change 31-Mar-2001 Cispecies: Date: Bession: E85822 A; Reference number: A85480; MUD:21074935; PMID:11206551 A; Reference number: A85480; MUD:21074935; PMID:11206551 A; Reference number: A85480; MUD:21074935; PMID:11206551 A; Residues: 1-2660 <

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1088	944	992	1048	1108	1153 1329	1201	1257	1296	1353	1409 1584	1464 1644	1513 1702	1566	1616 1806	1669 1860	1728	1783	1837
	TALQTFKVKKDGATDDETITVGKDGTQNGKTVNTLKLKGENGLTVATNKDGTVTFGINTQ 	SGLKAGDSTTLNKDGLSIKNPASNEQIQVGADGVKFAKVDKGNSSTGI :	DG-TSRITKDQIGFTGANGSLDTTKPHLTKDKLKVGEVEITNTGINAGGKKITNIQS	GDITQNSNDAVTGGRVYDLKTELESKINSAAKTAQNSLHEFSVADEQGNHFTVSNPYSSY	DTSKTSDVITFAGENGITTKVNKGVVRVGIDQTKGLTTPKLTVGN   :	NNGKGIVIDSKDGONTITGLSNTLANVTNDGAGHALSQGLANDTDKTR  :	AASIGDVLNAGFNLQGNGEAVDFVSTYDTVDFIDGNATTAKVTYDDTSKTSKVVYD	VNVDNKTISVTSDKKLGVKTTTLTKTSANGNATKFSAAD   :	GDALVKASDIATHLNTLAGDIQTAKGASQASSSASYVDADGNKVIYDSTDKKYYQVN  :	DKGQVDKNKEVAKDKLVAQAQTPDGTLAQMNVKSVINKEQVNDANKKQGINEDNAF	IKGLENAAKDIKTKNAAVIVGDLNAVAQIPLIFAGDIGITAKKLGEILIIKGGQT 	DINKLIDNNIGVVAGIDGFTVKLAKDLINLNSVNAGGIRIDEKGISFVD :	ANGQAKANTPVLSANGLDLGGKRISNIGAAVDDNDAVNFKQFNEVAKTVNNLN :   :   : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : : :   : : :   : :   : :   : :   : :   : :   : :   : :   : :   : : :   : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : : : :   : : : :   : : : : : :   :	NOSNSGASLPFVYTDANGKPINGTDGKPOKA-IKGADGKYYHANANGVPVD   :  :  :  :  :  :  :  :  :  :  :  :  :	KDGKPITDADKLANLAAHGKPLDAGHQVVASL-GGNSDAITLINIKSTLPQIDT	PNTGNANAGQAQSLPSLSAAQOSNAASVKDVLNVGFNLQTNHNQVDFVKAYDTVNFVNG- 	TGADITSVRSADGTMSNITVNTALAATDDDGNVLIKAKDGKFYKADDLMPNGSLK	AGKSASDAKIPIGESLVNPNACKGSTGDAVALNNLSKAVFKSKDGTTTTVSSD
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hemagglutinin/hemolysin-related protein NWB0493 [imported] - Neisseria meningitidis (C; Species: Neisseria meningitidis (C; Species: Neisseria meningitidis (C; Species: Neisseria meningitidis (C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 (C; Accession: H81193 ** N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Elsen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Oln, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M. ri, H.; Oln, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M. ri, H.; Oln, H.; Vamathevan, J.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A; Tatle: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8. A; Reference number: A81000; MUID:2017575 A; Accession: H81193 A; Status: preliminary A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-2703 <**TET>
A; Cross-references: GB: AE002405; GB: AE002098; NID: 97225708; PIDN: AAF40927.1; PID: 9722 A; Experimental source: serogroup B, strain MCS8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2254 VTGNSSTAHVASFIAADPSTIAATNS-----DLSTLKATVED--GSGNLIEGLTVYFALKS 2306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2189 GAERRIQNVAAGEVSATSTDAVNGSQLYKATQGIANATNELDHRIHONENKANAGISSAM 2248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGTNAPYVQVSAIDYSKNFSGEYKATVTGGGEGIATLIPVLNGVHQAGLSTTIGFTRAED 2465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSVALGSNSAISAGTHAGTQAKKSDGTAGTTTTAGATGTVKGFAGQTAVGAVSVG---AS 2188
----VSDTKQVTLIA----DAG---TAKLASLTSVYSFVVSTTEGATMTASVTDANGNPV 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2018 VQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGRQTQAGNQSIAIGDNAQATGDQSIAI 2077
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                                                                                       2000 EGIKVNFR-GTSVTLSSTSVETDDRGFAEILVTSTEVGLKTVSASLADKPTEV----IS
                                                                                                                                                                                                    2054 RLLNAKADINSATITSLEIPECQVMVAQDVAVKAHVNDQFGNPILNESVTFSAEPPEHMT
                                                                                                                                                                                                                                                             1928 VLGGKGNNDTEKLATGGVQVGVDKDGN-----ANGDLSNVWVKTQKD-----G
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                                                                                                                                                                                                                                                                                                                                                                  1971 SKKALLATYNAAGQTNYLTNNPAEAIDRINEQGIRF------FHVNDGNQEPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2078 GTGNVVTGKHSGAIGDPSTVKADNSYSVGNNNQFIDATQTDVFGVGN---NITV---TES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2249 AMASMPQAYIPG------RSMVTG---GIAT-----HNGQGAVAVGLSKLSD
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4.3%; Score 504.5; DB 2;
Best Local Similarity 20.4%; Pred. No. 1.4e-11;
Matches 557; Conservative 337; Mismatches 1044;
                                                                                                                                                        1892 NAGNDNADGNQVNIADIKKDPNSGSSSNRTVIKAG----
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ΟŸ	907 KDGTQNGKTVNTLKEKGENGLTVATNKDGTVTFGINTQS 945	
qq	1020 KDGLEDNSQGQKDQTTATFHLKNGSRIEANQWHVRDYHIETYKERIIENRPAHITVGG 1077	
ýo d	946 GLKAGDSTTLNKDG	
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δý	1035 GINAGGKKITNIQSGDITQNSNDAVT	
qq	1195 AVNGQRIHTGNVVSLNNATVTLPNSSLYTTHPDNKGWLVETDPQFADYRRWLGSD 1249	
δλ	1065 YDLKTELESKINSAAKTAQNSLHEFSVADEQGNHFTVSNPYSSYDTSKTSDVITFAGE 1122	
qq	QLDTNHLHKRLGDGYYEQKLVNEQIHQLTGYRRLDGYRSDEEQFKALM	
Qy	1123 NGITTKVNKGVVRVGIDQTKGLTTPKLTVGNNNGKGIVIDSKDG 1166	
QQ	1305 NGLTAAKTFGLTPGIALSAEQVARLTSDIVWMENQTVTLSDGSTQTVLVPKVYALARKGD 1364	
δλ	1167 QNTITGLSNTLANVTNDGAGHALSQGLANDTDKTRAASIGDVLNAGF 1213	
qq	1365 LNTSGGLISAEQVLLKLQNGNLTNSGTIAGRQAVLIQARNINSNGNIQADQIGLKAEKSI 1424	
Qy	VDFI	
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Qy	IEVTSDKKLGVKTTTLTKTSANGNATKFS	
qa	1481 NRTSDGILSLHASNDINLNAATVSNQVKDGTTQITAGN-NLNLGTIRTEHRE 1531	
δλ	1320 AKGASQASSSASYVDADGNKVIYDSTDKKYYQVNDKGQVDKNKEVAKDKLVAQAQTPDGT 1379	
q	1532 AYGTLDDENHRHVRQSTEVGSSIRTQNGA 1560	_
Qy	NEDNAFIKG	
qa	1561 LLRAGNDLKIRQGELEAEEGKTVLAAGRDVTISEGRQIT 1599	_
0y	1437 QTPLTFAGDTGTTAKKLGETLTIKGGGTDTNKLTDNNIGVVAGTDGFTVKLA 1488	
qq	1600 ELDISVSGKSKGILSSTKTHDRYRFSHDEAVGSNIGGGKMIVAAGQD 1646	
οy	1489 KDLTNLNSVNAGGTR-IDEKGISFVDANGQAKANTPVLSANGLDL 1532	
qq	1647INVRGSNLISDKGIVLKAGHDIDISTAHNRYTGNEYHESKKSGVMGTGGL 1696	_
Qy	1533 GGKRISNIGAAVDDNDAVNFKQFNEVAKTVNNLNNQSNSGASLPFVVTDANGKPINGTDG 1592	
qq	1697 -GFTIGN-RKTTDDTDRTNIVHTGSIIGSLNGDTVTVAGNRYRQTGSTVSSPEG 1748	
Qy	1593 KPQKAIKGADGKYYHANANGVPVDKDGKPITDADKLANLAAHGKPLDAGHQVVASLG 1649	_
QQ	1749 RNTVTAKSIDVEFANNRYATDYAHTQEQKGLTVALNVPVVQAAQNFIQAQNVGKSKN 1806	
Qy	1650 GNSDAITLINIKSTLPQIDTPNTGNANAGQAQSLPSLSAAQ-QSNAASVKDVLNVGFNLQ 1708	
QQ	1807 KRVNAMAAANAANQSYQATQQMQOFAPSSSAGGGNNNQSPSISVSITYGEQ 1858	
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QQ	1859 KSRNEQRRHYTEAAASQIIGKG-OTTLAATGSGEQSNINI-TGSDVIGHAGTALI 1911	
Οy	1769 KFYKADDLMPNGSLKAGKSASDAKTPTGLSL-VNPNAGKGSTGDAVALNNLSKAVFKSKD 1827	
qa	1912ADNHIRLQSAKQDGSEQSKNKSSGWNAGVAVKIGNGIRFGITAGGNIGKGKEQG 1965	
ò	1828 GTTTTIVSSDGISIQGKDNSSITLSKDGLNVGGKVISNVGKG1869	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;
"A protective protein antigen of Rickettsia rickettsii has tandemly repeated, near-identical sequences.";
Infect. Immun. 58:2760-2769(1990).
-!- FUNCTION: ELICITS PROTECTIVE IMMUNITY.
-!- PTH: GLYCOSYLATED (POSSIBLE).
-!- PTH: GLYCOSYLATED (POSSIBLE).
-!- AND IMMUNITY TO ROCKY MOUNTAIN SPOTTED FEVER.
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13 X APPROXIMATE TANDEM REPEATS.
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=783;
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01-OCT-1994 (Rel. 30, Last annotation update)
190 KDA ANTIGEN PRECURSOR (CELL SURFACE ANTIGEN)
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 TOXA_CLODI
YMJB_CAEEL
ICEA_PANAN
GTF2_STRDO
APU_THETU
PGCV_CHICK
ICEN_ERWHE
YDB6_SCHPO
SLAP_CAMFE
MSB2_YEAST
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MEDLINE=90354033; Pubmed=2117568;
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01-APR-1990 (Rel. 14, Last seq
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01-OCT-1994
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Best Local S Matches 522  Qy 261 ALGA  Db 36 ALGV  Qy 321 IKRR	OCBI SIMILBAILLY 23.0%; Pred. NO. / 88-10; 5 522; CONSELVATIVE 210; Mismatches 776; Indels 707; Gaps 114; 1 ALGADTRVDLDYGIALGYGSQILANNINNINRAYVPEGNGSNIKSSKATGNGLFSIGSST 320
06	:
376 145	5 KGGETQADKLTDNNNIGVYTDNNTGL
414	TVSTK
462	2 LKFTDNSNTALEDTT
503	3 KLKVGNSTLNNGGLTVNNTIGGSNKQIQVGADGIKFADVNVNVSNAAKF 551
552 351	2 GTTRITEEEIGFADADGKVDKKSPYLDKKQLQVGGVKITKDSGINAGDQKISNVKDATDD 611   :   :   :   :
612 393	2 TDAVTYKQLKQVQQDADGALQSFSIRDEKGQEFTISNLYSNGNTPNTFETITFAGEN 668
669	
724	4 RGLSPTLPSITNAGGVRTTEQGNTITSDEDKSRAASIGDILNTGFNLKNNSNSVGFVSTY 783 :::
784	4 NTVDFIDGNATTAKVTYDETNQTSKVTYDVNV 815
816 572	5 DEKTIELTGDNGKTNKIGVKTTTLTTNANGKATNESTTDNDALVNAKDIAENLNTLAKE 875 
876	6 IHTTKGTADTALQTEKVKKDGATDDETITVGKDGTQNGKTVNTLKLKGENGLTVAT 931
932	2 NKDGTVTFGINTQSGLKAGDSTTLNKDGLSIKNPASNEQIQVGADGVKFAKVD 984
985	K-GNSSTGIDGTSRITKDQIGF   ::               STGNANNGIVTFTGNSTVTGD-IGN
1041	1 KKITNIQSGDITQNSNDAVTGGRVYDLKTELESKINSAAKTAQNSLHEFS 1090
1091	
1148	8 KLTVGNNNGKGIVIDSKDGQNTITGLSNTLANVTNDGAGHALSQGLANDTDKTR 1201

1580 KVGAGNVTIAKGGKVKIGEIQGTGTNT-----LTLPAHFNLTG------SINKT 1622 NEQGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGRQTQAGNQ 2059 SIAIGDNAQATGDQSIAIGTGNVVTGKHSGAIGDPSTVKADNSYSVGNNNQFIDATQTDV 2119 1262 NKTIEVTSDKKLG---VKTTTLTKTSANGNATKFS-----AADGDALVKASDIA-THL 1310 965 TAT------LGGAVIKATT-TKLTDAASAVKFTNPVVVTGAIDNTGNANNGIVTFTGN 1015 1311 NTLAGDIQTAKGASQASSSASYVDADGNKVIYDSTDKKYYQVNDKGQVDKNKEVAKDKLV 1370 1142 AIDNTGNANNGIVTFTGNSTV--TGDIGNTNALATVNVGA-----GIT-LQAGGSLAAN 1192 1522 T-----PVLSANG-LDLGGKRISNI--GAAVDDNDA---VNFKQFNEVAKTVNNLNNQS 1569 1193 NIDFGARSTLEFNGPLDGGGRAIPYYFKGAIANGNNAILNVNTKLLTASHLTIGTV-AEI 1251 1570 NSGASLPFV-----VTDANGKPINGTDGKPQKAIKGADGKYYHANANGVPVDKDGKPI 1622 1623 TDADKLANLAAHG-----SPLDAGHQVVASL-----GGN-----SDAI 1655 1300 LAADLVAPGADEGTVVFNGGVNGLNVGSNVAGTARNIGDGGGNKFNTLLIYNAVTITDDV 1359 TLINIKSTLPQIDTPNTGNANAGQAQSLPSLSAAQQSNAASVKDVLNVGFNLQTNHNQVD 1715 1716 FVKAYDTVNFVNGTGADITSVRSADGTMSNITVNTALAATDDDGNVLIKAKDGKFYKADD 1775 1776 LMPNGSLKAGKSASDA--KTPTGLSLVNPNAGKGSTGDAVALNNLSKAVFKSKDGTTTTT 1833 1834 VSSDGISIQGKDNSSITLSKDG-LNVGGKVISNVGKGTKDTDAANVQQLNEVRNLLGLGN 1892 1893 AG---NDNAD-----GNQVNIADIKKDPNSGSSSNRTVIKAGTVLGGKGNNDTEKLA-- 1941 -TGGVQVGVDKDGNAN-GDLSNVWVKTQKDGSKKALLATYNAAGQTNYLTNNPAEAIDRI 1999 1016 STVTGNVCNTNALATVNVGAGLLQVQG---------------GVVKANTINLTDNAS 1057 -----NIGVVAGTDGFTVKLAKDLTNLN---SVNAGGTRIDEKGISFVDANGQAKAN 1521 1202 AASIGDVLNAGFNLQGNGEAVDFVSTYDTVDFIDGNATTAKVTYDDTSKTSKVVYDVNVD 1261 1371 AQAQTPDGTLAQMNVKSVINKEQVNDANKKQGINEDNAFIKGLENAAKDTKTKNAAVT--VGDLNAVAQTPLTFAGDTGTTAKKLGETLTIKGG--QTDTNKLTDN--------1429 1473 1656 1449 1492 1942 2000 2060 qq g οy ρp δ QQ qq ŏλ g QQ q δý qq οy g ò QQ ΩŽ ŏ Q δ qq δλ g ò οy Qγ qq ò g οŽ g ò δ δy

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CONFLICT
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-1- SIMILARITY: TO S.TYPHIMURLUM ORF NEAR CYSG (AC P25928).
-1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CODING FOR THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT BETWEEN AMINO ACIDS 839 AND 840.
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MEDLINE=92190338; P., Danchin A.;
Multiple IS insertion sequences near the replication terminus in
Escherichia coll K-12.";
                                                                      2175 AGQTAVGAVSVGA--SGAERRIQNVAAGEVSATSTDAVNGSQLYKATQGIANATN 2227
                                                                                                                       1748 TDTLTLNTTFDGAAKSGGNILIKSGSTLDLSGVSTLAL-------VVTATN 1791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                              P33666; P76087; P76088; P76856; P76859; P76859; O1-FEB-1994 (Rel. 28, Created) O1-OCT-2000 (Rel. 40, Last sequence update) O1-OCT-2000 (Rel. 40, Last annotation update) HYPOTHETICAL 205.9 KDA PROTEIN IN PAAY-ACPD INTERGENIC REGION. FRANCALARIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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MEDLINE=97251357; PubMed=9097039;
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SEQUENCE OF 464-2003 FROM N.A.
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STRAIN=K12 / MG1655;
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                                                                                                                                                                                                                                                                                     361 NGTGVKKKLGETLTIKGGETQADKLTDNNNIGVVTDNNTGLKVKL-----AKNLSGLE 413
                                                                                                                                                                                                                                                                                                                                                                                                                             414 TVSTKNLTASEKVTVGSGNNTAELQSGGLTFTPTTNASTDKTVYGTD--GLKFTDNSNTA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 GVS-----ADGATKWQYNHNGELVITGDNATVNNNGKT--TVDGKDSTGTEINGNNGKV 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1043 ITNIQSGDIT--QNSND-----AVTGGRVYDLKTELESKINSAAKTAQNSL-HEFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             855 TTGINSGTISLLQNGKDPAPSPIVLLATNGGSATNAGT-ITGKV-----TEQHSVFNKYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LED-----YLDKDKIKKY---GNSTLNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    311 GGTGTQINGDDATANNNGKTTVDGKDSTGTEINGNNGKVIQDGDLDVSGGGHGIDITGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTGTQINGDDATANNNGKT-----TVDG-----KDSTGTEIA----GNNGKVI
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                                                                                                                                                                                                                Indels 685;
                                                                                                                                              Length 2003;
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   495 I -> V (IN REF. 2).
205949 MW; B83A12C8B53220EE CRC64;
                                                                                                                                          Score 556.5; DB 1;
Pred. No. 7.5e-13;
                                                                                                                                                                        Best Local Similarity 22.4%; Pred. No. 7.5e-13;
Matches 492; Conservative 243; Mismatches 776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.8%;
495 49
2003 AA;
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24	40 63	99 15	59	14	26	26 07	33 50	26	36	45 98	79 58	35 12	36	33 15	93	53 80	91	54
102	124	129	135	141	146	152	158	162	168	174	177	183 161	188	193	199	205	211	216
: : :	NDGAGHALSQGLANDIDKTRAASIGDVLANG-FNLQGNGEAVDFVSTYDTVDFIDGNATT	. AKVTYDDTSKTSKUVYDVNVDNKTIEVTSDKKLGVKTTTLTKTSAN-GNATKFSAADGDA 	LVKASDIATHLNTLAGDIQTAKGASQASSSASYVDADGNKVIYDSTDKKYYQVNDKGQVD 	KNKEVAKDKLVAQAQTPDGTLAQMNVKSVINKEQVNDANKKQGINEDNAFIKGLE	NAAKDTK TKNAAVTVGDLNAVAQTPLTFAGDTGTTAKKLGETLTIKGGQTDT 	NKLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGTRIDEKGISFVDANGQAKANTPVLS	ANGLDLGGKRISNIGAAVDDNDAVNFKQFNEVAKTVN-NLNNQSNSGASLPFVYTDAN	GKPIN-GTDGKPQKAIKGADGKYYHANANGV-PVDKDGKPITDAD   :		SAAQQSNAASVKDVLNVGFNLQTNHNQVDFVKAXDTVN-FVNGTGADITSVRSADGTMSN	ITVN-TALAATDDDGNVLIKAKDGKEYKADDLMPN 	GSLKAGKSASDAKTPTGLSLVNPNAGKGSTGDAVALNNLSKAVFKSKDGTTTTTVS 	SDGISIQGKDNSSITLSKDGLNVGGKVISNVGKGTKDTDAANVQQLNEVRN	LLGLGNAGNDNADGNQVNIADIKKDPNSGSSSNRTVIKAGTVLGGKG	NNDTEKLATGGVQVGVDKDGNANGDLSNVWVKTQKDGSKKALLATYNAAGGTNYLTNNPA 	EAIDRINEQGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQAKADGEAAVAIGRQ : :	TQAGNQSIAIGDNAQATGDQSIAIGTGNVYTGKHSGAIGDPSTVKADNSYSVGNNNQFID	ATQTDVFGVGNNITVTESNSVALGSNSAISAGTHAGTQAKKSDGTAGTTTT-
2967	1182	1241	1300	1360	1415	1467	1527	1584	1627	1687	1746	1780	1836	1887	1934	1994	2054	2114
qq	0y 0p	Oy Op	Oy Op	Oy Op	δλ	Oy Dp	Qy Dp	Qy Dp	Qy Dp	Oy Dp	Oy Dp	OY Db	oy ob	Oy Dp	Oy Db	Oy Dp	Oy Dp	Oγ

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-1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY. 656 PNTFETITFAGENGISISNDIAKGKVKVGIDPINGLTTPKLTVGSDKDGKTQLVIEQVAS 715 68 PNA--VITANANNGINLNTPAGS-----FNGLFL-----SNANNLAVTVSEDTTL 110 716 G--NDTKNIIRGLSPTLPSITNAGGVRT-TEQGNTITSDEDKSKAASIGDILNTGFNLKN 772 773 NSNSVGFVSTYNTVDFIDGNATTAKVTYDETNQTSKVTYDVNVDEKTIELTGDNGKTNK- 831 Indels 539; Caps 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 49, Last sequence update)
30-MAY-2000 (Rel. 40, Last annotation update)
01-0CT-2000 (Rel. 40, Last annotation update)
0UTER MEMBRANE PROTEIN B PRECURSOR (168 KDA SURFACE-LAYER PROTEIN)
(SURFACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SCAS) (ROMP B)
(CONTAINS: 120 KDA SURFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTIGEN)
(120 KDA OUTER MEMBRANE PROTEIN OMPB); 32 KDA BETA PEPTIDE). FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR Uchiyama T.;
"Sequencing of the gene encoding the protein rOmp B of Rickettsia
"Sequencing of the gene encoding the protein rOmp B of Rickettsia
"Sequencing of the EMBL/GenBank/DDBJ databases.

1- FOUCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
SIMILARITY). Length 1656; 120 KDA SURFACE-EXPOSED PROTEIN.
32 KDA BETA PEPTIDE.
POLY-GLY.
7M; 3132A69C9DD5999F CRC64; Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsieae; Rickettsia. NCBI\_TaxID=35790; Query Match 4.2%; Score 492.5; DB 1; Best Local Similarity 22.7%; Pred. No. 1.1e-10; Matches 419; Conservative 198; Mismatches 690; 2211 NGSQLYKATQGIANATNELDHRIHQNENKANAGISS 2246 1930 NLS--YAKSQRTASLAGAGSQHFNVDDGQKGGGINS 1963 PRT; 1656 AA. Ψ., EMBL; AB003681; BAA20138.1; -. Antigen; S-layer; Cell wall. CHAIN 1339 1656 CHAIN 1339 1656 DOMAIN 528 533 SEQUENCE 1656 AA; 168097 M STANDARD; = Rickettsia japonica [1] SEQUENCE FROM N.A. OMPB\_RICJA STRAIN-YH; OMPB\_RICJA 2165 g QQ ò οğ g q οχ ò δ

NALI-VNGANGTLNVT 217	LNTLAKEIHTTKGTAD 884 	GENGLIVATINKDGTVTFGINT 943    :        NGOLIANAGPANAVIGTNN 326	VKFAKVDKGNSSTGIDGTSRITKDQI 1003        ::       -FVVSVDNGKAAT-IDGQVYAKDMVI 357	SGDITONSNDAVTGGR 1063          VAITONSNEGTT 400	NPXSSYDTSKTSDVIT 1118 	KLTVGNNNGKG 1158 :  :	LANVINDGAGHAL-SQGLANDIDK 1199 ::                      DIGNGGGGAALQSITLANDAIK 547	TTAKVTYDDTSKTSKV 1254 	-TKTSANGNATKFSAADGDALVKASDIA 1307 	VNDKGQVDKNKEVAKD 1367 	NAFIKGLENAAKDTKTKNA 1425 : I : LYATNITTTDANVGSF 740	ETLIKGGQT 1464 	NAGGTRIDEKGISFVDANG 1516   ::    :  VSGPGNVVVNEIGNAGN 856	KOFNEVAKTV-NNLNNQSNSGASL 1575         :         GNTIPLTIKSTVGNETAEGFSV 909	VPVDKDGKPITDADKLANLA 1632            :    VIADGQVIGDQNNIVGLGLGS 940	IDTPNTGNANAGQAQSLPSLS 1687 	YDTVNFVNGTG 1730 :   :    TDFDGKITLGSVNGN- 1045	DDLMPNGSLKAGKSAS 1789
NDLSGLGTIDFGAAASTLVFDLANPTTQKAPLILADNALI	IGVKTTTLTTINANCKAINESTIDNDALVNAKDIAENLNTLAKEIHTTKGTAD 	TALQTFKVKKDGATDDETITVGKDGTQNG-KTVNTLKLKGENGLTVATNKDGTVTFGINT     :   :	OSGLKAGDSTTLNKDGLSIKNPASNEQIQVGADGVKFAKVDKGNSSTGIDGTSRITKDQI 	GFTGANGSLDTTKPHLTKDKLKVGEVEITNTGINAGGKKITNIQSGDITQNSNDAVTGGR 	VYDLKTELESKINSAAKTAQNSLHEFSVADEQGNHFTVSNPYSSYDTSKTSDVIT 	FAGENGITTKVNKGVVRVGIDQTKGLTTPKLTVGNNNGKG 	IVIDSK	TRAASIGDVLNAGFNLQGNGEAVDFVSTYDTVDFIDGNATTAKVTYDDTSKTSKV 	VYDVNVDNKTIEVTSDKKLGVKTTTLTKTSANGNATK 	THLNTLAGDIQTAKGASQASSSASYVDADGNKVIYDSTDKKYYQVNDKGQVDKNKEVAKD :	KLVAQAQTPDGTLAQMNVKSVINKEQVNDANKKQGINEDNAFIKGLENAAKDTKTKNA 	AVTVGDLNAVAQTPLTFAGDTGTTAKKLG	DINKLIDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGTRIDEKGISFVDANG 	QAKANT PVLSANGLDLGGKRISNIGAAVDDNDAVNFKQFNEVAKTV-NNLNNQSNSGASL 	PEVVIDANGKPINGIDGKPQKAIKGADGKYYHANANGVPVDKDGKPITDADKLANLA	AHGKPLDAGHQVVASLGGNSDAITLTNIKSTLPQIDTPNTGNANAGAQSLPSLS 	AAQOSNAASVKDVLNVGFNLQTNHNQVDFVKAYDTVNFVNFTG  ::	ADITSVRSADGTMSNITVNTALAATDDDGNVLIKAKDGKF-YKADDLMPNGSLKAGKSAS
167 N	832 - 218 N	885 T 274 I	327 0	358 0	1064 v	1119 E	1159 1 494 T	1200 1	1255 V 605 -	1308 T 651 N	1368 F	1426 #	1465 I	1517 C	1576 F	1633 - 941 E	1688 p	1731 2
QQ	ç d	Qy	Qy Dp	S Q	oy Db	Qy Dp	95 Pp	O <sub>Y</sub>	Q <sub>Y</sub>	Qy Dp	Qy	Oy Dp	oy Dp	Oy Dp	Oy Dp	Qy Db	QY	, VO

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1197
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                    TTTVSSDGISIQGKDNSSI---TLSKDGLNVGGKVI----SNVGKGTKDTDAANVQQLNEVR 1885
                                                                                                                          1886 NLLGLGNAGNDNADGNQVNIADIKKDPNSGSSSNRTVIKAGTVLGGK--GNNDTEKLATG 1943
                                                                                                                                              1944 GVQVGVDKDGNANGDLSNVWVKTQKDGSKKALLATYNAAGQTNYLTNNPAEAIDRINEQG 2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: OUTER MEMBRANE.
MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPMA
MAY BE RESPONSIBLE FOR PORE FORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Uphoff T.S., Welch R.A.;
"Nucleotide sequencing of the Proteus mirabilis calcium-independent hemolysin genes (hpmA and hpmB) reveals sequence similarity with the Serratia marcescens hemolysin sees (shlA and shlB).";
J. Bacteriol. 172:1206-1216(1990).
-:- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPFURE BY MECHANISMS NOT CLEARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPMA REQUIRES HPMB FUNCTION.
                                                                                Proteus mirabilis.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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01-AUG-1990 (Rel. 15, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
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SEQUENCE FROM N.A., AND SEQUENCE OF 30-43.
STRAIN-ISOLATE 477-12;
MEDLINE-90170827; Pubmed-2407716;
DAKTP-TGLSLVNPNAGKGSTGDA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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P16466;
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                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1090 SVADEQGNHFTVSNPYSSYDTSKTSDVITFAGENGITTKVNKGVVRVGIDQTKGLTT--P 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---TRAASIGDVLNAGFNLQGNGEAVDFVSTYDTVDFIDGNATTAKVTYDDTSKTSKVVY 1256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVNVDNKTIEVTSDKKLGVKTTT---LTKTSANGNATKFSAADGDALVKASDIATHLNTL 1313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                621
                                                                                                                                                                                                                                                                                                                                                                                                                                GNTPNTFETITFAGENGISISNDIAKGKVKVGIDPINGLTTPKLTVGSDKDGKTQLVIEQ 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ASLILNE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAKEIHTTKGTADTALQTFKVKKDGATDDET----ITVGKDGTQNGKTVNTLKLKGENGL 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------DSQVRYDSYDKDGSENYQNYRGGITVNNSG--SSQTLTKTELKGKN-- 326
                                                                                                                                                                                                                                                                                                                                                                SGINAGDQKISNVKDATDDTDAVTYKQLKQVQQDADGALQSFSIRDEKGQEFTISNLYSN 652
                                                                                                                                                                                                                                                                                                                                                                                               44 SAVNGGTQVINIV---TPNNEGISHNQYQDFNVGKPGAV--FNNALEAGQSQLAGHLNAN 98
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----INAGNNLAIN------ANKDIHINGLVEKESRSENGNKRNHTSRLESGSW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -NTGFNLKNNSN--SVGFVSTYNTVDFID------GNATTAKVTYDETNQTSKVTYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QLKGYSTLNNTNLLSLG-KNGLNTTGLLDLIAPRIDSRGKITAAEISAFTGQNTFSQHFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VNVDEKTIELTGDNGKTNKIGVKTTTLTTTNANG-KATNFSTTDNDALVNAKDIAENLNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVATNKDGTVTFGINTQSGLKA ---- GDSTTLNKDGLSIKNPASNEQIQVGADGVKFAKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DKGNSSTGIDG-----TSRIT--KDQIGFTGA-----NGSLDTTKPHLTKDKLKVGEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                713 VASGNDT----KNIIRGLSPTLPSITNAGGVRTTEQGNTITSDEDKSKAASIGDIL----
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                                                                                                                                                                                                                                                                                                                               Indels 603;
                                                                                                                                                                                                                                                                                                DB 1; Length 1577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLTVGNNNGKGIVIDSKDGQNTITGLSNTLANVTNDGAGHALSQGLANDTDK---
                                                                                                                                                                                                                                              SEQUENCE 1577 AA; 165869 MW; 175975E0C924B2D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.9%; Score 450.5; DB 1; Best Local Similarity 21.1%; Pred. No. 3.3e-09; Matches 389; Conservative 249; Mismatches 605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----PNGOY----
SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA)
                                                                                                                                                                                               Hemolysis; Toxin; Outer membrane; Signal
                                                                                                                                                                                                                                HEMOLYSIN
                                                                                                                                                             EMBL; M30186; AAA25657.1; -.
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                                                                                                                                                                                                                  SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITSVRSADGTMSNITVNTALAATDDDGNVLIKAKDGKFYKADDLMPNGSLKAGKSASDAK 1792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1014 ITVAIKGEGO----TTDNALMET------KAKGSOFTSNGDISINVGENAHYEGAOFD 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1793 TPTGLSLVNPNAG-----AVFKSK 1826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGGKVISNVGKGTKDTDAANVQQLNEVRNLLG------LGNAGNDNADGN--- 1901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----QVNIADIKKDPNSG----SSSNRTVIKA--GTVLG--GKGNNDT-----EKLAT- 1942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----GGVQVGVD-----KDGNANGDLSNVWVKTQKD-----GSKKALLATYNAAGQTNY 1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDPSTVKADNSYSVGNNNQFIDATQTDVFGVGNNITVTESNSVALGSNSAISAGTHAGTQ 2151
1314 AGDIQTAKGASQASSSASYVDADGNKVIYDSTDKKYYQVNDKGQVDKNKEVAKDKLVAQA 1373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GASLPFVVTDANG--KPINGTDGKPQKAIKGADGKYYHANANGVPVDKDG-----KPIT 1623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQKGKTVINAGGDLTLAQATDTHSESQSNVNGSANLKVGTTPESKDYGGGFNAGTTHHSK 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --SKDGLN 1857
                                                                                                                                                                                                                                                                                       1421 KTKNAAVTVGDENAVAQTPEJFAG-DTGTTAKKLGETLTIKGG-----QTDTNKLTDNNI 1474
                                                                                                                                                                                                                                                                                                                                                                                                                                        1475 GVVAGTDGFTVKLAKDLTNLNSVNAGGTRID---EKGISFVDANGQAKANTPV----LS 1526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1527 ANGLDL--------GGKRISNIGAAVDDNDAVNFKQFNEVAKTVNNLNNQSNS 1571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1624 DADKLANLA--AHGKPLDAGHQVVASLGGNSDAITLTNIKSTLPQIDTPNTGNANAGQAQ 1681
                                                                                                                                                                                                                                                                                                                                                           715 EQANSTISGANVDLQANKDVTFAGSDLKTTA----GNASITGDNVAFVSTENKKQTDNTD 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            868 GVNL----DYSGVTKPV-----KKAIE------DGVNTTKPGNNTDLTKKVT 904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              905 ARDAIANLANLSTPNVGVEVGIKGGGSQQSQTDSQAVST----SINAGKIDIDSNN 959
                                                                ----OTSTG-SELISDAQLTVVSGN------DVNVIGSLIK----SADKLGIH-
                                                                                                                                                                                       771 TTISGGFSYT------GGVDKVGSKADFQYDKQHTQTEVTKNRGSQTEVAGDLTIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IHNIGGKLLVNVEDQQKTSHQNATLETGTLTINSNKDLTLSGANVTADSVTGNVGGSLNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLPSLSAAQQSNAASVKDVLNVGFNLQTNHNQVDFVKAYDTVNFVNG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 QKAGSHAK------GKESIAIGGDVLAEGDASIAIGSDDLYLDRNSTNSKYPN 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 IAFGTTGNNDNASASNEASIAIGSLAKA------HANQAIAIGGSKPDPRNQAAN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       508 ELVSSAQLEVRGQREVALDDAS-----SARGMTVVAAGALAARNLQSKGAIGVQGGEAV 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         562 SVANANSDAELRVRGRGOVDLHDLSAARGADI---SGEGRVNIGRARSDSDVKVSAHGAL 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 DEDYGIALGYGSQILNNNNNNNKAYVPEGNGS----NIKSSKA---TGNGLFSIGSSTI 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 VAECAKSHSGSSSSTAGQVGSSPVIRLTRVATLAIL---VIGATL---NGSAYAQNNSK 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STAEGNYSLAVGLTAK - - - - - AEKGYTIAIGSNAQAINYGALALGADTRV - - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEQUENCE OF 1-3261 FROM N.A. MEDIINE-89202384; PubMed-2539596; MEDIINE-89202384; PubMed-2539596; MEDIINE-80-4, Domenightini M., Tuomanen E., Rappuoli R., Falkow S.; "Filamentous hemagglutinin of Bordetella pertussis: nucleotide sequence and crucial role in adherence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 GLLSTLIQNHTVLRQIRDSNGSQKYRRTAAEGHASTAVGAMAYAKGHFANAFGTR----
                                                                                                                                                                                                                                                                                                                                           S:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 3.8%; Score 448; DB 1; Length 3591; Best Local Similarity 19.5%; Pred. No. 1e-08; Matches 599; Conservative 358; Mismatches 1069; Indels 1050;
                                                                                                                                                                                                                                                                                                                                       Relman D.A., Domenighini M., Tuomanen E., Rappuoli R., Falkow "Genetic characterization of Bordetella pertussis filamentous haemagglutinin: a protein processed from an unusually large
                                                                                                                                                                                               Bordetella pertussis.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 86:2637-2641(1989).
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                                                                                          01-0CT-1989 (Rel. 12, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
FEB-1996 (Rel. 33, Last annotation update)
FILAMENTOUS HEMAGGLUTININ.
                                                        PRT; 3591 AA
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-90355839; PubMed-23388559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M60351; AAA22974.1; -.
EMBL; M60351; AAA22975.1; ALT_INIT.
EMBL; M60351; AAA22976.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: SURFACE.
                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Microbiol. 4:787-800(1990).
                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antigen; Hemagglutinin.
SEQUENCE 3591 AA; 36
                                                                                                                                                                                                                                                     NCBI_TaxID=520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFECTION.
                                                        FHAB_BORPE
                                                                                                                                                                                                                                                                                                                                                                                                      precursor.
                RESULT 5
FHAB_BORPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224
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qq	619	SIDSMTALGAIGVQAGGSVSAKDMRSRGAVTVSGGGAVNLGDVQS 663
Qy	322	DTDAVNVAQLKAVENLAKRQITFKGDDNGTGVKKKLG
qa	664	AGDALQAGFLKSAG-AMTVNGR
δλ	381	QADKLTDNNNIGVYTDNNTGLKVKLAKNLSGLETVSTKNLTASEKVTVG 429
qq	714	GELTV
oy .	430	SGNNTAELSG-GLTFTPTTNASTDKTVYGTDGLKFTDNSNTALE
වූ .	774	SVNSASRVAISAHGALDVGKVSAKSGIGLEGWGAVGADSLGSDGAISVSGRDAVRV
δ	474	DTTRITKDKDKLKVGNS :
QQ	830	DQARSLADISLGAEGGATLGAVEAAGSIDVRGGSTVAANSLHANRDVRVSGKDAVRVTAA
δō i	510	TLNNKGLTVNNTIGGSNKQIQVGA
qq	890	T-SGGGLHVSSGRQLDLGAVQARGALALDGGAGVALQSAKASGTLHVQGGE 93
ΟŊ	561	IGFADADGKVDKKSPYLDKKQLQVGGVKITKDSGINAGDQKISNVKDATDDT :
qq	940	HL
Qγ	613	DAVTYKQLKQVQQDADGALQSFSIRDEKGQEFTISNLYSNGNTPNTF 659
qa	991	QARAQQKLELGSVKSDGGLQAAAGGALSLAAAEVAGALELSGQGVTVDRASASR 1044
Qy	099	
qq	1045	ARIDSTGSVGIGALKAGAVEAASPRRARRALRQDFFTPGSVVVRAQGNVTVGRGDPHQGV 1104
Qy	692	TPPKLTVGSDKDGKTQLVIEQVASGNDTKNIIRGLSPTLPSITNAGGVRTTEQGNTI 748
qq	1105	;
Οy	749	TSDEDKSKAASIGDILNTGFNLKNNSVG
qq	1147	ESKISQSVLAAKGDKGKPAVSVKVAKKLFLNGTLRAVNDNNETMSGRQIDVVDGRPQ 1203
δλ	795	TAKVTYDETNQTSKVTYDVNVDEKTIELTGDNGKTNKIGVKTTTLTTT 842
qq	1204	
Qy	843	NANGKATNESTTÖNDALVNAKDIAENLNTLAKEIHTTKGTADTALQTFKVKKDGATDDET 902
QQ	1251	KENGASVTVRTTGNLVNKGYISAGKQGV-LEVGGALTNEF 1289
Qy	903	ITVGKDGTQ96KTVNTLKLKGENGLTVATNKDGTVTFGINTQSG946
qq	1290	EAQRI
ΟŽ	947	LKAGDSTTLNKDGLSIKNPASNEQIQVGADGVKFAKVDKGNSSTGIDGTSR 997
qα	1349	GGSPTVTAGAKATTSANKLSVDVASWDNAGSLDIKKGGAQVTVAGRYAEHGEVSIQGDYT 1408
Qy	866	ITKDQIGFTGANGSLDTTKPHLTKDKLKVGEVEITNTGINAGGKKITNIQSGD 1050
qq	1409	VSADAIALAAQVTQRGGAANLTSRHDTRFSNKIRL
Qy	1051	ITQNSNDAVTGGRVYDLKTELESKINSAAKTAQNSLHEFSVADEQGNHF
qq	1461	
ΟY	1101	VSNPYSSYDTSKTSDVITFAG-ENGITTKVNKGVVRVGIDQTKGLTTPKLTVGNNNGKGI 1159
qq	1514	VSNP-GTFTAGKDITVTSRGFDNEGKMESNKDIVIKTEQFSNGR 1557
δy	1160	VIDSK-DGONTITGLSNTLANVINDGAGHALS-QGLANDTDKTRAASIGDVLNAGFNLOG 1217

qq	1558	VLDAKHDLTVTASGQADNRGSLKAGHDFTVQAQRIDNSCTMAAGHDATLKAP-HLRN	1613
δλ	1218	NGEAV	1247
qq	1614	TGQVVAGHDIHIINSAKLENTGRVDARNDIALDVADFTNTGSLYAEHDATLTLAQGTQRD	1673
οy	1248	TSKTSKVVDVNVDNK-TIEVTSDKKLGVK	1276
qq	1674	LVVDQDHILPVAEGTLRVKAKSLTTEIETGNPGSLIAEVQENIDNKQAIVVGKD	1727
Qy Dp	1277	TTLTKTSANGNATKFSAADGDALVKASDIATHLNTLAGDIQTAKGASQASSSASYVDAD	1336 1769
ò	1337	GNKVIYDSTDKKYYQVNDKGQVDKNKEVAKD-KLVAQAQTPDGTLAQMNVKSVINKEQVN	1395
. a		: : :  :    : GNARLTAAVALLNKLGRIRAGEDMHLDAPRIENTAKLSGEVQRKGVQDVGGGEH	1823
ογ	1396	DANKKQGINEDNAFIKGLENAAKDTKTKNAAVTVGDLNAVAQTPLTFAGDTGTTAKK- :	1452
qq	1824	GRWSGIGYVNYWLRAGNGKKAGTIAAPWYGGDLTA-EQSLIEVGKDLYLNAGARKD	1878
λο d	1453	IGETLTIKGGOTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGTR	1503
ga	6/81	EHRHLLNEGVIQAGGHGHIGGDVDNRSVVRIVSAMEYFRIPLFVSLIALDNRAGLSFA	1936
à à	1937		1528 1996
3	)  -	THE KOLL BUILD BEDENKLET THOSE FILLERS WE ENNEDED LY FOR THE MEN	
r d	1529	GLDLGGKRISNIGAAVDDNDAVNFKQFNEVAKTVNNLNNQ 	1568 2047
3		7	1
6	1569	SNSGASLPEVYTDANGKPINGTDGKPQ	1595
3 3	* 0	DOĞRI GRADGOTIDABİ REYDƏ İLÇEF AADLIRI YLANÇADÇAL LUABLIDIN AQVIL NƏÇLDA	707
<u> </u>	1596	VDT ON TOOL DUMIN AND TO THE OWN THE O	162/
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δō	1628	LANLAAHGKPLDAGHQVVASLGGNSDAITLTNIKSTLP	1665
QQ	2168	AGAGLTLSNGAIHNGENAAQNRGRPEGLKIGAHSATSVSGSFDALRDVGLEKRLDIDDAL	2227
οy	1666	OIDTPNTCNANA	1677
а	2228	AAVLVNPHIFTRIGAAQTSLADGAAGPALARQARQAPETDGMVDARGLGSADALASLASL	2287
٥y	1678	GQAQSLKDVLNVGFN	1706
QQ	2288	DAAQGLEVSGRRNAQVADAGLAGPSAVAAPAVGAADVGVEPVTGDQVDQPVVAVGLEQPV	2347
٥y	1707		1736
qq	2348	ATVRVAPPAVALPRPLFETRIKFIDQSKFYGSRYFFEQIGYKPDRAARVAGDNYFDTTLV	2407
οy	1737	RSADGTMSNITV-NTALAATDDDGNVLIKAKDGKF-YK	1772
qq	2408	REQVRRALGGYESRLPVRGVALVAKLMDSAGTVGKALGLKVGVAPTAQQLKQADRDFVWY	2467
οy	1773	ADDLMPNGSLKAGKSASDAKTPTGLSLVNPNAGKGSTGDAVALNNL-	1818
QQ	2468	:	2525
οy	1819	SKAVFKSKDGTTTTTVSSDGISIQGKD	1858
QQ	2526	QGRSVKVDAGKGKVVVADSKGAGGGIEADDEVDVSGRDIGIEGGKLRGKDVRLKADTVKV	2585
δy	1859		1890
Db	2586	2586 ATSMRYDDKGRLAAR-GDGALDAQGGQLHIEAKRLETAGATLKGGKVKLDVDDVK-LGGV	2643

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MEDLINE-DULLINE, MEDLINE-STATES, PubMed-2122457; MEDLINE-DOBSON M.E., Ching W.M., Dasch G.A.; Carl M., Dobson M.E., Ching W.M., Dasch G.A.; Characterization of the gene encoding the protective paracrystallinesurface-layer protein of Rickettsia prowazekii: presence of a truncated identical homologin Rickettsia typhi."; Proc. Natl. Acad. Sci. U.S.A. 87:8237-8241(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----TGGIATH----NGQGAVAVGLSKLS 2285
                                                                                                                                                           EAHAGRGMTAGAEVKVGYRASHEQSS---ETEKSYRNANLNFGGGS--VEAGNVLDIGGA 2814
                                                                                                                                                                                                                                                                                            OMPB_RICPR STANDARD; PRT; 1643 AA.
0553020; 092CM0;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
(SURFACE PROTEIN B PRECIPINSON (168 KDA SURFACE-LAYER PROTEIN)
(SURFACE PROTEIN ANTIGEN) (CELL SUFFACE ANTIGEN)
(CONTAINS: 120 KDA SURFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTIGEN)
(120 KDA OUTER MEMBRANE PROTEIN OMPB); 32 KDA BETA PEPTIDE].
GNAGNDNAD-----GNQVNIADIKKDPNSGSSSNR--TVIKAGTVLGGKGNNDTEKLAT
                   2644 YEAGSSYENKSSTPLGSLFAILSSTTETNQSAHANHYGTRIEAGTLEGKMQNLEIE----
                                                                   -----GSKKAL
                                                                                                   GGSVDAAHTDLSVARDARFKAAADFAHAEHEKDVRQLSLGAKVGAGGYEAGFSLGSESGL
                                                                                                                                    LA-----TYNAAGQTNYLTNNPAEAIDRINEQGIRFFHVNDGNQEPVVQGRNGIDSSAS
                                                                                                                                                                                                      GKHSVAIGFQAKADG------EAAVAIGRQT-QAGNQSIAIGDNAQA----
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                                                                                                                                                                                                                                                                                                                                          SVGNNNQF-----IDATQTDV-----FGVGNNITVTESNSVAL------GSN
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moron C.G., Yu X.J., Walker D.H.; Sequence analysis of ompB of Rickettsia prowazekii."; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                     GG-----VQVGVDKDGNANGDLSNVWVKTQKD-----VQVGVDKDGNANGDLSNVWVKTQKD-----
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-BREINL;
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                                                                                                                                                                                                                                                                                                        Hackstadt T., Messer R., Cieplak W. Jr., Peacock M.G.;
"Evidence for proteolytic cleavage of the 120-kilodalton outer
membrane protein of rickettsiae: identification of an avirulent mutant
                                                                                                                                                                                                                                                                                                                                                                Infect. Immun. 60:159-165(1992).
-!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
STRUCTION: THE 120 KDA SURFACE.
VIRULENCE PACTOR AND/OR IMMUNOGEN DURING INFECTION.
-!- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.
-!- SUBCELLULAR LOCATION: ECLL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.
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   TTQEAPLTLGA -> INSRSSSYHLVS (IN REF. 1).
   T -> I (IN REF. 1).
   Q -> L (IN REF. 1).
   D -> G (IN REF. 2).
   T -> S (IN REF. 2).
   T -> S (IN REF. 2).
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                                                    Andersson S.G.E., Zomorodipour A., Andersson J.O., Scheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Eriksson A.-S., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the origin of
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                                                                                                                                                                                         Ching W.M., Carl M., Dasch G.A.; "Mapping of monoclonal antibody binding sites on CNBr fragments the S-layer protein antigens of Rickettsia typhi and Rickettsia
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ilarity 21.4%; Pred. No. 5.1e-09;
Conservative 216; Mismatches 713;
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                                       MEDLINE=99039499; PubMed=9823893;
Andersson S.G.E., Zomorodipour A.
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MEDLINE=92114896; PubMed=1370573;
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IDENTIFICATION OF CLEAVAGE SITE.
MEDLINE=92104668; PubMed=1729180;
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Mol. Immunol. 29:95-105(1992).
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942 NANTLYSGIRTTKNNQG----TVTLSGGMPNN-------PGTIYGLGLENGSP 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 394 SNFGSTN-FGNLDTQIVVPDTKILKGNFIGDVKNNGNTAGVITFNANGALVSASTDPNIA
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                                                                                                                                                                                                                                                                     1049 GDITQNSNDAVTGGRVYDLKTELESKINSAAKTAQNSLH-----EFSVADE----QG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         337 VD---NGNAATISGQVYAKNMVIQSANAGGQVTFEHIVDVGLGGTTNFKTADSKVIITEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 767 ILDNGTTVKFLGDT-TFNGGTKIEGKSILQISNNYTTDHVESADNTGTLEFVNTDPITVT
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                                                                                                 ---TOSGLKAGDST----TLNKD-
                                                                                                                                                             178 AAPSVLEFNLINPTTQEAPLTLGANSKIVNGGNGTLNITNGFIQVSDNTFAGIKTINIDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1133 VVRV-----GIDQTKGLTTPKLTVGNNN-----GKGIVIDSKDGQNTITGLSNTLA-
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                                                                                              ---TNKDGTVTFGIN----
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1504 VTPMAGLSYLKSSNENYKETGTTVANKRINSKFSDRV-----DLIVGAKVAGSTVNITDI 1558
1079 PVASVRFTGND-----SGAGLQGNIYSQNIDFGTYNLTIL----NSNVILGGGTTAINGE 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LATGGVQVGVDKDGNANGDLSNVWVKTQKDGSKKALLATYNAAGQTNYLTNNPAEAIDRI 1999
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                                                                                                                                                    130 IDLLTNNLIFANGTSTWGDNTSISTTL---NVSSGNIGOVVIAEDAO--VNATTTGTTTI 1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---DGQTAPFISQP 1594
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
00TER MEMBRANE PROTEIN B PRECURSOR (168 KDA SURFACE-LAYER PROTEIN)
(SURPACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SOMP B)
(CONTAINS: 120 KDA SURFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTICEN)
(120 KDA OUTER MEMBRANE PROTEIN OMPB); 32 KDA BETA PEPTIDE].
                                                                                                                                                                                                                                                                                                                                                                                                                                 - VAGSATGAVSSGDEAEVSYGVWAKPFYNIAEQDKKGGIAGYKAKTTG---VVVGLDTLA
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Gilmore R.D. Jr., Cleplak W. Jr., Policastro P.F., Hackstadt T.;
"The 120 Kilodatton outer membrane protein (rOmp B) of Rickettsia rickettsii is encoded by an unusually long open reading frame: evidence for protein processing from a large precursor.";
Mol. Microbiol. 5:2361-2370(1991).
                                                                                                                                                                                                                                                                                                    1185 KIQDNANANFSGTQAYTLIQGGARFNGTLGAPNFAVTGSNIFVKYELIRDSNQDYVLTRT
                                                                                                                                                                                                                                                                                                                                                                                    NEVRNLL -- GLGNAGNDNADGNQVNIADIKKDPNSGSSSNRTVIKAGTVLGGKGNNDTEK
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                                                                            DDLMPNGSLKA-GKSASDAKTPTGLSLVNPNAGKGSTGDAVALNNLSKAVFKSKDGTTTT
                                                                                                                                                                                                                                TVSSDGIS-----IQGKDNSSITLSKDGLNVGGKVISNVGKGTKDTDAANV-QQL
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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STRAIN-R.
MEDLINE-90136087; PubMed=2515418;
Gilmore R.D. Jr., Joste N., McDonald G.A.;
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Q53047;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    831 KIGVKTTTLTTTN----ANGKATNFSTTDNDALVNAKDIAENLNTLAKEIHTT----KGTA 883
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-!- FUNCTION: THE 120 KDA SURPAGE-EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRGIENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
-!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BILAXER WITH HEXAGONAL SYMMETRY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1654;
                                                                                                                                                                                                                                                                                                                                                                               120 KDA SURFACE-EXPOSED PROTEIN.
32 KDA BETA PEPTIDE.
POLY-THR.
                                                                                                                                                                                                                                                                                                                                                                                                                                         1654 AA; 168184 MW; D7AB70FB7087F618 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.8%; Score 444.5; DB 1;
ilarity 21.8%; Pred. No. 5.6e-09;
Conservative 182; Mismatches 728;
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CHAIN 1 1333
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IDENTIFICATION OF CLEAVAGE SITE.

MEDLINE-92104668; Pubmed-1729180;

MEDLINE-92104668; Pubmed-1729180;

A Hackstadt T., Messer R., Cieplak W., Peacock M.G.;

Hackstadt T., Messer R., Cieplak W., Peacock M.G.;

Hackstadt T., Messer R., Cieplak W., Peacock M.G.;

The membrane protein of rickettsiae: identification of an avirulent of membrane protein in processing.";

Thiest. Infect. Immun. 60.159-165(1992).

C.:- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROPEIN MHYCH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.

THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.

C.:- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.

C.:- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A STANKETRY.
2208 DAVNGSQLYKATQGIANATNELDHRI------HQNENKANAGISSAMAMASMPQAYIP 2259
                                                                               |: ::| | :: : | | :: : | | 1573 PEVHAFVVHKVTGRLSKTQSVLDGQVTPCINQPDRTTKTSYNLGLSASIRSDAKMEYGIG 1632
                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
OUTER MEMBRANE PROTEIN B PRECURSOR (168 KDB SURFACE-LAYER PROTEIN)
(SURRACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SCA5) (ROMP B)
[CONTAINS: 120 KDA SURFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTIGEN)
(120 KDA OUTER MEMBRANE PROTEIN OMPB); 32 KDA BETA PEPTIDE].
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MEDLINE=92114896; PubMed=1370573;
Ching W.M., Carl M., Dasch G.A.;
"Mapping of monoclonal antibody binding sites on CNBr fragments the S-layer protein antigens of Rickettsia typhi and Rickettsia prowazekii.";
Mol. Immunol. 29:95-105(1992).
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Antigen; S-layer; Transmembrane; Cell wall.
Antigen; S-layer; Transmembrane; Cell wall.
11353 120 KDA SURFACE-EXPOSED PROTEIN.
11353 32 KDA BETA PEPTIDE
11455 32 KDA BETA PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=785;
                                                                                                                                                                                                                                                                     PRT; 1645 AA.
                                                                                                                                 2260 GRSMVTGGIATHNGQGAVAV 2279
                                                                                                                                                                     1633 YDAQISSKYTAHQGTLKVRV 1652
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                                                                                                                                                                                                                                                                     STANDARD;
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PARTIAL SEQUENCE.
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CONFLICT 657 657 H -> N (IN REF. 2).  CONFLICT 842 W -> I (IN REF. 2).  CONFLICT 1071 1071 G -> A (IN REF. 2).  CONFLICT 1306 1306 G -> S (IN REF. 2).  SEQUENCE 1645 AA; 169698 MW; 0CB5641C7EB185EE CRC64;	y Match 3.7%; Score 438.5; DB 1; Length 1645; Local Similarity 22.1%; Pred. No. 9.1e-09; hes 390; Conservative 209; Mismatches 570; Indels 599; Gaps 101;	725 GLSPTLPSITNAGGVRTTEQGNTITSDEDKSKAASIGDILNTGFNLKN-NSNSVGFVSTY 783	784 NTVDFIDGNATTAKVTYDETNOTSKVTYDVNVDEKTIELTGDNGKTNKIGVKTTLLTTN 843	ET 90	903 ITVGKDGTQNGKTVNTLKLKGENGLTVATNKDGTVTFGINTOSGLKAGDSTTLNKDG 959   1	960 LSIKNPASNEQIQVGADGVKFAKVDKGNSSTGIDGTSRITKDQIGFTGAN 1009   :	010 GSLDTTKPHLTKDKLKVGEVEITNTGINAGGKKITN	050 DITQNSNDAVIGGRVYDLKTELESKINSAAKTAQNSLHEFSVADEQ 1095 	096GNHFTVSNPYSSYDTSKTSDVITFAGENGITTKVNKG 1132	133VVRVGIDQTKGLTTPKLTVGNNNGKGIVIDSKDGQNTITGLSNTLAN- 1179	180VTNDGAGHALSQGLANDTDKTRAASIGDVLNAGFNLQGNGEA 1221 	222 VDFVSTYDTVDFIDGNATTAKVTYDDTSKTSKVVYDNKTIEVT-SDKKLGVKTT 1278  1	279 TLTKTSANGNATKFSAADGDALVKASDIATHLNTLAGDIQTAKGASQASSSASYVD 1334	335 ADGNKVIYDSTDKKYYQVNDKGQVDKNKEVAKDKLVAQAQTPDGTLAQMNVKSVINK-EQ 1393	394 VNDANKKQGINEDNAFIKGLENAAKDTKTKNAAVTVGDLNAVA 1436 	437 QTPLTFAGDTGTTAKKLGETLTIKGGQTDTNKLTDNNIGVVAGT 1480 	481 DGFTVKLAKDLTNLNSVNAGGTRIDEKGISFVDANGQAKANTPVLSANGLDLGG 1534
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1085 --FTGNDSGVGLQGNIHSQNID---FGTYNLTILNSDVILGG------GTTAINGEI 1130
                                                                                                                                                                    ITLTNIKSTLPQIDTPNTGNANAGQAQSLPSLSAAQQSNAASVKDVLNVGFNLQTNH--- 1711
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                                   1535 KRISNIGAAVDDNDAVNFKQFNEVAKTVNNLNNQSNSGASLPFVVTDANGKPINGTDGKP 1594
                                                                                                   1595 QKAIKGADGKYYHANANGVPVDKDGKPITDADKLANLAAHGKPLDAGHQVVASLGGNSDA 1654
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                                                                                                                           887 VLTIKSTVG-----NGT-VDNFNAPILVVSGIDSMINNGQVIGDQKNIIALSLGSDNS 938
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002470;
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 36, Last annotation update)
PII-TYPE PROTEINASE PRECURSOR (EC 3.4.21.96) (LACTOCEPIN) (CELL WALL-ASSOCIATED SERINE PROTEINASE) (LP151).
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Bacieria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
Lactobacillus;
NCBI_TaxID=1597;
                                                      2066 NAQA--TGDQSIAIGTGNVVTGKHSGAIGDPSTVKADNSYSVGNNNQFI-----DATQT
821 DPITVTLNKQGAYFGVLKQVMVSGPGNIAFNEIG-----NGVAHA-
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                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                             Purification and N-terminal amino acid sequence determination of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                           SPECIFICITY, ALTHOUGH SOME SUBSITE PREFERENCE HAVE BEEN NOTED, E.G. LARGE HYDROPHOBEC RESIDUES IN THE P1 AND P4 POSITIONS, AND PRO IN THE P2 POSITION. BEST KNOWN FOR ITS ACTION ON CASEINS, ALTHOUGH IT HAS BEEN SHOWN TO HYDROLYSE HEMOGLOBIN AND OXIDIZED
                                                                                                                                                                                                       paracasei.";
J. Gen. Microbiol. 138:313-318(1992).
J. Gen. Microbiol. PROTEASE WHICH BREAKS DOWN MILK PROTEINS DURING THE GROWTH OF THE BACTERIA ON MILK.
-!- CATALYTIC ACTIVITY: ENDOPEPTIDASE ACTIVITY WITH VERY BROAD
                                                              "Cloning, sequencing and expression of the gene encoding the cell-
envelope-associated proteinase from Lactobacillus paracasei subsp.
                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. CELL WALL. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
CHARGE RELAX SYSTEM (BY SIMILARITY).
CHARGE RELAX SYSTEM (BY SIMILARITY).
CHARGE RELAX SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1902;
                                                                                                                                                                                            cell-wall-bound proteinase from Lactobacillus paracasei subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEMBRANE ANCHOR (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protease; Cell wall; Zymogen; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PII-TYPE PROTEINASE.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.5%; Score 407.5; DB 1; 21.1%; Pred. No. 1.4e-07;
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PROSITE; PS00343; GRAM_POS_ANCHORING; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
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                                                                                                         Gen. Microbiol, 138:1353-1364(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS, PRO0723, SUBTILIBIN.
PROSITE, PS00136, SUBTILIASE_ASP, 1.
PROSITE; PS00137, SUBTILASE_HIS; 1.
                                                                                                                                                  MEDLINE=92226694; PubMed=1564442;
Naes H., Nissen-Meyer J.;
                                        MEDLINE=92381481; PubMed=1512565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00746; Gram_pos_anchor;
Pfam; PF00082; Peptidase_S8; 3.
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281
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                                                                                                                                      SEQUENCE OF 189-196.
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                                                     Holck A., Naes H.;
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                                                                                            paracasei NCDO 15
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109;

567; Gaps

Indels

400 GLKVKLAKN--LSGLETVSTKNLTA----SEKVTVGSGNNTAELQSGGLTFTPTTNASTD 453 

g

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Best Local Similarity 21.1%; Pred. No. 1.4e-07; Matches 450; Conservative 262; Mismatches 856;

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1012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1142 ----KGLTTPKLTV-----GN-NNGKGIVIDSKDG--QNTITGLSNTLANVINDGAGHA 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1189 LSQGLANDTDKTRAASIGDVLNAGFNLQGNGEAVDFVSTYDTVDFIDGNATTAKVTYDDT 1248
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                                                                                        157 FSTKVRVVDIPKLKQIAGVKTVTLAKVYYPTDAKANSMANVQAVWSNYKYKGEGTVVSVI
---- ATQLAAKGIDY-NKLNKVQQQDTYVDVIVQMSAAPASEN
                                                                                                                                                                                                                                                                                                            | | | | | | | | | | DTGIDP---THKDMR-LSDDKDVKLTKYDV--EKFTDTAKHGRYFTSKVPYGFN----YA
                                                                                                                                                                                                                                                                                                                                                                                                                                          DNNDTITDDT------GTGDDPTKSVVGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SP----TLPSITNAGGVRTTEQGNTITSDEDKSKAASIGDILNTGFNLKNNSNS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       306 APEAQLLAMKVFTNSDFSATTGSATLVSAIEDSAKIGA--DVLNMSLGSDSGNQTLEDPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----GATDDET----ITVGKDGTQN-GKTVNTLKLKGENGLTVATNKDGTV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     967 SNEQIQ--VGADGVKFAKVDKGNSSTGIDGTSRITKDQIGFTGANGSL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           589 SNLSFKPDITAPGGNIWSTQNNNGYTNMSGTSMASP----FIAGSQALLKQALNNKNNPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     645 YADYKQLKGTALTDFLKTVEMN-TAQPIN------DI--NYNNVIVSPRRQGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           810 FLNFKGSDGSRLNLPYMGFFGDWNDGK--1VDSLNGITYSPAGGNYGTVPLLTNKNTGHQ
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                                                      GGLTVNNTIGGSNKQIQVGADGIKFADVNVNVSNAAKFGTTRITEEEIGFADADGKV---
                                                                                                                                                             571 -DKKSPYLDKKQL-QVGGVKIT-------KDSGINA-------GDQKISNVK
                                                                                                                                                                                                                                                                             DATDDTDAVTYKQLKQVQQDADGALQSFSIRDEKGQEFTISNLYSNGNTPNTFETITFAG
                                                                                                                                                                                                                                                                                                                                                                                      ENGISISNDIAKGKVKVGIDPINGLTTPKLTVGSDKDGKTQLVIEQVASGNDTKNIIRGL
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2GIN 1404 DAGT 1058L 1457 SFDL 1113	151	NNL- 1565 :  FDLK 1221	1615 5DNT 1274	TINI 1660 EF 1319	3-VK 1718   1   CVV 1379	(ADD 1775 : .S 1435	SKDG 1828  :   SENN 1485	sTKD 1872 :- :- :YQD 1542	(AGT 1927 : \SAK 1601	DGSKKAL 1975 :   AINQL 1652	ISVA 2035 	ibps 2095	SAIS 2143 : :: LKTKVA 1786	QNVAAG 2200  : -NIPTK 1841		
NDKGQVDKNKEVARDKLVAQAQTPDGTLAQMNVKSVINKEQVNDANKKQGIN	TIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGTRIDEKGIS	F VENNGÇARANIYY DSANGEDIGGARKI SONIÇAAN DÜNDAVNEKÇENEYAKIYNNIYAKIYNNI- 	-NNQSNSGASLPFVVTDANGKPINGTDGKPQKAIKGADGKYYHANANGVPV	DRDGKPITDADKLANLAAHGKPLDAGHQVVASLGGNSDAITLINI 	KSTLPQIDTPNTGNANAGQAQSLPSLSAAQQSNAASVKDVLNVGFNLQTNH-NQVDF-VK 	AYDTVNFVNGTGAD-ITSVRSADGTMSNITVNTALAATDDDGNVLIKAKDGKFYKADD	LMPNGSLKAGKSASDAKTPTGLSLVNPNAGKGSTGDAVALNNLSKAVFKSKDG 	TTTTVSSDQISIQGKDNSSITLSKDGLNVGGKVISNVGKGTKD 	TDAANVQ-QLNEVRNLLGLGNAGNDNADGNQVNIADIKKDPNGGSSSNRTVIKAGT	WVKTOK	LATYNAAGQTNYLTNNPAEAIDRINEQGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVA 	IGEOAKADGEAAVAIGRQTQAGNQSİAIGDNAQATGDQSIAIGTGNVYTGKHSGAIGDPS 	ı s	RRI	.DHR 2232   TER 1876	1848 AA.
NDKGQVDKNKEVAKDKLVAQAQTPDGTLAQMNVKSVIN	TIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTN	ADANTEV LOANGEDEGGEREISNIGE 	3ASLPFVVTDANGKPINGTDGK :	-DKDGKPITDADKLANLA  :	OTPNTGNANAGQAQSLPSLSAAQQS             ::   DPKTGIATITGKVKHPTTTLQVDG	/NGTGAD-ITSVRSADGTMSNITVN 	(AGKSASDAKTPTGLSLVNPNAGKG   :   :    :    ASQYADININSGKP	TTTTTVSSDGISIQGKDN	QLNEVRNLLGLGNAGNDNADGNQV 	VLGGKGNNDTEKLATGGVQVGVDKDGNANGDLSNV 	LATYNAAGGTNYLTNNPAEAIDRINEGGIRFF 	OGEAAVAIGRQTQAGNQSIAIGDNA                 DDLVAQAQAGTQTADQL	TVKADNSYSVGNNNQFIDATQTDVFGVGNNITVTESNSVALGSN	AGTHAGTQAKKSDGTAGTTTTAGATGTVKGFAGQTAVGAVSVGASGAE 	EVSATST DAVNGSQLYKATGGIANATNELDHR :	STANDARD; PRT; 1
1353 1007 VALSAKTE 1405 EDNAFIKG 1059 TADGYTK	1458 TIKGGQTE:     :		1566 -NNQSNSG     :  1222 FNNGSDQT	1616DK 	1661 KSTLPQID :  : 1320 NATSAKFY	1719 AYDTVNFV   1 1380 VGDTTQ	1776 LMPNGSLK       1436 LAINGSHV	1829 TTTTTVSS     :: 1486 TTTKKIT-	1873 TDAANVQ-       1543 VPAAGVTV	1928 VLGGKGNND 	1976 LATYNAAG     1653 AAKLPADK	2036 IGFQAKAD       1689 KTFTAALD	2096 TVKADNSY :11 1731 -IKAATPA	2144 AGTHAGTQ     1787 AAVEAAKT	2201 EVSATST- :     1842 PATTTSTS	RESULT 10 CBPA_CLOCL ID CBPA_CLOCL AC P38058;
da da	oy oy	G G	Oy Dp	Qy Dp	Qy Db	Qy Dp	Qy Dp	Qy Dp	Qy Dp	Qy	QY	Qy Dp	Oy Dp	Qy Db	Qy Dp	RESULT CBPA_C ID C

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.5%; Score 406; DB 1; Length 1848;
Best Local Similarity 20.6%; Pred. No. 1.5e-07;
Matches 452; Conservative 277; Mismatches 800; Indels 668; Gaps 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 ------QAANQKAGSHAKGKESI--AIGGDVLAEGDASIAIGSDDLYLDRNSTNS 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 NDYSFDASSSTPVVNPKVTGYIGGAKVLGTAPGPDV----PSSIINPTSATFDKNVTKQ 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 KYPNGLLSTLIQNHTVLRQIRDSNGSQKYRRTAAEGHASTAVGA--MAYAKGHFANAFGT 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 A---DVKTTMTLNGNTFKTITDANG-----TALNASTDYSVSGNDVTISKAYLAKQSVG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 RSTAEGNYSL--------AVGLT---AKAEKGYTIAIGSNAQAINYGALAL- 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264 TTTLNFNFSAGNPQKLVITVVDTPVEAVTATIGKVQVNAGETVAVPVNLTKVPAAGLATI 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GADTRVDLDYGIALGYGSQILNNNNNNNNNKAYVPEGNGSNIK-----SS 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307 KATGNGLFSIGSSTIKRKIIN -----VGAGYEDTDAVNVAQLK----AVENLAKRQITF 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 AQNNSKIAFGTTGNNDNASASNEASIAIG---SLAKAHANQAIAIGG--SKPDPRN---- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 SSSTAGQVGS-SPVIRLTRVATLAILV-------IGATLNGSAY 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
MEDLINE-92228810; PubMed-1565642;
MASSEYOV O., Takagi M., Goldstein M.A., Doi R.H.;
Primary sequence analysis of Clostridium cellulovorans cellulose
                                                                                                                                                                                                                                                                               binding protein A.";
Proc. Natl. Acad. Sci. U.S.A. 89:3483-3487(1992).
-I- FUNCTION: BINDS TO CELLULOSE FIBERS AND COORDINATES CELLULASE
                                                                               CBPA.
Clostridium cellulovorans.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat; Signal; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cellulose degradation; Cell wall; Repeat, Signal; Glycoprotein.
SIGNAL
1 28 POTENTIAL.
CHAIN 29 1848 CELLULOSE BINDING PROTEIN A.
DOMAIN 29 189 CELLULOSE-BINDING (BY SIMILARITY).
SEQUENCE 1848 AA; 189152 MW; 85FA6CE6F771AFIA CRC64;
01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-1998 (Rel. 37, Last annotation update)
CELLULOSE BINDING PROTEIN A PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                          -!- PTM: THE N-TERMINUS IS BLOCKED.
-!- PTM: CONTAINS ABOUT 10% OF CARBOHYDRATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M73817; AAA23218.1; -. PIR; A44140. HSSP; Q06851; 1NBC.
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InterPro; IPR002102; -.
Pfam; PF00942; CBD_3; 1.
Pfam; PF00963; Cohesin;
                                                                                                                                                              NCBI_TaxID=1493;
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428 416 465 472 510 525 548 601	638 694 698 698 754 736 814 816 838	921 883 978 928 1033 1073	1123 1068 1181 1119 1236 1238 1238 1328
KGDDNGTGVKKKLGGTLTIKGGETQADKLTDNNNIGVVDDAQLQEKPCAVNPGTVTI KGDDNGTGVKKKLGGTLTIKGGETQADKLTDNNNIGVVTDNNTGLKVKLAKNLSGLETVS	LIGYTENGITGLITSDYSISGNVVKIS	TLAKEIHTTKGTADTALQTFKVKKDGATDDETITYGKDGTQNGKTVNTLKL	KINSAAKTAQNSLHEFSVADEQCNHFTVSNPYSSYDTSKTSDVITFAGEN
374 357 429 417 473 511 526 584	602 643 639 699 755 737 737	871 839 922 884 979 929 1034	1036 1124 1169 1182 1180 1237 1179 1239
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1332 --KAVPSTGTTPVAISGTPVFADGTLAEVQYKTVAGSVTIAAADIKAVKAT-----VG 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SASYVDADGNKVIYDSTDKKYYQVNDKGQVDKNKEVAKDKLVAQAQTPDGTLAQMNVKSV 1388
                                            1389 INKEQVNDANKKQGINEDNAFIKG-LENAAKDTKTKNAAVTVGDLNAVAQTPLTFAGDTG 1447
                                                                                                                                                                                                                                                                               1448 TTAKKLGETLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLN--SVNAGGTRID 1505
                                                                                                                                                                                                                                                                                                                        1506 EKGISFVDANGQAKANTPVLSANGLD--LGGKRISNIGAAVDDNDAVNFKQFNEVAKTVN 1563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1432 P----SVNFSSVVNGSTIKILFLDDTLGSQLISKDGVFA----TVNFK----VKSTAT 1477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1564 N-------LNNQSNSG--ASLP-FVVTDANGKPINGTDGKPQKA-- 1597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1598 --IKGADGKYYHANANGVPVDKDGKPITDADKLANLAAHGKPLDAGHQVVASLGGNSDAI 1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TL-----TNIKSTLPQIDTPNTGNANAGQAQSLPSLSAAQQSNAASVKDVLNVGFN 1706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1707 LQTNHNQVDFVKAYDTVNFVNGTGADITSVRSADGTM--SNITVNTALAATDDDGNVLIK 1764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1765 -- AKDGKFYK------ADDLMPNGSLKAGK----SASDAKTPTGLSLVNPNAGKGST 1809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1810 GDAVALNNLSKAVFK-SKDGTTTTTV-SSDGISIQGKDNSSITLSKDGLNVGGKVISNVG 1867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1868 KGTKDTDAANVQQLNEVRNLLGLGNAGN-----DNADGNQVNIAD----IKKDPNSG 1915
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"Molecular characterization of the hemolysin determinant of Serratia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Bacteriol. 170:3177-3188(1988).
-!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1735 ----KVGNVCVAEYKISFDSSVLTYVGTTAGTSIK---NPAVNFS-----
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Serratia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1916 SSSNRTV-IKAGTVLGGKGNNDTE--KLAT--GGVQV 1947
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01-APR-1990 (Rel. 14, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
HEMOLYSIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1608 AA
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SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.
STRAIN=SN8;
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1090 SVADEQGNHFTVSNPYSSYDTSKTSDVITFAGENGITTKVNKGVVRVGIDQTKGLTTPKL 1149 1031 ITNTGINAGGKKITNIQSGDITQNSNDAVTGG-RVYDLKTELESKINSAAKTAQNSLHEF 1089 1150 TVGNNNGKGIVIDSKDGQNTITGLSNTLANVTNDGAGHALSQGLANDTDKTRAASIGDVL 1209 1258 -VNVDNKTIEVTSDKKLG---VKTTTLTKTSANGNA----TKFSAADGDALVKASDIATH 1309 VAQAQTPDGTLAQMNVKSVINKEQVNDANKKQGINED-NAFIKGLENAAKDTKTKNAAVT 1428 1210 NAGFNLQGNGEAVDFVSTYDTVDFIDGNATTAKVTYDDTSKTSKVYYD----- 1257 1310 LNTLAGDIQTAKGASQASSSASYVDADGNKVIYDSTDKKYYQVNDKGQVDKNKEVAKDKL 1369 1429 VGDLNAVAQTPLTFAGDTGTTAKKLGETLTIKGGQTDTNKLTDNNIGVVAGTDGFTVKLA 1488 1489 KDLTNLNSVNAGGTRIDEKGISFVDANGQAKANTPVLSANGLDLGGKRISNIGAAVDDND 1548 1549 AVNFKQFNEVAKTVNN--LNNQSNSGASLPFVVTDANGKPINGTDGKPQKAIKGADGKYY 1606 1607 HANANGVPVDKDGKPITDADKLANLAAHGKPLDAGH-QVVASLGGN-----SDAI 1655 1656 TLTNIKSTLPQIDTPNTGNANAG-----QAQSLPSLSAAQQSNAASVKDV-LNVGFNLQ 1708 1709 TNHNQVDFVKAYDTVNFVNGTGADITSVRSADGTMSNITVNTALAATDDDGNVLIKAKDG 1768 1769 KFYKADDLMPNGSLKAGKSASDAKTPTGLSLVNPNAGKGSTGDAVALNNLSKAVFKSKDG 1828 | :|:: | :|: | :|120 | 1178 KL------SGNIDLGAGSSDSKEKTG------GNLSAGGAFDIAKVNESATERQG- 1220 1829 TTTTVSSDG---ISIQGKDNSSITLSKDGLNVGGKVISNVGKGTKDTDAANVQQLNEVR 1885 1886 NLLGLGNAGNDNADGNOVNIADI--KKDPNSGSSSNRTVIKAGTVLGGKGNNDTEKLATG 1943 525 QKTANAKAVRDDKTSWGGIGGGDNKNNSNRREISHASELTSGGTLRLN------GQQG 576 :| || | | |:| | |:| | |:| | | | | |:| | | | |:| | | |:| | |:| | |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |: 627 HKAD------NSYQSSTASEL---KSDTNLTLVSHKDADVIGSQVASG---GEL 668 SVESKTG-NINVKAAERQQNIDEQKTAL--TVN---GYAKEAG-----DKQ-----Y 709 1944 ------GSKKALLATYNAA 1982 GOTNYLTINNPAEAI-DRINEOGIRFFHVNDGN-QEPVVQGRNGIDSSASGKH-SVAIGFQ 2039 710 RAGLRIEHTRDSEKTTRTENSASSLSGGSVKLKAEKDVTFSGSKLVADKGDASVSGNKVS 769 :|| || || || :|: 943 ------KSVQAGSIDINAKG-EVRDQGTQYQAGS--------KGAVNLTADSHRSE 982 909 INDIG------GIGAPNVGLDIGAQGGSSE--KRSSSSQAVV-----699 ò g QQ δý g Op οy ò P δ σg οy Op g δ ŏ qq à Db QQ ò οy g ò q ò g òγ ò

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PIR; S32920;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOTIF REPRATED 31 TIMES.
SIMILARITY: THE REPEATED MOTIF IN THE C-TERMINUS HAS SOME
SIMILARITY TO THE REPEAT IN E.COLI RHS GROUP OF PROTEINS (RHSA-D).
                  2040 AKADGEAAVAIGR-----QTQAGNQSIA-IGDNAQATGDQSIAIGTGNVVTGKHSGA 2090
                                                               1437 PQQDTTGAVSFSKAEGKVTLPATPAGEKPQGPLWDRGART-----VGGAVKDSITGP 1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN: HAS TWO LIGAND-BINDING DOMAINS; THE N-TERMINUS, HAS THREE 101 AA REPEATS WHICH ARE RESPONSIBLE FOR CELL WALL BINDING; THE C-TERMINUS CONSISTS OF TWO BLOCKS OF RESIDUES WITH A CONSERVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ø
                                                                                                           2091 IGDPSTVKADNSYSVGNNNQFIDATQTDVFGVGNNITVTESNSVAL--GSNSAISAGTHA
                                                                                                                                                     1489 AGRQGHLKV--NADVVNNN-----AVGEQSAIAGKNGVALQVGGQTQLTGGEIR
                                                                                                                                                                                                    --TAGTTTTAGAT--GTVKGFACQTAVGAVSVGASGAER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular analysis of three major wall-associated proteins of Bacillus subtilis 168: evidence for processing of the product of gene encoding a 258 kDa precursor two-domain ligand-binding
                                                                                                                                                                                                                                            1536 SQQGKVELGGSQVSQQDVNGQRYQGGGRVDAAATVGGLLGGAAKQSVAGNVP----
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2334 AA
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WALL-ASSOCIATED PROTEIN PRECURSOR
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MEDLINE=95219088; PubMed=7704263;
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                                                                                                                                                                                                                                                                                        2193 RIQNVAAGEVSATSTDAVNG 2212
                                                                                                                                                                                                                                                                                                                                    1588 ----FASGHASTQQADAKAG 1603
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                                                                                                                                                                                                    2149 GTQAKKSDG--
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D29985;
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Gaps 122;
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                                                      OR 32 (POTENTIAL).
WALL-ASSOCIATED PROTEIN.
3 X 101 AA APPROXIMATE TANDEM REPEATS.
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258 MTDSKLDELSGEVERSDKVSYKLEKNEEGYLLHLTADENWLKDPERVYPVSIDPSTSLSV
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                                                                                                                                                            K(4)-G-X(4)-[YF]-X-D-X(2)-G-X(4).
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            Subtilist; BG10797; wa
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GNDTKNIIRGLSPTLPSITNAGGVRTTEQGNTITSDEDKSKAASIODI 763 	LNTGFNLKNNSNGYGFVS-TYNTVDFIDGNATTAKVTYDETNQTSKVT 810 	YDVNVDEKTIELTGDNGKTNKIGVKTTLTTTNANGKATNFSTTDNDA 858  KIWPTSAEIKAGKYALHLKDGSGAELPIN-PGPTYKNAGGDGAKRNYSFKIIAYNKDGEA 737		GKTVNTLKLKGENGLTVATNKDGTVTFGINTQSGLKAGDSTTLNKDGLSIKNPASNE 969 	QIOVGADGVKFAKVDKGNSSTGIDGTSRITKDQIGFTGANGSLD 1013	TTKPHLTKDKLKVGBVEITNTGINAGGKKITNIQSGDITQNSNDAVTGGRV 1064 	YDLKTELESKINSAAKTAONSLHEFSVADEOGNHFTVSNPYSSYDTSKTS 1114	DVITFAGENGITIKVNKGVVRVGIDQTKGLTTPKLTVGNNNGKGIVIDSK 1164 	DGQNTITGLSNTLANVTNDGAGHALS-QGLANDTDKTRAASIGDVLNAGFNLQGNGEAVD 1223 	EVSTYDTVDEIDGNATTAKVTYDDTSKTSKVVYDVNVDNKTIEVTS 1269 		E 136 : VTD 124	VAKDKLVAQAQTEDGTLAQMNVKSVINKEQVNDANKKQGINEDNAFIKGLE 1414		-QTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGTR 1503 	IDEKGISFVDANGQAKANTPVLSANGLDLGGKRISNIGAAVDD 1546 	NDAVNFKQFNEVAKTVNNLNNQSNSGASLPFVVTDANGKPINGTDGKPQKAIKGAD 1602     :
GNDTKNIIRGLSP 	LNTGFNLKNNSNS       : QAPSAKGYNNGNA	YDVNVDE :: KIWPTSAEIKAGK	LVNAKDI: : : IASPAATPALPDI!	GKTVNTLKLKGENG      :  :  G-YVNLIWEKVQN	QIQVGADGVKFAKY :	TTKPHLTKI 	YDLKTELESKINSA   :: PGLGLSRI	OVITEAGENGI    :  : OG-TYQPPTGVYLE	OGQNTITGLSNTLA :      NQLTAITDASGRKI	FVSTYDTVDFIDGN 	SRKVQYGYNEAGNP	'LAGDIQTAKGASQ          -PNDVGTGK	AKDKLVAQAQTPD 	NAAKDTK  :   : TASKDRRKISVIAD	OTDINK             KTDLAKSRAYFNI	DEKG	DAVNFKQFNEVAKT     :     DDVSLKAARTSAS(
716	764	811	859 738	913	970	1014	924	1115 E	1165 1	1224 E	1270 -	1312 T 1196 -	1364 V : 1249 I	1415 N 1307 T	1463 - 1367 I	1504 I : 1424 V	1547 N      1484 N
Oy Dp	Qy Db	Oy Op	Qy Db	Qy	Qy Dp	og Og	Oy Op	Qy Db	Oy Dp	Qy Db	Qy Dp	Oy.	oy op	Qy Db	Oy Dp	QQ V	Qy Db

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GKYYHANANGVPVDKDGKPITDADKLANLAAHGKPLDAGHQVVASLGGNSDAITLTNIKS 1662
                                                      1663 TLPQIDTPNTGNANAGGAQSLPSLSAAQQSNAASV---KDVLNVGFNLQT-----NHNQ 1713
                                                                          1714 VDFVKAYDTVNFVNGTGADITSVRSAD-------GTMSNITVN---TALAAT 1755
                  DDDGNVL---IKAKDGKFYKAD-DLM-----PNGSLKAGK-SASDAKTPTGLSLVNP 1802
                                                                                                                                                                                        1852 SKDGLNVGGKV----- 18NVGKGTKDTDAANVQQLNEVRNLLG---- 1889
                                                                                                                                                                                                                              NAGKGSTG----DAV---ALNNLSKAVFK-SKDGTTTTTVSSDGISIQGK--DNSS-ITL 1851
                                                                                                                                                                                                                                                                                                             1795 LIDR---GGSQTWTYPSDSDKLKTFSWIHGDQKGTNQFTYNKLDQMIEMKDSTSSYSFDY 1851
                                                                                                                                                                                                                                                                                                                                             1890 ------SSSNRTVIK--- 1924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIP_LACLC STANDARD; PRT; 1902 AA.
P16271;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PI-TYPE PROTEINASE PRECURSOR (EC 3.4.21.-) (WALL-ASSOCIATED SERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1983 GQTNYLTNNPAEAIDRINEQGI------RFFHVND------GNQEPVV-
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1013 -----DITKPHLTKDKLKVGEVEITNTGINAGGKKITNIQSGDITQNSNDAVT---- 1060
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                                                         --RIDYSSTAEIQQETNKVIAAQASV-----KAAVEQVTQQTAG--ESYGYVVNGFSTK 160
                                                                                                                                                                                                                                                 687 GAGLVDVKAAIDALEKNPSTVVAENGYPAVELKDFTSTDKTFKLTFTNSTTHELTYQMDS 746
   ATDTTAATTNQAIA----TQLAAKGIDY-NKLNKVQQQDIYVDVIVQMSAAPASENGTL- 110
                                                                                                                                                                                                                               SISNDIAKGKVKVGIDPINGLTTPKLTVGSDKDGKTQLVIEQVASGNDTKNIIRGLSP-- 728
                                                                                                                                                                                                                                                                                               ---TLPSITNAGGVRTTEQGNTITSDEDKSKAASIGDILNTGFNLKNNSNSVGFVSTYNT 785
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                                                                                                                               161 VRVVDIPKLKQIAGVKTVTLAKVYYPTDAKANSMANVQAVWSNYKYKGEGTVVSVIDSGI
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                                  VNNTIGGSNKQIQVGADGIKFADVNVNVSNAAKFGTTRITEEEIGFADADGKV----DKK
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                                                                                                 SPYLDKKQL-QVGGVKIT-----KDSGINA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                           Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. CELL WALL. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
MEMBRANE ANCHOR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.4%; Score 392.5; DB 1; Length 1902; 21.0%; Pred. No. 4.6e-07;
                                Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris)
                                                                                                                                                          MEDLINE-88149035; PubMed-3278687;
KOK J., Leenhouts K.J., Haandrikman A.J., Ledeboer A.M.,
"Nucleotide sequence of the cell wall proteinase gene of
Streptococcus cremoris Wq2.";
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W; 2901C7F19B2E5D0B CRC64;
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Pfam; PF00082; Peptidase_S8; 3.
PRINTS; PR00723; SUBTILIASIN.
PROSITE; PS00136; SUBTILIASE_HS9; 1.
PROSITE; PS00138; SUBTILASE_HS9; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
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Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KAYDTVNFVNGTGAD-ITSVRSADGTMSNITVNTALAATDDDGNVLI--KAKDGKFYKAD 1774
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                 1058 TTADGYTK-IETPLSDEQ----AQALGNGDNSAELYLTDNASNATDQDASVQKPGSTSFD
                                                                              1510 SFVDANGQAKANTPVLSANGLDLGGKRISNIGAAVDDNDAVNFKQFNE----VAKTVNNL
                                                                                                                                                                                 --NNQSNSGASLPFVVT---DANGKPINGTDGKPQKAIKGADGKYYHANANGVPV----
                                                                                                                                                                                                   1274 TIKVTATDEDGNTTTEQKTITSSYDPDMLKNSVT----FDQG----VTFGAN-----E
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                                                           LTIKGGQTDTNKLTDNNIGVVAGTDG-----FTVKLAKDLTNLNSVNAGGTRIDEKGI
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NEDNAFIKGLENAAKDTKTKNAAVTVGDLNAVAQTPLT----FAGDTGTTAKKLGET
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P2P\_LACLA STANDARD; PRT; 1902 AA. P15293; 01-APR-1990 (Rel. 14, Created) 01-APR-1990 (Rel. 14, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update)

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EXTRACELLULAR (POTENTIAL).
MEMBRANE ANCHOR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                    PII-TYPE PROTEINASE PRECURSOR (EC 3.4.21.96) (LACTOCEPIN) (CELL WALL-ASSOCIATED SERINE PROTEINASE) (LP151).
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                                                               Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                    INSULIN B-CHAIN.
SUBCELLULAR L'ACATION: TYPE I MEMBRANE PROTEIN. CELL WALL.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
SUBTILASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00082; Peptidac___.
PRIMYS; PR00723; SUBTILISIN.
PROSITE; PS00137; SUBTILASE_ASP; 1.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS001343; GYAM_POS_ANCHORING; 1.
PROSITE; PS00343; GYAM_POS_ANCHORING; 1.
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                                       Lactococcus lactis (subsp. lactis) (Streptococcus lactis)
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HSSP; P00782; 2SBT.
MEROPS; S08.019; -.
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Oy Dp	458	GTDGLKFTDNSNTALEDTTRITKDKIGFSNKACTVDENKPYLDKDKLKVGNSTLNNGGLT 517
0y Dp	518	VNNTIGGSNKQIQVGADGIKFADVNVNVSNAAKFGTTRITEEEIGFADADGKVDKK
Oy Dp	574	
oy Dp	611	
Qy	671	SISNDIAKGKVKVGIDPINGLTTPKLTVGSDKDGKTQLVIEQVASGNDTKNIIRGLSP
Oy Dp	729	TLPSITNAGGVRTTEQGNTITSDEDKSKAASIGDILNTGFNLKNNSVGFVSTYNT : -
Oy Db	786	VDFIDGNATTAKVTYDETNQTSKVTYDVNVDEKTIELTGDNGKTNKIGVKTTTLTTTNAN 845   ::
Oy Og	846	GKATNFSTTDNDALVNAKDIAENLNTLAKEIHTTKGTA-DTALQTFKVKKDGATDDE 901
Oy Dp	902	TITVGKDGTQNGKTVN-TLKLKGENGLTVATNKDG 935
oy ep	936	TV963    TV963    TATPVTSMALTTTFPTFGLSSVTGGKLVDWVAAHPDDSLGVKIALTLVPNQKYTEDKMSD 581
Q Dp	964	NPASNEQIQVGADGVKFAKVDKGNSSTGIDGTSRITKDQIGFTGANGSL 1012
Qy Dp	1013 638	OY NNKNNPFYAYYKOLKGTALTUFLEVELTUTGINAGGKKITNIQSGDITQNSNDAVT- 1060  NNKNNPFYAYYKOLKGTALTDFLKTVEMN-TAQPINDINYNNVIVS 682
Qy Dp	1061	
Qy	1106	SSYDTSKTSDVITFAGENGITTKVNKGVVRVGIDQT
QY Db	1142	
Qy Db	1182 861	NDGAGHALSQCLANDTDKTRAASIGDVLNAGFNLQGNGEAVDFVSTYDTVDFIDGNATTA 1241
Qy Db	1242	KVTYDDTSKTSKVVYDVNVDNKTIEVTSDKLGVKTTLTKTSANGNATKFSAADGDAL- 1300   :
Oy Dp	1301	VKASDIATHLNTLAGDIOTAKGASQASSSASYVDADGNKVIYDSTDKKYYQV 1352  CN
δ	1353	NDKGQVDKNKEVAKDKLVAQAQTPDGTLAQMNVKSVINKEQVNDANKKQGINE 1405

1459 IKGCQTDTNKLTDNNIGVVAGTDG-----FTVKLAKDLTNLNSVNAGGTRIDEKG--- 1508 1562 VNNL--NNQSNSGASLPFVVT---DANGKPINGTDGKPQKAIKGADGKYYHANANGVPV- 1615 1375 PFGVVVGDTTQNKT----FQEALTFILDAVAPTLSLDSSTDAPVYTNNPNFQITGT---- 1426 1760 NVLIKAKDGKFYKADDLMPNGSLKAGKSASDAKTPTGLSLVNPNAGKG---STGDAVAL- 1815 1646 OT------GINQLAAKLPADKKTSLL--NQLQSVKAALETDL------GNQ----- 1682 2079 DNAFIKGLENAAKDTKTKNAAVTVGDLNAVAQTPLT----FAGDTGTTAKKLGET---LT 1458 1509 ---ISFVDANGQAKANTPVLSANGLDLGGKRISNIGAAVDDNDAVNFKQFNE----VAKT 1561 1616 ------DKDG-----KPIT---DADKLANLAAHGKPLDAGHQVVASLGGNSDAI 1655 1656 TLTNIKSTLPQIDTPNTGNANAGQAQSLPSLSAAQQSNAASVKDVLNVGFNL----- 1707 ---EFNATSAKFYDPKTGIATITGKVKHPTTTLQVDGKQIPIKDDLTFSFTLDLGTLGQK 1374 -----QTNHNQVDFVKAYDTVNFVNGTGADITSV-RSADGTMSNITVNTALAATDDDG 1759 1816 ---NNLSKAVFKSKDGTTTTTVSSDGISIQGKDN-----SSITLSKDGLNV 1858 1859 GGKV--ISNVGKGTKDTDAANVQ-QLNEVRNLLGLGNAGNDNADGNQVNIADIKKDP--- 1912 1913 -NSGSSSNRTVIKAGTVLGGKGNND-----TEKLATG--GVQVGVDKDGNANGDL 1959 1586 LQAAKQELTNLIASAKTLSASGKYDDATTTALAAATQKAQTALDQTNASVDSLTGANRDL 1645 1960 SNVWVKTQKDGSKKALLATYNAAGQTNYLTNNPAEAIDRINEQGIRFFHVNDGNQEPVVQ 2019 1683 -----TDSSTGK-----TFTAALDDLVA-----QAQAGTQT----DDQLQATLAKVLDAVL 1724 2080 GNVVTGKHSGAIGDPSTVKADNSYSVGNNNQFIDATQTDVFGVGNNITVTESNSVALGSN 2139 1725 AKLAEG-----IKAATPAEVGNAK---DAATGKTWYADIADTLTSGQASADASD 1770 2140 ------SAISAGTHAGTQAKKSDGTAGTTTTAGATGT---VKGFAGQTAVGAVS 2184 1771 KLAHLQALQSLKTKVAAAVEAAKTVCKGDGTTGTSDKGGGGGTPAPTPCDICKDKGDEGS 1830 2020 GRNGIDSSASGKHSVAIGFQAKADGEAAVAIGRQTQAGNQSIAIGDNAQATGDQSIAIGT 2185 VGASGAERRIQNVAAGEVSATST---DAVNGSQLYKATQGIANATNELDHR 2232 1831 QPSSGG-----NIPTNPATTTSTSTDDTTDRNGQLTSGKGALPKTGETTER 1876 PRT; 1183 AA CNA\_STAAU STANDARD; 6 053654; 15-DEC-1998 (Rel. 37, Created) RESULT 15 CNA\_STAAU ID CNA\_ST AC Q53654 DT 15-DEC 1406 1318 1708 1427

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patti J.M., Boles J.O., Hocock M., "Identification and biochemical characterization of the ligand binding domain of the collagen adhesin from Staphylococcus aureus."; Biochemistry 32:11428-11435(1993).
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LIS/PRO-RICH (CELL WALL-SPANNING).
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aureus adhesin.";
Nat. Struct. Biol. 4:833-838(1997).
-!-FUNCIION MEDIATES ATTACHMENT OF STAPHYOCOCCAL CELLS TO COLLAGEN-CONTAINING SUBSTRATA.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN CELL WALL.
-!- SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 169-318.

MEDLINE-97475225; PubMed=9334749;
Symersky J., Patti J.M., Carson M., House-Pompeo K., Teale M., Moore D., Jin L., Schneider A., DeLucas L.J., Hoeoek M.,

Narayana S.V.L.;
Structure of the collagen-binding domain from a Staphylococcus
                                                                                                                                                                                                                                                        Patti J.M., Jonsson H., Guss B., Switalski L.M., Wiberg K., Lindberg M., Hoeoek M.;
Wolccular characterization and expression of a gene encoding staphylococcus aureus collagen adhesin.";
J. Blol. Chem. 267:4766-4772(1992).
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Lindberg M., Hoeoek M.;
J. Biol. Chem. 269:11672-11672(1994).
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MEMBRANE ANCHOR (POTENTIAL)
CYTOPLASMIC (POTENTIAL)
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                                                                                                       Bacteria; Firmleutes; Bacillus/Clostridium gre
Bacillus/Staphylococcus group; Staphylococcus
NCBI_TaxID=1280;
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
COLLAGEN ADHESIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COLLAGEN-BINDING
                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=EDA 574;
MEDLINE=92165839; Pubmed=1311320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94032261; PubMed-8218209;
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PDB; IAMX; 24-JUN-98.
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                                                                                     Staphylococcus aureus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-FDA 574;
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289 NNNKAYVPEG-NGSNIKSSKATGNGLFSIGSSTIKRKIINVGAGYEDTDAVNVAQLKA-- 345
                                                                                                                                                                                                 346 --VENLAKR-QITFKGDDNGTGVKKKLGETLTIKGGETQADKLTDNNNIGVVTDNNTGLK 402
                                                                                                                                                                                                                                                                                                    VKLAKNLSGLETVSTKNLTASEKV-TVGSGNNTAELQSGGLTFTPTTNASTDKTVYGTDG 461
                                                                                                                                                                                                                                                                                                                                 LKETDNSNTALEDTTRITKDKIGFSNKAGTVDENKPYLDKDKLKVGNSTLNNGGLTVNNT 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 VFYYKTGDMLPEDTTHVR----WFLN----INNEKSYVSKD------ITIKD- 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGGSNKQIQVGADGIKFADVNVNVSNAAK---FGTTRITEEEIGFADADGKVDKKSPYLD 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----VTIPQGYGSYNSFSINYK-----TKITNEQGKEFVNNSQAWYQEHGKEE 306
                                                                                                                               639 EKGQEF--TISNLYSNGNTPNTFETITFAGENGISISNDIAKGKVKVGIDPINGLTTPKL 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVGSDKDGKTQLVIEQVASGNDTKNIIRGLSPTLPSITNAGGV-------RTTE 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       395 APREPTIFOKDKEYPFTMKDTDNQGY-----FTTIE----NAKAIEKTKDVS 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNEQIQVG--ADGVKFAKVDKGNSSTGIDGTSRITK----DQIGFTGANGSLDTTKPHLT 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1021 KDKLKVGEVEITNTGINAGGKKITNIQSGDITQN--SNDAVTGGRVYDLKTELESKINSA 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1079 AKTA----QNSLHEFSVADEQGNHFTVSNPYSSYDTSKTSDVITFAGENGITTKVNKGV 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1192 GLANDTDKTRAASIGDVLNAGFNLQ-----GNGEAVDFVSTYDTV-DF----IDGNATTAK 1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       336 -LKQDKDTKAPIANVKFKLSKKDGSVVKDNQKEIEIITDANGIANIKALPSGDYILKEIE 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         804 NQ-----TSKV------TYDVNVDEKTIELTGDNGKTNKIGVKTTTLTTTN----ANG 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            847 KATNESTTDNDALVNAKDIAENLNTLAKEIHTTKGTADTALQTFKVKKDGATDDETITVG 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            495 KAIKY-----G 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           907 KDGTQNGKTVNTLKLKGENGLTVATNKDGTVTFGINTQSGLKAGDSTTLNKDGLSIKNPA 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1134 VRVGIDQTKGLTTPKLTVGNNNGKG-IVIDSKDGQNTITGLSNTLANVTNDG-AGHALSQ 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               437 AQKVWEGTQKVKPIIYFKLYKQDDNQNTTPV--DKAEIRKLEDGTTKVTWSNLPENDKNG 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----DMGNLIVINKYTPETTSISGEKVWDDKDNQ-------DGKRPEKVSV 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKQLQVGGVKITKDSGINAGDQKISNVKDATDDTDAVTYKQLKQVQQDADGALQSFSIRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          744 QGNTITSDEDKSKAASIGDILNTGFNLKNNSNSVGFVSTYNTVDFIDGNATTAKVTYDET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----VKGELKV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - EKVSVNLLANGEKVKTLDVTSETNWKYEFKDLPKYDEGKKIEYT------VŢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDTTPECYT -----KKENGLVVINTEKPIETTSI---SGEKVWDDKD-NQDG---KRP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             601 EDHVKDYTTDINGTITT--NKYTPGETSATVTKNWDDNNNQDGKRPTEIKVELYQDGKAT
3.2%; Score 379; DB 1; Length 1183;
llarity 21.1%; Pred. No. 7.9e-07;
Conservative 182; Mismatches 543; Indels 430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             307 VNGKSFNHTVHNINANAGIEGT-----
                             Similarity
                          Local Simhes 309;
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Qy 1243 VTYDDTSKTSKVVYD Db 807 YTPGETSATVENWDD QY 1285 -ANGNATKFSAADGD     :    :    Db 867 KAKGQQVKTYVE QY 1342 YDSTDKKYYQVNDKG           Db 917 WDDKDN QY 1399 KKQGINEDNAFIK           Db 967 KKIEYTVTEDH QY 1457 LTTKGQCTDTNKLTD           Db 1010 NNNODGKRPT QY 1517 -QAKANTPVLSANGLI   Db 10168 QQVKYTVDELT QY 1576 PEVVTDANGKPINGTI   Db 1058 QQVKYTVDELT QY 1576 PEVVTDANGKPINGTI   Db 1068 LLYTNKYTI   QY 1628 LANLAAHGKPL   Db 1138 KDNKTKPENPLKELPI	VTYDDTSKTSKVVYDVNVDNKTIEVTSDKKLGVKTTTLFKTS-; 1284   :	-angnatkesaadgdalvkasdiathlntlagdigtakgasgassasyvdadgnkvi 1341 	YDSTDKKYYQVNDKGQVDKNKEVAKDKLVAQAQTPDGTLAQMNVKSVINKEQVNDAN 1398 	KKQGINEDNAFIKGLENAAKDTKTKNAAVTVGDLNAVAQTPLTFAGDTGTTAKKLGET 1456 	LTIKCGQTDTNKLTDNNIGVVAGTDGFTVKLAKDLTNLNSVNAGGTRIDEKGISFVDANG 1516 	-QAKANTPVLSANGLDLGGKRISNIGAAVDDNDAVNFKQFNEVAKTVNNLNNQSNSGASL 1575 	1576 PFVVTDANGKPINGTDGKPQKAIKGADGKYYHAN-ANGVPVDKDGKPITDADK 1627 	DACHQVVAS 1647     :::   KTGMKIITS 1161	
•					1457 LTIKGGQTDTNKLTDNNIGVV 		576   PFVVTDANGKPINGTDGKPQK	1628 LANLAAHGKPLDAGHQVVAS 1647 	

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